

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..161
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576112
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3229:

Met Ala Arg Ser Pro Ala Ala Ser Ser Ser Tyr Thr Asp Ser Thr
1 5 10 15
Gly Ser Ser Ser Asp Ser Gly Ser Thr Ser Ser Gly Ile Asp Arg Arg
 20 25 30
Arg His Glu Arg Glu Arg Arg Arg Ser Ala Ser Asp Asp Asp Ser Tyr
 35 40 45
Ser Thr Ser Ser Tyr Asp Ser Asp Arg Glu Val Ser Gly Arg Ser Arg
50 55 60
Lys His Lys Lys Ser Ser Arg Ser Arg Lys Ser Arg Glu Arg Glu Arg
65 70 75 80
Ser Lys Asp Arg His His Lys Arg Asp Lys Ser Lys His Lys Glu Lys
 85 90 95
Lys Glu Ser Glu His Ala Asp Gly Pro Val Gln Leu Ser Lys Phe Leu
 100 105 110
Gly Arg Asp Lys Glu Lys Glu Glu Gly Thr Gln Arg Ser Ala Ile Ser
 115 120 125
Gly Lys Lys Ile Met Met Lys Leu Glu Lys Thr Lys Glu Asp Lys Ala
130 135 140
Ala Glu Ser Lys Arg Asn Glu Leu Leu Lys Phe Leu Asn Ala Ser Tyr
145 150 155 160
Asp

- (2) INFORMATION FOR SEQ ID NO:3230:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 921 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..921
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576129
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3230:

atcttttagac gacaccccta cccgacccga tcggcgggag agcacgagac gccagcgcca 60
tccatcgcg caaaaagccga gacgacccag gaatctcggc accgtcgccc cccttttctct 120
ctcgctcaaa agttgctgct ggagccctct cccctctctc cgaccaccaa ccatggatga 180
ggcgcaagtt gtggagtcaa aggatggaac catctcggtt gcttctgcat ttgctggtta 240
tcaggaagct gtgcaagaca gggatcacaa attcttgaca maagcagtgg aagaagcata 300
tcgaggagtc gattgcggtg acggaggtcc attcggagca gttgtcgtct gtaatgacga 360
agTagtagtc agctgccata acatggttct gaagcacact gaccctactg cgcattgctga 420
agtaactgca attagagagg cttgcaaaaa gcttgggaaa attgagctct cagactgcga 480
aatttacgcg tcctgcgagc catgcccatt gtgctttagt gcagttcctc tctcccgaat 540
caagaggctg gtttatggg ccaaggcaga ggctgccatc gccattggat ttgatgactt 600
cattgcagat gctctgagag gcaactgggt ctaccagaag gccaaacttg agatcaagaa 660
agctgacggc aatggtgcat tgatcgctga gcaagtcttt gaaaagacta aagagaagtt 720
ccagatgtac tgatgctgag cagaagagag atctcagatt tgtacaatgc ttactcataa 780
ggacaagaaa taatacagtg cccaaatgtc cattgtttcg ggaaaaaaat ctcaattcca 840
ctgttcaaca ttttgatgat gcctgaattt cttgttaaca gacacaagat tgttatttgc 900
tgtaaaatgt gcagttgatg g

(2) INFORMATION FOR SEQ ID NO:3231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..243
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3231:

Phe Leu Asp Asp Thr Pro Thr Arg Pro Asp Arg Arg Glu Ser Thr Arg
1 5 10 15
Arg Gln Arg His Pro Ser Arg Gln Lys Pro Arg Arg Pro Arg Asn Leu
20 25 30
Gly Thr Val Ala Pro Leu Ser Leu Ser Leu Lys Ser Cys Cys Trp Ser
35 40 45
Pro Leu Pro Ser Leu Arg Pro Pro Thr Met Asp Glu Ala Gln Val Val
50 55 60
Glu Ser Lys Asp Gly Thr Ile Ser Val Ala Ser Ala Phe Ala Gly Tyr
65 70 75 80
Gln Glu Ala Val Gln Asp Arg Asp His Lys Phe Leu Thr Xaa Ala Val
85 90 95
Glu Glu Ala Tyr Arg Gly Val Asp Cys Gly Asp Gly Gly Pro Phe Gly
100 105 110
Ala Val Val Val Cys Asn Asp Glu Val Val Val Ser Cys His Asn Met
115 120 125
Val Leu Lys His Thr Asp Pro Thr Ala His Ala Glu Val Thr Ala Ile
130 135 140
Arg Glu Ala Cys Lys Lys Leu Gly Lys Ile Glu Leu Ser Asp Cys Glu
145 150 155 160
Ile Tyr Ala Ser Cys Glu Pro Cys Pro Met Cys Phe Ser Ala Val His
165 170 175
Leu Ser Arg Ile Lys Arg Leu Val Tyr Gly Ala Lys Ala Glu Ala Ala
180 185 190
Ile Ala Ile Gly Phe Asp Asp Phe Ile Ala Asp Ala Leu Arg Gly Thr
195 200 205
Gly Phe Tyr Gln Lys Ala Asn Leu Glu Ile Lys Lys Ala Asp Gly Asn
210 215 220
Gly Ala Leu Ile Ala Glu Gln Val Phe Glu Lys Thr Lys Glu Lys Phe
225 230 235 240
Gln Met Tyr

(2) INFORMATION FOR SEQ ID NO:3232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3232:

Met Asp Glu Ala Gln Val Val Glu Ser Lys Asp Gly Thr Ile Ser Val
1 5 10 15
Ala Ser Ala Phe Ala Gly Tyr Gln Glu Ala Val Gln Asp Arg Asp His
20 25 30
Lys Phe Leu Thr Xaa Ala Val Glu Glu Ala Tyr Arg Gly Val Asp Cys

35 40 45
Gly Asp Gly Gly Pro Phe Gly Ala Val Val Val Cys Asn Asp Glu Val
50 55 60
Val Val Ser Cys His Asn Met Val Leu Lys His Thr Asp Pro Thr Ala
65 70 75 80
His Ala Glu Val Thr Ala Ile Arg Glu Ala Cys Lys Lys Leu Gly Lys
85 90 95
Ile Glu Leu Ser Asp Cys Glu Ile Tyr Ala Ser Cys Glu Pro Cys Pro
100 105 110
Met Cys Phe Ser Ala Val His Leu Ser Arg Ile Lys Arg Leu Val Tyr
115 120 125
Gly Ala Lys Ala Glu Ala Ala Ile Ala Ile Gly Phe Asp Asp Phe Ile
130 135 140
Ala Asp Ala Leu Arg Gly Thr Gly Phe Tyr Gln Lys Ala Asn Leu Glu
145 150 155 160
Ile Lys Lys Ala Asp Gly Asn Gly Ala Leu Ile Ala Glu Gln Val Phe
165 170 175
Glu Lys Thr Lys Glu Lys Phe Gln Met Tyr
180 185

(2) INFORMATION FOR SEQ ID NO:3233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..455
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3233:

aaatggatgg cattatgaac acggcctccg caagcatgtc catgtacgct taccttgctc	60
tectcaagcc ccagggaag atgacccctgc ttggcctgcc tgagaagcct ctgcagatct	120
ccgccttctc ttgtgttact gggggcaaga ctctggcccg gagctgcatg gggagcatca	180
gggacacgca ggagatgatg gacttcgcag ccaagcacgg gttgacagcg gacatcgaac	240
tgatcggcac cgaagaagtt aatgaggcca tggaacNgyc tcgccaaagg cgaggNtcag	300
gtaccgcttc gtcacgcaca tcggcaacac catcagcgcg gcatcactag ggagctcgcc	360
ggtcccagct ctgtagctgc gacacttggt cctgcttgga tatatcgtgc gataagcaag	420
tatatattgga ataaaaagga actcaatttta aacgc	

(2) INFORMATION FOR SEQ ID NO:3234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3234:

Met Asp Gly Ile Met Asn Thr Ala Ser Ala Ser Met Ser Met Tyr Ala
1 5 10 15
Tyr Leu Ala Leu Leu Lys Pro Gln Gly Lys Met Ile Leu Leu Gly Leu
20 25 30
Pro Glu Lys Pro Leu Gln Ile Ser Ala Phe Ser Leu Val Thr Gly Gly
35 40 45
Lys Thr Leu Ala Gly Ser Cys Met Gly Ser Ile Arg Asp Thr Gln Glu
50 55 60
Met Met Asp Phe Ala Ala Lys His Gly Leu Thr Ala Asp Ile Glu Leu
65 70 75 80

Ile Gly Thr Glu Glu Val Asn Glu Ala Met Glu Xaa Xaa Arg Gln Gly
85 90 95
Arg Xaa Ser Gly Thr Ala Ser Ser Ser Thr Ser Ala Thr Pro Ser Ala
100 105 110
Arg His His
115

(2) INFORMATION FOR SEQ ID NO:3235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3235:

Met Asn Thr Ala Ser Ala Ser Met Ser Met Tyr Ala Tyr Leu Ala Leu
1 5 10 15
Leu Lys Pro Gln Gly Lys Met Ile Leu Gly Leu Pro Glu Lys Pro
20 25 30
Leu Gln Ile Ser Ala Phe Ser Leu Val Thr Gly Gly Lys Thr Leu Ala
35 40 45
Gly Ser Cys Met Gly Ser Ile Arg Asp Thr Gln Glu Met Met Asp Phe
50 55 60
Ala Ala Lys His Gly Leu Thr Ala Asp Ile Glu Leu Ile Gly Thr Glu
65 70 75 80
Glu Val Asn Glu Ala Met Glu Xaa Xaa Arg Gln Gly Arg Xaa Ser Gly
85 90 95
Thr Ala Ser Ser Thr Ser Ala Thr Pro Ser Ala Arg His His
100 105 110

(2) INFORMATION FOR SEQ ID NO:3236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..518
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3236:

aaacgcactc tcctatatcc gccgccatcg tctcgggctc tcctctctaa tcttcgggtt 60
cgcgctgcag tgtcttccgc ccgggctacc accatgccga agcagatcca cgagatcaag 120
gacttcctgc tgactgcgcg gcggaaggac gcacggtcgg tgcggatcaa gcgggccaag 180
gacgccgtca agttcaaggt gcgctgctcc aggtacctct acaccctctg cgtccacgac 240
gccgacaagg ccaacaagct caagcagtcg ctcccgccag gtctgactgt ccaggagatt 300
taaggtatca agccacaaac tgtgcttttt ttgcgggtgtc agggacgttt gctccagtgt 360
tactttagtt tgtaggtggg ctccattgct gtgtttgaat gaattatgaa gtttgagttt 420
gggatgcgaa tgatgtgtcg aacctatgag Gcctgtgttg taatggttac cccagaccgc 480
aaaggatggc aatctatcat aagttaaact gatttccg

(2) INFORMATION FOR SEQ ID NO:3237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..100
(D) OTHER INFORMATION: / Ceres Seq. ID 1576139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3237:

Lys Arg Thr Leu Tyr Pro Pro Pro Ser Ser Arg Ala Leu Ile Ser
1 5 10 15
Asn Leu Arg Val Arg Val Ala Val Ser Ser Ala Arg Ala Thr Thr Met
20 25 30
Pro Lys Gln Ile His Glu Ile Lys Asp Phe Leu Leu Thr Ala Arg Arg
35 40 45
Lys Asp Ala Arg Ser Val Arg Ile Lys Arg Ala Lys Asp Ala Val Lys
50 55 60
Phe Lys Val Arg Cys Ser Arg Tyr Leu Tyr Thr Leu Cys Val His Asp
65 70 75 80
Ala Asp Lys Ala Asn Lys Leu Lys Gln Ser Leu Pro Pro Gly Leu Thr
85 90 95
Val Gln Glu Ile
100

(2) INFORMATION FOR SEQ ID NO:3238:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..69
(D) OTHER INFORMATION: / Ceres Seq. ID 1576140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3238:

Met Pro Lys Gln Ile His Glu Ile Lys Asp Phe Leu Leu Thr Ala Arg
1 5 10 15
Arg Lys Asp Ala Arg Ser Val Arg Ile Lys Arg Ala Lys Asp Ala Val
20 25 30
Lys Phe Lys Val Arg Cys Ser Arg Tyr Leu Tyr Thr Leu Cys Val His
35 40 45
Asp Ala Asp Lys Ala Asn Lys Leu Lys Gln Ser Leu Pro Pro Gly Leu
50 55 60
Thr Val Gln Glu Ile
65

(2) INFORMATION FOR SEQ ID NO:3239:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1034 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1034
(D) OTHER INFORMATION: / Ceres Seq. ID 1576144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3239:

accaaagatg	ttgccgtggc	ctcgccgcac	aagaaaaatca	cagcagtaca	gcaccagaaa	60
cagaaaggta	gtagatcaag	gaacgccagt	gcggcgacaa	tgaccggcag	tggaagcacg	120
ggcgccaatg	gcaagagcca	gagatccagg	gccaaggcaa	tgctgttcgc	cttgggcaag	180
agcttttctg	accaagtctt	gcctcaggag	aagggtgtgg	agagctacct	ccaagaaagc	240
agctgcgacg	atcccgccac	caggggccaag	cttcagcgcc	tttgacgac	tacaacagtg	300
aagacaaggt	acactgttat	gtccaaggag	ctattggata	agcaccaga	gctgaagatg	360
gaGggtactc	cgacactgac	acctcgccct	gacatctgca	atgccgcggt	gatcgacctt	420
ggtgctgccc	cagCtcgcgc	tgcccttgac	gaatggggtc	gccctgcagc	tgatattacc	480
cacctcatct	acatctcatc	cagtgcacct	cgtctcccag	ggggcgacct	tcacctggct	540

gctcgccttg gccttagccc aaacacocgtg cgcacttccc ttctcttccct tggctgctcc 600
ggtggtgctg ctgcctcccg cactgccaag gacattgctg agaacaatcc agggagccgt 660
gtcctagtaa cagctgctga gaccactgtg ctaggcttcc ggccaccaag ttatgaccgt 720
ccttatgacc ttgttggtst gcgctgtttg gtgatgggtgc atcagccgtg attataggag 780
caggtcccat gacaccagca gaaaatcctt tcttggagct tgagttctcc acgcaggagt 840
tcctacctgg gactgataag gtaattgatg gcaaaatctc agaggaagga attaatTTTA 900
aactagggcg tgatttgcct gagaagattg aaagccgcac agaaggtttc tgcaggactc 960
tcatgaacca ggtagggata aaggatttca acgatatatt ttgggctgtg catcctgggtg 1020
gaccagcaat attg

(2) INFORMATION FOR SEQ ID NO:3240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1576145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3240:

Thr Lys Asp Val Ala Val Ala Ser Pro His Lys Lys Ile Thr Ala Val
1 5 10 15
Gln His Gln Lys Gln Lys Gly Ser Arg Ser Arg Asn Ala Ser Ala Ala
20 25 30
Thr Met Thr Gly Ser Gly Ser Thr Gly Ala Asn Gly Lys Ser Gln Arg
35 40 45
Ser Arg Ala Lys Ala Met Leu Phe Ala Leu Gly Lys Ser Phe Pro Asp
50 55 60
Gln Val Leu Pro Gln Glu Lys Val Val Glu Ser Tyr Leu Gln Glu Ser
65 70 75 80
Ser Cys Asp Asp Pro Ala Thr Arg Ala Lys Leu Gln Arg Leu Cys Thr
85 90 95
Thr Thr Thr Val Lys Thr Arg Tyr Thr Val Met Ser Lys Glu Leu Leu
100 105 110
Asp Lys His Pro Glu Leu Lys Met Glu Gly Thr Pro Thr Leu Thr Pro
115 120 125
Arg Leu Asp Ile Cys Asn Ala Ala Val Ile Asp Leu Gly Ala Ala Ala
130 135 140
Ala Arg Ala Ala Leu Asp Glu Trp Gly Arg Pro Ala Ala Asp Ile Thr
145 150 155 160
His Leu Ile Tyr Ile Ser Ser Ser Asp Leu Arg Leu Pro Gly Gly Asp
165 170 175
Leu His Leu Ala Ala Arg Leu Gly Leu Ser Pro Asn Thr Val Arg Thr
180 185 190
Ser Leu Leu Phe Leu Gly Cys Ser Gly Gly Ala Ala Ala Leu Arg Thr
195 200 205
Ala Lys Asp Ile Ala Glu Asn Asn Pro Gly Ser Arg Val Leu Val Thr
210 215 220
Ala Ala Glu Thr Thr Val Leu Gly Phe Arg Pro Pro Ser Tyr Asp Arg
225 230 235 240
Pro Tyr Asp Leu Val Gly Xaa Arg Cys Leu Val Met Val His Gln Pro
245 250 255

(2) INFORMATION FOR SEQ ID NO:3241:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

SEQUENCE - 1576145

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1576146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3241:

Met Thr Gly Ser Gly Ser Thr Gly Ala Asn Gly Lys Ser Gln Arg Ser
1 5 10 15
Arg Ala Lys Ala Met Leu Phe Ala Leu Gly Lys Ser Phe Pro Asp Gln
20 25 30
Val Leu Pro Gln Glu Lys Val Val Glu Ser Tyr Leu Gln Glu Ser Ser
35 40 45
Cys Asp Asp Pro Ala Thr Arg Ala Lys Leu Gln Arg Leu Cys Thr Thr
50 55 60
Thr Thr Val Lys Thr Arg Tyr Thr Val Met Ser Lys Glu Leu Leu Asp
65 70 75 80
Lys His Pro Glu Leu Lys Met Glu Gly Thr Pro Thr Leu Thr Pro Arg
85 90 95
Leu Asp Ile Cys Asn Ala Ala Val Ile Asp Leu Gly Ala Ala Ala Ala
100 105 110
Arg Ala Ala Leu Asp Glu Trp Gly Arg Pro Ala Ala Asp Ile Thr His
115 120 125
Leu Ile Tyr Ile Ser Ser Ser Asp Leu Arg Leu Pro Gly Gly Asp Leu
130 135 140
His Leu Ala Ala Arg Leu Gly Leu Ser Pro Asn Thr Val Arg Thr Ser
145 150 155 160
Leu Leu Phe Leu Gly Cys Ser Gly Gly Ala Ala Ala Leu Arg Thr Ala
165 170 175
Lys Asp Ile Ala Glu Asn Asn Pro Gly Ser Arg Val Leu Val Thr Ala
180 185 190
Ala Glu Thr Thr Val Leu Gly Phe Arg Pro Pro Ser Tyr Asp Arg Pro
195 200 205
Tyr Asp Leu Val Gly Xaa Arg Cys Leu Val Met Val His Gln Pro
210 215 220

(2) INFORMATION FOR SEQ ID NO:3242:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..203

(D) OTHER INFORMATION: / Ceres Seq. ID 1576147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3242:

Met Leu Phe Ala Leu Gly Lys Ser Phe Pro Asp Gln Val Leu Pro Gln
1 5 10 15
Glu Lys Val Val Glu Ser Tyr Leu Gln Glu Ser Ser Cys Asp Asp Pro
20 25 30
Ala Thr Arg Ala Lys Leu Gln Arg Leu Cys Thr Thr Thr Thr Val Lys
35 40 45
Thr Arg Tyr Thr Val Met Ser Lys Glu Leu Leu Asp Lys His Pro Glu
50 55 60
Leu Lys Met Glu Gly Thr Pro Thr Leu Thr Pro Arg Leu Asp Ile Cys
65 70 75 80
Asn Ala Ala Val Ile Asp Leu Gly Ala Ala Ala Ala Arg Ala Ala Leu
85 90 95
Asp Glu Trp Gly Arg Pro Ala Ala Asp Ile Thr His Leu Ile Tyr Ile
100 105 110
Ser Ser Ser Asp Leu Arg Leu Pro Gly Gly Asp Leu His Leu Ala Ala

115 120 125
Arg Leu Gly Leu Ser Pro Asn Thr Val Arg Thr Ser Leu Leu Phe Leu
130 135 140
Gly Cys Ser Gly Gly Ala Ala Leu Arg Thr Ala Lys Asp Ile Ala
145 150 155 160
Glu Asn Asn Pro Gly Ser Arg Val Leu Val Thr Ala Ala Glu Thr Thr
165 170 175
Val Leu Gly Phe Arg Pro Pro Ser Tyr Asp Arg Pro Tyr Asp Leu Val
180 185 190
Gly Xaa Arg Cys Leu Val Met Val His Gln Pro
195 200

(2) INFORMATION FOR SEQ ID NO:3243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3243:

gagaganana ngcgargaar gavggagaga gcacgggggc ttgatcgaag atgggatgccg 60
gagcaaaggt ggtgaagaag gccgcggcgg ggcgtcgcgg cgggggcaag tacttcttcc 120
acgagcagat ttcaaggcat cgcaccatca tgaatatctt tgacaaaacc cctcatgtgc 180
ataaagacgc atttgttgct ccaagtgcac cccttattgg tgatgttcaa gtcgggtcag 240
gagcttccat ttggtatggg tgcgtcttaa gaggggatgc aaacatcata caaattggat 300
ctgggaccaa tatacaagac aattctctta tacatgtggc taaatctaata ctaagtggga 360
aggtctttcc aacaaccatt ggtaataacg tcacagtagg tcatagtgtc gtgttacaag 420
gatgcacggt tgaggatgag gctttgttg gcattggggc aaccctatta gatggtgttg 480
ttgttgaaaa gcacggaatg gtggcttgct ggagccctcg tacggcagaa tactaggatc 540
ccttggtggag aggtatgggg agggaaccCt gccaaatttc tgaggaagct cacagatgac 600
gagatcagtt tcattgcgga atcagctgcc aactattcca atctgtccaa ggtccatgct 660
gctgagaatg ccaaacctct tgaaaagatt gagtttgaga aggtgttggg caagaagttt 720
gctcaccagg atgagtatga ttctctgatt ggcgtcactg aaggggcacc accagagctc 780
acgtccccaa atccagccca atgaacctct gtttctgttt tctctttggc gccttaatca 840
ttttctggtg gacagtgtg gatcgttgat cgggtgactg ttccatgaca ctggtggtt 900
atgtttactt ttctcccca ataactcttg atcgagcgat gttataaagc tggccatgca 960
cttcttccag attctgtatt cggtatgttt aagatgtgct ccctttcata acctcaagag 1020
tagttttagc accgtccata ttctgtcatg gttctgtact atgctttctg gcccgcgctg 1080
tatgaacat ctttataaaa atctctt

(2) INFORMATION FOR SEQ ID NO:3244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3244:

Met Asp Ala Gly Ala Lys Val Val Lys Lys Ala Ala Ala Gly Arg Arg
1 5 10 15
Gly Gly Gly Lys Tyr Phe Phe His Glu Gln Ile Ser Arg His Arg Thr
20 25 30
Ile Met Asn Ile Phe Asp Lys Thr Pro His Val His Lys Asp Ala Phe
35 40 45
Val Ala Pro Ser Ala Ser Leu Ile Gly Asp Val Gln Val Gly Ser Gly

50	55	60
Ala Ser Ile Trp Tyr Gly Cys Val Leu Arg Gly Asp Ala Asn Ile Ile		
65	70	75
Gln Ile Gly Ser Gly Thr Asn Ile Gln Asp Asn Ser Leu Ile His Val		80
	85	90
Ala Lys Ser Asn Leu Ser Gly Lys Val Phe Pro Thr Thr Ile Gly Asn		95
	100	105
Asn Val Thr Val Gly His Ser Ala Val Leu Gln Gly Cys Thr Val Glu		110
	115	120
Asp Glu Ala Phe Val Gly Ile Gly Ala Thr Leu Leu Asp Gly Val Val		125
130	135	140
Val Glu Lys His Gly Met Val Ala Cys Trp Ser Pro Arg Thr Ala Glu		
145	150	155
Tyr		160

(2) INFORMATION FOR SEQ ID NO:3245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3245:

Met Thr Arg Ser Val Ser Leu Arg Asn Gln Leu Pro Thr Ile Pro Ile	
1	5 10 15
Cys Pro Arg Ser Met Leu Leu Arg Met Pro Asn Leu Leu Lys Arg Leu	
	20 25 30
Ser Leu Arg Arg Cys Trp Ala Arg Ser Leu Leu Thr Arg Met Ser Met	
	35 40 45
Ile Pro Arg Leu Ala Ser Leu Lys Gly His His Gln Ser Ser Arg Pro	
	50 55 60
Gln Ile Gln Pro Asn Glu Pro Leu Phe Leu Phe Ser Leu Trp Arg Leu	
65	70 75 80
Asn His Phe Leu Leu Asp Ser Ala Gly Ser Leu Ile Gly Val Leu Phe	
	85 90 95
His Asp Thr Gly Gly Leu Cys Leu Leu Phe Leu Pro Asn Asn Leu Gly	
	100 105 110
Ser Ser Asp Val Ile Lys Leu Ala Met His Phe Phe Gln Ile Leu Tyr	
	115 120 125
Ser Val Cys Leu Arg Cys Ala Pro Phe His Asn Leu Lys Ser Ser Phe	
130	135 140
Ser Thr Val His Ile Arg His Glu Phe Cys Thr Met Leu Ser Gly Pro	
145	150 155 160
Ala Cys Met Asn His Leu Tyr Lys Asn Leu	
	165 170

(2) INFORMATION FOR SEQ ID NO:3246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3246:

116-117-118-119-120-121-122-123-124-125-126-127-128-129-130-131-132-133-134-135-136-137-138-139-140-141-142-143-144-145-146-147-148-149-150-151-152-153-154-155-156-157-158-159-160-161-162-163-164-165-166-167-168-169-170-171-172-173-174-175-176-177-178-179-180-181-182-183-184-185-186-187-188-189-190-191-192-193-194-195-196-197-198-199-200-201-202-203-204-205-206-207-208-209-210-211-212-213-214-215-216-217-218-219-220-221-222-223-224-225-226-227-228-229-230-231-232-233-234-235-236-237-238-239-240-241-242-243-244-245-246-247-248-249-250-251-252-253-254-255-256-257-258-259-260-261-262-263-264-265-266-267-268-269-270-271-272-273-274-275-276-277-278-279-280-281-282-283-284-285-286-287-288-289-290-291-292-293-294-295-296-297-298-299-300-301-302-303-304-305-306-307-308-309-310-311-312-313-314-315-316-317-318-319-320-321-322-323-324-325-326-327-328-329-330-331-332-333-334-335-336-337-338-339-340-341-342-343-344-345-346-347-348-349-350-351-352-353-354-355-356-357-358-359-360-361-362-363-364-365-366-367-368-369-370-371-372-373-374-375-376-377-378-379-380-381-382-383-384-385-386-387-388-389-390-391-392-393-394-395-396-397-398-399-400-401-402-403-404-405-406-407-408-409-410-411-412-413-414-415-416-417-418-419-420-421-422-423-424-425-426-427-428-429-430-431-432-433-434-435-436-437-438-439-440-441-442-443-444-445-446-447-448-449-450-451-452-453-454-455-456-457-458-459-460-461-462-463-464-465-466-467-468-469-470-471-472-473-474-475-476-477-478-479-480-481-482-483-484-485-486-487-488-489-490-491-492-493-494-495-496-497-498-499-500-501-502-503-504-505-506-507-508-509-510-511-512-513-514-515-516-517-518-519-520-521-522-523-524-525-526-527-528-529-530-531-532-533-534-535-536-537-538-539-540-541-542-543-544-545-546-547-548-549-550-551-552-553-554-555-556-557-558-559-560-561-562-563-564-565-566-567-568-569-570-571-572-573-574-575-576-577-578-579-580-581-582-583-584-585-586-587-588-589-590-591-592-593-594-595-596-597-598-599-600-601-602-603-604-605-606-607-608-609-610-611-612-613-614-615-616-617-618-619-620-621-622-623-624-625-626-627-628-629-630-631-632-633-634-635-636-637-638-639-640-641-642-643-644-645-646-647-648-649-650-651-652-653-654-655-656-657-658-659-660-661-662-663-664-665-666-667-668-669-670-671-672-673-674-675-676-677-678-679-680-681-682-683-684-685-686-687-688-689-690-691-692-693-694-695-696-697-698-699-700-701-702-703-704-705-706-707-708-709-710-711-712-713-714-715-716-717-718-719-720-721-722-723-724-725-726-727-728-729-730-731-732-733-734-735-736-737-738-739-740-741-742-743-744-745-746-747-748-749-750-751-752-753-754-755-756-757-758-759-760-761-762-763-764-765-766-767-768-769-770-771-772-773-774-775-776-777-778-779-780-781-782-783-784-785-786-787-788-789-790-791-792-793-794-795-796-797-798-799-800-801-802-803-804-805-806-807-808-809-810-811-812-813-814-815-816-817-818-819-820-821-822-823-824-825-826-827-828-829-830-831-832-833-834-835-836-837-838-839-840-841-842-843-844-845-846-847-848-849-850-851-852-853-854-855-856-857-858-859-860-861-862-863-864-865-866-867-868-869-870-871-872-873-874-875-876-877-878-879-880-881-882-883-884-885-886-887-888-889-890-891-892-893-894-895-896-897-898-899-900-901-902-903-904-905-906-907-908-909-910-911-912-913-914-915-916-917-918-919-920-921-922-923-924-925-926-927-928-929-930-931-932-933-934-935-936-937-938-939-940-941-942-943-944-945-946-947-948-949-950-951-952-953-954-955-956-957-958-959-960-961-962-963-964-965-966-967-968-969-970-971-972-973-974-975-976-977-978-979-980-981-982-983-984-985-986-987-988-989-990-991-992-993-994-995-996-997-998-999-1000-1001-1002-1003-1004-1005-1006-1007-1008-1009-1010-1011-1012-1013-1014-1015-1016-1017-1018-1019-1020-1021-1022-1023-1024-1025-1026-1027-1028-1029-1030-1031-1032-1033-1034-1035-1036-1037-1038-1039-1040-1041-1042-1043-1044-1045-1046-1047-1048-1049-1050-1051-1052-1053-1054-1055-1056-1057-1058-1059-1060-1061-1062-1063-1064-1065-1066-1067-1068-1069-1070-1071-1072-1073-1074-1075-1076-1077-1078-1079-1080-1081-1082-1083-1084-1085-1086-1087-1088-1089-1090-1091-1092-1093-1094-1095-1096-1097-1098-1099-1100-1101-1102-1103-1104-1105-1106-1107-1108-1109-1110-1111-1112-1113-1114-1115-1116-1117-1118-1119-1120-1121-1122-1123-1124-1125-1126-1127-1128-1129-1130-1131-1132-1133-1134-1135-1136-1137-1138-1139-1140-1141-1142-1143-1144-1145-1146-1147-1148-1149-1150-1151-1152-1153-1154-1155-1156-1157-1158-1159-1160-1161-1162-1163-1164-1165-1166-1167-1168-1169-1170-1171-1172-1173-1174-1175-1176-1177-1178-1179-1180-1181-1182-1183-1184-1185-1186-1187-1188-1189-1190-1191-1192-1193-1194-1195-1196-1197-1198-1199-1200-1201-1202-1203-1204-1205-1206-1207-1208-1209-1210-1211-1212-1213-1214-1215-1216-1217-1218-1219-1220-1221-1222-1223-1224-1225-1226-1227-1228-1229-1230-1231-1232-1233-1234-1235-1236-1237-1238-1239-1240-1241-1242-1243-1244-1245-1246-1247-1248-1249-1250-1251-1252-1253-1254-1255-1256-1257-1258-1259-1260-1261-1262-1263-1264-1265-1266-1267-1268-1269-1270-1271-1272-1273-1274-1275-1276-1277-1278-1279-1280-1281-1282-1283-1284-1285-1286-1287-1288-1289-1290-1291-1292-1293-1294-1295-1296-1297-1298-1299-1300-1301-1302-1303-1304-1305-1306-1307-1308-1309-1310-1311-1312-1313-1314-1315-1316-1317-1318-1319-1320-1321-1322-1323-1324-1325-1326-1327-1328-1329-1330-1331-1332-1333-1334-1335-1336-1337-1338-1339-1340-1341-1342-1343-1344-1345-1346-1347-1348-1349-1350-1351-1352-1353-1354-1355-1356-1357-1358-1359-1360-1361-1362-1363-1364-1365-1366-1367-1368-1369-1370-1371-1372-1373-1374-1375-1376-1377-1378-1379-1380-1381-1382-1383-1384-1385-1386-1387-1388-1389-1390-1391-1392-1393-1394-1395-1396-1397-1398-1399-1400-1401-1402-1403-1404-1405-1406-1407-1408-1409-1410-1411-1412-1413-1414-1415-1416-1417-1418-1419-1420-1421-1422-1423-1424-1425-1426-1427-1428-1429-1430-1431-1432-1433-1434-1435-1436-1437-1438-1439-1440-1441-1442-1443-1444-1445-1446-1447-1448-1449-1450-1451-1452-1453-1454-1455-1456-1457-1458-1459-1460-1461-1462-1463-1464-1465-1466-1467-1468-1469-1470-1471-1472-1473-1474-1475-1476-1477-1478-1479-1480-1481-1482-1483-1484-1485-1486-1487-1488-1489-1490-1491-1492-1493-1494-1495-1496-1497-1498-1499-1500-1501-1502-1503-1504-1505-1506-1507-1508-1509-1510-1511-1512-1513-1514-1515-1516-1517-1518-1519-1520-1521-1522-1523-1524-1525-1526-1527-1528-1529-1530-1531-1532-1533-1534-1535-1536-1537-1538-1539-1540-1541-1542-1543-1544-1545-1546-1547-1548-1549-1550-1551-1552-1553-1554-1555-1556-1557-1558-1559-1560-1561-1562-1563-1564-1565-1566-1567-1568-1569-1570-1571-1572-1573-1574-1575-1576-1577-1578-1579-1580-1581-1582-1583-1584-1585-1586-1587-1588-1589-1590-1591-1592-1593-1594-1595-1596-1597-1598-1599-1600-1601-1602-1603-1604-1605-1606-1607-1608-1609-1610-1611-1612-1613-1614-1615-1616-1617-1618-1619-1620-1621-1622-1623-1624-1625-1626-1627-1628-1629-1630-1631-1632-1633-1634-1635-1636-1637-1638-1639-1640-1641-1642-1643-1644-1645-1646-1647-1648-1649-1650-1651-1652-1653-1654-1655-1656-1657-1658-1659-1660-1661-1662-1663-1664-1665-1666-1667-1668-1669-1670-1671-1672-1673-1674-1675-1676-1677-1678-1679-1680-1681-1682-1683-1684-1685-1686-1687-1688-1689-1690-1691-1692-1693-1694-1695-1696-1697-1698-1699-1700-1701-1702-1703-1704-1705-1706-1707-1708-1709-1710-1711-1712-1713-1714-1715-1716-1717-1718-1719-1720-1721-1722-1723-1724-1725-1726-1727-1728-1729-1730-1731-1732-1733-1734-1735-1736-1737-1738-1739-1740-1741-1742-1743-1744-1745-1746-1747-1748-1749-1750-1751-1752-1753-1754-1755-1756-1757-1758-1759-1760-1761-1762-1763-1764-1765-1766-1767-1768-1769-1770-1771-1772-1773-1774-1775-1776-1777-1778-1779-1780-1781-1782-1783-1784-1785-1786-1787-1788-1789-1790-1791-1792-1793-1794-1795-1796-1797-1798-1799-1800-1801-1802-1803-1804-1805-1806-1807-1808-1809-1810-1811-1812-1813-1814-1815-1816-1817-1818-1819-1820-1821-1822-1823-1824-1825-1826-1827-1828-1829-1830-1831-1832-1833-1834-1835-1836-1837-1838-1839-1840-1841-1842-1843-1844-1845-1846-1847-1848-1849-1850-1851-1852-1853-1854-1855-1856-1857-1858-1859-1860-1861-1862-1863-1864-1865-1866-1867-1868-1869-1870-1871-1872-1873-1874-1875-1876-1877-1878-1879-1880-1881-1882-1883-1884-1885-1886-1887-1888-1889-1890-1891-1892-1893-1894-1895-1896-1897-1898-1899-1900-1901-1902-1903-1904-1905-1906-1907-1908-1909-1910-1911-1912-1913-1914-1915-1916-1917-1918-1919-1920-1921-1922-1923-1924-1925-1926-1927-1928-1929-1930-1931-1932-1933-1934-1935-1936-1937-1938-1939-1940-1941-1942-1943-1944-1945-1946-1947-1948-1949-1950-1951-1952-1953-1954-1955-1956-1957-1958-1959-1960-1961-1962-1963-1964-1965-1966-1967-1968-1969-1970-1971-1972-1973-1974-1975-1976-1977-1978-1979-1980-1981-1982-1983-1984-1985-1986-1987-1988-1989-1990-1991-1992-1993-1994-1995-1996-1997-1998-1999-2000-2001-2002-2003-2004-2005-2006-2007-2008-2009-2010-2011-2012-2013-2014-2015-2016-2017-2018-2019-2020-2021-2022-2023-2024-2025-2026-2027-2028-2029-2030-2031-2032-2033-2034-2035-2036-2037-2038-2039-2040-2041-2042-2043-2044-2045-2046-2047-2048-2049-2050-2051-2052-2053-2054-2055-2056-2057-2058-2059-2060-2061-2062-2063-2064-2065-2066-2067-2068-2069-2070-2071-2072-2073-2074-2075-2076-2077-2078-2079-2080-2081-2082-2083-2084-2085-2086-2087-2088-2089-2090-2091-2092-2093-2094-2095-2096-2097-2098-2099-2100-2101-2102-2103-2104-2105-2106-2107-2108-2109-2110-2111-2112-2113-2114-2115-2116-2117-2118-2119-2120-2121-2122-2123-2124-2125-2126-2127-2128-2129-2130-2131-2132-2133-2134-2135-2136-2137-2138-2139-2140-2141-2142-2143-2144-2145-2146-2147-2148-2149-2150-2151-2152-2153-2154-2155-2156-2157-2158-2159-2160-2161-2162-2163-2164-2165-2166-2167-2168-2169-2170-2171-2172-2173-2174-2175-2176-2177-2178-2179-2180-2181-2182-2183-2184-2185-2186-2187-2188-2189-2190-2191-2192-2193-2194-2195-2196-2197-2198-2199-2200-2201-2202-2203-2204-2205-2206-2207-2208-2209-2210-2211-2212-2213-2214-2215-2216-2217-2218-2219-2220-2221-2222-2223-2224-2225-2226-2227-2228-2229-2230-2231-2232-2233-2234-2235-2236-2237-2238-2239-2240-2241-2242-2243-2244-2245-2246-2247-2248-2249-2250-2251-2252-2253-2254-2255-2256-2257-2258-2259-2260-2261-2262-2263-2264-2265-2266-2267-2268-2269-2270-2271-2272-2273-2274-2275-2276-2277-2278-2279-2280-2281-2282-2283-2284-2285-2286-2287-2288-2289-2290-2291-2292-2293-2294

Met Leu Leu Arg Met Pro Asn Leu Leu Lys Arg Leu Ser Leu Arg Arg
1 5 10 15
Cys Trp Ala Arg Ser Leu Leu Thr Arg Met Ser Met Ile Pro Arg Leu
20 25 30
Ala Ser Leu Lys Gly His His Gln Ser Ser Arg Pro Gln Ile Gln Pro
35 40 45
Asn Glu Pro Leu Phe Leu Phe Ser Leu Trp Arg Leu Asn His Phe Leu
50 55 60
Leu Asp Ser Ala Gly Ser Leu Ile Gly Val Leu Phe His Asp Thr Gly
65 70 75 80
Gly Leu Cys Leu Leu Phe Leu Pro Asn Asn Leu Gly Ser Ser Asp Val
85 90 95
Ile Lys Leu Ala Met His Phe Phe Gln Ile Leu Tyr Ser Val Cys Leu
100 105 110
Arg Cys Ala Pro Phe His Asn Leu Lys Ser Ser Phe Ser Thr Val His
115 120 125
Ile Arg His Glu Phe Cys Thr Met Leu Ser Gly Pro Ala Cys Met Asn
130 135 140
His Leu Tyr Lys Asn Leu
145 150

(2) INFORMATION FOR SEQ ID NO:3247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 922 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..922
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3247:

aaaactgttc	tgcttcgctc	gcrggcgctc	atctccactc	ctccgatggc	gccgccaccc	60
accagcccct	cattcctcgc	cccgccgcgc	ctgccacacc	acccgcaccc	tcgcctcctt	120
ttgcgacctc	cctccgcctc	ttccgcgcgc	gccgaaatac	tcggcggtcg	gggcctctgc	180
aatggtgagg	tcggcggtcc	caaagaactc	gcacccgggt	ccaccacctc	ctcgcccgcg	240
ccctctcctc	ctccttcgac	agattctcct	ccgcccgcgc	ttgatccgga	cgcgttcgag	300
aaggagatga	tgggcctcac	aggcggcttc	cctggcggtg	aggtcggcct	caaggacttc	360
gtagccaaga	acccgcctcc	tcccaagaaa	tcagaatccc	agccccaagc	cacgctctcc	420
gcgcgcgcgc	ggccgcgcga	gctgcgcgct	ttcttgcccg	gcattggtgt	gctggtcaag	480
aaccccaaca	acgcctacca	catgtactgc	ggtatcgtgc	agcgcgtcag	CGacggcaag	540
gNtcgcggtg	ctcttcgagg	gaggagtgtg	ggacaggctc	atcaccttca	acctcgacga	600
gctcgagggc	agggagaagg	gaccccttat	ggccaacccc	aagtccgtgg	tgctagagga	660
tcttgtcgcg	gagctcgagg	atgacgatga	tgataaggag	gacgaagcgg	ccaagaagaa	720
ggaaccggag	ggcgcgccgc	cgcgcgcgac	atgaccaggc	ttcttggttc	tggtatacac	780
atcctctgta	tgtatgcatg	tatacagctc	aaataaaaata	tttgagagta	attaaaaagg	840
aacgataata	taactcttat	tatgaagtat	atagtttgaa	tgttagtgtg	aattggggca	900
tggaagaatt	gccatacggt	tg				

(2) INFORMATION FOR SEQ ID NO:3248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..227
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3248:

Lys Thr Val Leu Leu Arg Ser Xaa Ala Leu Ile Ser Thr Pro Pro Met

U.S. PAT. & TRADEMARK OFFICE

1 5 10 15
Ala Pro Pro Pro Thr Ser Pro Ser Phe Leu Arg Pro Pro Pro Leu Pro
20 25 30
His His Pro His Pro Arg Leu Leu Leu Arg Pro Pro Ser Ala Ser Phe
35 40 45
Arg Val Ala Glu Ile Leu Gly Gly Arg Gly Leu Cys Asn Gly Glu Val
50 55 60
Gly Val Arg Lys Glu Leu Ala Ser Gly Ser Thr Thr Ser Ser Pro Ala
65 70 75 80
Pro Ser Pro Pro Pro Ser Thr Asp Ser Pro Pro Pro Ala Val Asp Pro
85 90 95
Asp Ala Phe Glu Lys Glu Met Met Gly Leu Thr Gly Gly Phe Pro Gly
100 105 110
Gly Glu Val Gly Leu Lys Asp Phe Val Ala Lys Asn Pro Pro Pro Pro
115 120 125
Lys Lys Ser Glu Ser Gln Pro Gln Ala Thr Leu Ser Ala Pro Pro Arg
130 135 140
Pro Pro Glu Leu Pro Leu Phe Leu Pro Gly Met Val Val Leu Val Lys
145 150 155 160
Asn Pro Asn Asn Ala Tyr His Met Tyr Cys Gly Ile Val Gln Arg Val
165 170 175
Ser Asp Gly Lys Xaa Arg Gly Ala Leu Arg Gly Arg Ser Val Gly Gln
180 185 190
Ala His His Leu Gln Pro Arg Arg Ala Arg Gly Gln Gly Glu Gly Thr
195 200 205
Pro Tyr Gly Gln Pro Gln Val Arg Gly Ala Arg Gly Ser Cys Arg Gly
210 215 220
Ala Arg Gly
225

(2) INFORMATION FOR SEQ ID NO:3249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..212
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3249:

Met Ala Pro Pro Pro Thr Ser Pro Ser Phe Leu Arg Pro Pro Pro Leu
1 5 10 15
Pro His His Pro His Pro Arg Leu Leu Leu Arg Pro Pro Ser Ala Ser
20 25 30
Phe Arg Val Ala Glu Ile Leu Gly Gly Arg Gly Leu Cys Asn Gly Glu
35 40 45
Val Gly Val Arg Lys Glu Leu Ala Ser Gly Ser Thr Thr Ser Ser Pro
50 55 60
Ala Pro Ser Pro Pro Pro Ser Thr Asp Ser Pro Pro Pro Ala Val Asp
65 70 75 80
Pro Asp Ala Phe Glu Lys Glu Met Met Gly Leu Thr Gly Gly Phe Pro
85 90 95
Gly Gly Glu Val Gly Leu Lys Asp Phe Val Ala Lys Asn Pro Pro Pro
100 105 110
Pro Lys Lys Ser Glu Ser Gln Pro Gln Ala Thr Leu Ser Ala Pro Pro
115 120 125
Arg Pro Pro Glu Leu Pro Leu Phe Leu Pro Gly Met Val Val Leu Val
130 135 140
Lys Asn Pro Asn Asn Ala Tyr His Met Tyr Cys Gly Ile Val Gln Arg
145 150 155 160

Val Ser Asp Gly Lys Xaa Arg Gly Ala Leu Arg Gly Arg Ser Val Gly
165 170 175
Gln Ala His His Leu Gln Pro Arg Arg Ala Arg Gly Gln Gly Glu Gly
180 185 190
Thr Pro Tyr Gly Gln Pro Gln Val Arg Gly Ala Arg Gly Ser Cys Arg
195 200 205
Gly Ala Arg Gly
210

(2) INFORMATION FOR SEQ ID NO:3250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1576162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3250:

Met Met Gly Leu Thr Gly Gly Phe Pro Gly Gly Glu Val Gly Leu Lys
1 5 10 15
Asp Phe Val Ala Lys Asn Pro Pro Pro Pro Lys Lys Ser Glu Ser Gln
20 25 30
Pro Gln Ala Thr Leu Ser Ala Pro Pro Arg Pro Pro Glu Leu Pro Leu
35 40 45
Phe Leu Pro Gly Met Val Val Leu Val Lys Asn Pro Asn Asn Ala Tyr
50 55 60
His Met Tyr Cys Gly Ile Val Gln Arg Val Ser Asp Gly Lys Xaa Arg
65 70 75 80
Gly Ala Leu Arg Gly Arg Ser Val Gly Gln Ala His His Leu Gln Pro
85 90 95
Arg Arg Ala Arg Gly Gln Gly Glu Gly Thr Pro Tyr Gly Gln Pro Gln
100 105 110
Val Arg Gly Ala Arg Gly Ser Cys Arg Gly Ala Arg Gly
115 120 125

(2) INFORMATION FOR SEQ ID NO:3251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 627 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..627

(D) OTHER INFORMATION: / Ceres Seq. ID 1576221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3251:

aaggtgtttt gccctcttct tcgcgarcnc ccccgccgca acccgagcc gcatcgagg 60
acccgagcc gccgatggcg aagaagcaca gggaccagc ctctgargcc gcgagcggcg 120
actccccggc cgcgctccatc cgctccctct tctccgcgga caaMcccgtt ccgcccgaag 180
gcctctacgg aggagcccc cgcgactcct gcacccgcca cgacgcccct ccccatgcaa 240
cccagccgtg acgccaggga tgccgagccg tcctcgaaga agaataagaa gagcaaggag 300
gagggccccg gcgcgaagcg gaagcgrgac gaggtaggag ccggccggga gcggcgcgga 360
ggcgcgaggaga atccgtcgag agttggggag aagaggaagg ctcccgaaga cgcgccacag 420
ggggccgggg aggacgagga ggaggctttc gacgacgaga gcaagctgct caggaccgtg 480
ttcgtgggga acctgccgct gcggwccaag cgcaaggtgc tcatcaagga gttcgtcaa 540
aaaggacagg caggcagctg cctcccccca tgttatgatg acaaaactct agtagctagg 600
aaaggaatca cggtgacctt ttgtttc

(2) INFORMATION FOR SEQ ID NO:3252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..209
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576222
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3252:

Lys Val Phe Cys Pro Leu Leu Arg Xaa Xaa Pro Arg Arg Asn Pro Gln
1 5 10 15
Pro His Arg Glu Thr Arg Ser Arg Arg Trp Arg Arg Ser Thr Gly Thr
20 25 30
Gln Pro Leu Xaa Pro Arg Ala Ala Thr Pro Arg Pro Arg Pro Ser Ala
35 40 45
Pro Ser Ser Pro Arg Thr Xaa Pro Phe Arg Arg Lys Ala Ser Thr Glu
50 55 60
Glu Pro Pro Ala Thr Pro Ala Pro Ala Thr Thr Pro Leu Pro Met Gln
65 70 75 80
Pro Ser Arg Asp Ala Arg Asp Ala Glu Pro Ser Ser Lys Lys Asn Lys
85 90 95
Lys Ser Lys Glu Glu Gly Pro Arg Arg Lys Arg Lys Xaa Asp Glu Leu
100 105 110
Glu Ala Gly Arg Glu Arg Arg Arg Gly Ala Glu Asn Pro Ser Arg Val
115 120 125
Gly Glu Lys Arg Lys Ala Pro Asp Asp Ala Ala Gln Gly Ala Gly Glu
130 135 140
Asp Glu Glu Glu Ala Phe Asp Asp Glu Ser Lys Leu Leu Arg Thr Val
145 150 155 160
Phe Val Gly Asn Leu Pro Leu Arg Xaa Lys Arg Lys Val Leu Ile Lys
165 170 175
Glu Phe Ala Gln Lys Gly Gln Ala Gly Ser Cys Leu Pro Pro Cys Tyr
180 185 190
Asp Asp Lys Thr Leu Val Ala Arg Lys Gly Ile Thr Val Thr Phe Cys
195 200 205
Phe

- (2) INFORMATION FOR SEQ ID NO:3253:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..131
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576223
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3253:

Met Gln Pro Ser Arg Asp Ala Arg Asp Ala Glu Pro Ser Ser Lys Lys
1 5 10 15
Asn Lys Lys Ser Lys Glu Glu Gly Pro Arg Arg Lys Arg Lys Xaa Asp
20 25 30
Glu Leu Glu Ala Gly Arg Glu Arg Arg Arg Gly Ala Glu Asn Pro Ser
35 40 45
Arg Val Gly Glu Lys Arg Lys Ala Pro Asp Asp Ala Ala Gln Gly Ala
50 55 60
Gly Glu Asp Glu Glu Glu Ala Phe Asp Asp Glu Ser Lys Leu Leu Arg
65 70 75 80
Thr Val Phe Val Gly Asn Leu Pro Leu Arg Xaa Lys Arg Lys Val Leu

85 90 95
Ile Lys Glu Phe Ala Gln Lys Gly Gln Ala Gly Ser Cys Leu Pro Pro
100 105 110
Cys Tyr Asp Asp Lys Thr Leu Val Ala Arg Lys Gly Ile Thr Val Thr
115 120 125
Phe Cys Phe
130

(2) INFORMATION FOR SEQ ID NO:3254:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1576224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3254:

Met Pro Ser Arg Pro Arg Arg Arg Ile Arg Arg Ala Arg Arg Arg Ala
1 5 10 15
Arg Gly Ala Ser Gly Ser Xaa Thr Ser Trp Arg Pro Ala Gly Ser Gly
20 25 30
Gly Glu Ala Arg Arg Ile Arg Arg Glu Leu Gly Arg Arg Gly Arg Leu
35 40 45
Pro Thr Thr Arg His Arg Gly Pro Gly Arg Thr Arg Arg Arg Leu Ser
50 55 60
Thr Thr Arg Ala Ser Cys Ser Gly Pro Cys Ser Trp Gly Thr Cys Arg
65 70 75 80
Cys Xaa Pro Ser Ala Arg Cys Ser Ser Arg Ser Ser Leu Lys Lys Asp
85 90 95
Arg Gln Ala Ala Ala Ser Pro His Val Met Met Thr Lys Leu
100 105 110

(2) INFORMATION FOR SEQ ID NO:3255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..750

(D) OTHER INFORMATION: / Ceres Seq. ID 1576229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3255:

gcttccacca tcgcacccac cgggagcgcc tcctcttctc cagcgtcgga tccccattcc 60
ccacctctcc tccctccgcc gccagctccc gcmcccttct ctcccctcct cgccctcccg 120
cgcgcgcggt tttataaggg tttaagcgga ggcgcccggt cgctggcgat ggccgamgac 180
ggcgggagcc acgagggcag cggcgggcggc ggaggcgctc gggagcagga ccggttcctg 240
cccatcgcca acatcagccg gatcatgaag aargCcgccc cggccaacgg caagatcgcc 300
aaggacgcta aggagaccgc tgcaaaaccg aggggtgctga aacagagatg attctggttt 360
ggcccgtaga agcgatgcaa aaggtcgtct cccaaggtaa cgacgaatga tggAcagcgg 420
gggtgctctt gctctctaca agttgatgac aactagctgg ttgccttttg aaagcaccog 480
tgcatgtgat ctgacgaatg aaaacaaagt gatgggtgta aacgtgtaaa gactttaaac 540
tggtgccaat aaatattacg tatttatgta aatgcacgga tctgatggaa tgcacatatg 600
gtgcccatac atctgggcat tgcgcgctgc cgaatgtctg gttaaagcgcg ctattttcatg 660
gttggtgtgcg tccgagaaaa ggcaatggcc gtgcaaaagt ttcttcgacg gatggttgca 720
gatgttagca gtacaggatg ttttcttgt

(2) INFORMATION FOR SEQ ID NO:3256:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

```
(A) NAME/KEY: peptide
(B) LOCATION: 1..60
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3257:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1															
Met	Ala	Xaa	Asp	Gly	Gly	Ser	His	Glu	Gly	Ser	Gly	Gly	Gly	Gly	Gly
1				5				10						15	
Val	Arg	Glu	Gln	Asp	Arg	Phe	Leu	Pro	Ile	Ala	Asn	Ile	Ser	Arg	Ile
			20					25					30		
Met	Lys	Xaa	Ala	Val	Pro	Ala	Asn	Gly	Lys	Ile	Ala	Lys	Asp	Ala	Lys
		35					40					45			
Glu	Thr	Ala	Ala	Lys	Pro	Arg	Val	Leu	Lys	Gln	Arg				
	50					55				60					

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

```
(A) NAME/KEY: peptide
(B) LOCATION: 1..59
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3258:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

Met	His	Gly	Ser	Asp	Gly	Met	His	Ile	Trp	Cys	Pro	Ser	Ile	Trp	Ala
1			5					10						15	
Leu	Arg	Ala	Ala	Glu	Cys	Leu	Val	Lys	Arg	Ala	Ile	Ser	Trp	Leu	Cys
			20					25					30		

Ala Ser Glu Lys Arg Gln Trp Pro Cys Lys Ser Phe Phe Asp Gly Trp
35 40 45
Leu Gln Met Leu Ala Val Gln Asp Val Phe Leu
50 55

(2) INFORMATION FOR SEQ ID NO:3259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 934 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..934
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3259:

aaaaattgca	aaaatctctg	ccgtgcctct	cgtctctctt	ctcargcgcc	acgcaaaacg	60
gtctccgttt	tccctctccg	gatccggccc	gcgggagcca	ggagccatcg	atgatccgga	120
ccgcaacggt	gcgagcgcg	ctcctcctat	cgcgcctcta	cgtagcacag	gcaaaggcag	180
cttctcgctg	gcctctcgtc	cgtcggaagg	cttcgcctct	tggatctgta	cgctctttct	240
atcagatgga	cattacaagg	caatacaaaa	ataaaaattt	gactgcaaga	gggtgccata	300
gctccccctg	gagtcagaaa	ttagcaatga	aaagctgtgt	tccatgcaac	totaaggatt	360
taggtcccat	gtcagaagat	tctgctaaaa	agttgcttga	acaggtgaat	ggttggaac	420
tgatcactga	aggtggtgtt	ctgaaattac	atagaacatg	gaaggtgaag	aactttgtta	480
aaggacttga	gttctttcag	cttggtgctg	ctatcgctga	ggaagaagg	caccatccag	540
atcttcatct	tggtggttgg	aataatgtga	aaattgatgt	ttggactcat	tctgtcagag	600
gtttaacaag	taatgatttc	atccttgctg	cgaagatcaa	tcattctact	ttagacggca	660
ttataaggaa	gaaagctaaa	tagccaatgt	ctcagaagca	actcaaatat	gcagctcgta	720
tttgtttgga	attttgtag	cgcagcgatg	gagaagccaa	atggtgagga	cacctcgccc	780
tgtgtgagat	taacttgctg	aaatgtagtg	ccttattcag	tagctcattt	taccttgta	840
tttaattagta	atttgcata	gtagacgttg	aatccatcat	tgtacttggt	tacctactta	900
cottacctgt	cagttttgaa	aagacacatg	gtcg			

(2) INFORMATION FOR SEQ ID NO:3260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..226
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3260:

Lys	Leu	Gln	Lys	Ser	Leu	Pro	Cys	Leu	Ser	Ser	Leu	Phe	Ser	Xaa	Ala
1			5					10						15	
Thr	Gln	Asn	Gly	Leu	Arg	Phe	Pro	Ser	Pro	Asp	Pro	Ala	Arg	Gly	Ser
		20					25					30			
Gln	Glu	Pro	Ser	Met	Ile	Arg	Thr	Ala	Thr	Val	Arg	Ala	Arg	Leu	Leu
		35					40					45			
Leu	Ser	Arg	Ser	Tyr	Val	Ala	Gln	Ala	Lys	Ala	Ala	Ser	Arg	Trp	Pro
		50				55					60				
Leu	Val	Arg	Trp	Lys	Ala	Ser	His	Leu	Gly	Ser	Val	Arg	Ser	Phe	Tyr
		65			70				75					80	
Gln	Met	Asp	Ile	Thr	Arg	Gln	Tyr	Lys	Asn	Lys	Ile	Leu	Thr	Ala	Arg
			85				90							95	
Gly	Cys	His	Ser	Ser	Pro	Glu	Ser	Gln	Glu	Leu	Ala	Met	Lys	Ser	Cys
			100				105						110		
Val	Pro	Cys	Asn	Ser	Lys	Asp	Leu	Gly	Pro	Met	Ser	Glu	Asp	Ser	Ala
			115				120						125		
Lys	Lys	Leu	Leu	Glu	Gln	Val	Asn	Gly	Trp	Glu	Leu	Ile	Thr	Glu	Gly

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3262:

Met Asp Ile Thr Arg Gln Tyr Lys Asn Lys Ile Leu Thr Ala Arg Gly
1 5 10 15
Cys His Ser Ser Pro Glu Ser Gln Glu Leu Ala Met Lys Ser Cys Val
20 25 30
Pro Cys Asn Ser Lys Asp Leu Gly Pro Met Ser Glu Asp Ser Ala Lys
35 40 45
Lys Leu Leu Glu Gln Val Asn Gly Trp Glu Leu Ile Thr Glu Gly Gly
50 55 60
Val Leu Lys Leu His Arg Thr Trp Lys Val Lys Asn Phe Val Lys Gly
65 70 75 80
Leu Glu Phe Phe Gln Leu Val Ala Ala Ile Ala Glu Glu Glu Gly His
85 90 95
His Pro Asp Leu His Leu Val Gly Trp Asn Asn Val Lys Ile Asp Val
100 105 110
Trp Thr His Ser Val Arg Gly Leu Thr Ser Asn Asp Phe Ile Leu Ala
115 120 125
Ala Lys Ile Asn His Leu Thr Leu Asp Gly Ile Ile Arg Lys Lys Ala
130 135 140
Lys
145

(2) INFORMATION FOR SEQ ID NO:3263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 698 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..698
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3263:

aaagaaaagg aaggaagaag ggcctcctgt atcctctcac ttccctcagt cctcgctccgt	60
ctgctccctc ctctckctas ctagctctag ctagccttcc tgtagcgcg gtagatggc	120
tgccctgcc tccaccacg cgcgcgcg ggcagcgctg ctgctgctgc tcctcctgtc	180
gctcgccgcg gcggcggnac atgtcgatcg tgtcctacgg ggagcgcgagc brcraggagg	240
cgcgcgcgat gtacgcgagg tggatggcg cgacggccg gacctacaam gccgtcggcK	300
aggaggagcg gcggtaccag gtgttccggg acaacctccg ctacatcgac gcgcacaacg	360
ccgccgccga cgcgggcgtc cactccttcc gcctcgAgcc tcaaccgCtt cgccgacctc	420
accaacgacg agtaccgcgc cacctacctc ggcgccagga ccaggccgca gaggggagagg	480
aagctcgcg ccaggtacca cgccgccgac aacgaggacc tgccggagtc cgtcgactgg	540
agggccaagg gcgcgctcgc cgaggtcaag gaccagggca gctgcgggag ctgttgggct	600
ttctcaacaa tagcagctgt ggaaggcatc aaccagattg ttacaggcga cttgatctcc	660
ttgtctgaac aagagcttgt cgactgtgac mytcgtac	

(2) INFORMATION FOR SEQ ID NO:3264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..221
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3264:

Arg Lys Gly Arg Lys Lys Gly Leu Leu Tyr Pro Leu Thr Ser Leu Ser
1 5 10 15
Pro Arg Pro Ser Ala Pro Ser Ser Xaa Xaa Leu Ala Leu Ala Ser Leu
20 25 30
Pro Val Ala Arg Gln Arg Trp Leu Pro Leu Pro Pro Pro Arg Arg Arg

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1576247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3265:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..155
(D) OTHER INFORMATION: / Ceres Seq. ID 1576248
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3266:

Met Ser Ile Val Ser Tyr Gly Glu Arg Ser Xaa Xaa Glu Ala Arg Arg
1 5 10 15
Met Tyr Ala Glu Trp Met Ala Ala His Gly Arg Thr Tyr Xaa Ala Val
20 25 30
Gly Xaa Glu Glu Arg Arg Tyr Gln Val Phe Arg Asp Asn Leu Arg Tyr
35 40 45
Ile Asp Ala His Asn Ala Ala Ala Asp Ala Gly Val His Ser Phe Arg
50 55 60
Leu Glu Pro Gln Pro Leu Arg Arg Pro His Gln Arg Arg Val Pro Arg
65 70 75 80
His Leu Pro Arg Arg Gln Asp Gln Ala Ala Glu Gly Glu Glu Ala Arg
85 90 95
Arg Gln Val Pro Arg Arg Arg Gln Arg Gly Pro Ala Gly Val Arg Arg
100 105 110
Leu Glu Gly Gln Gly Arg Arg Arg Arg Gly Gln Gly Pro Gly Gln Leu
115 120 125
Arg Glu Leu Leu Gly Phe Leu Asn Asn Ser Ser Cys Gly Arg His Gln
130 135 140
Pro Asp Cys Tyr Arg Arg Leu Asp Leu Leu Val
145 150 155

(2) INFORMATION FOR SEQ ID NO:3267:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 988 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..988
(D) OTHER INFORMATION: / Ceres Seq. ID 1576267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3267:

cgatagtatg ctaggaagga gagaaaatcc aggggagcat gaagcgatgc gcaagatgaa 60
gaatgaattt atggtaaaatt gggatgggtt ggcactaaa gataaggagc gtgtgcttgt 120
tcttggtgct acaaataggc cttttgacct cgacgaggct gtgattagga gggtcccccg 180
cagggttaatg gtaaaactgac ccgatgcacg aaatagggag aaaattctaa aagtaatttt 240
ggcaaaaagaa gagctgggat ctgatgttga tatggactcg cttgccaata tgactgatgg 300
ttattcagga agcgacctga agaattctgtg tgtvaccgag ggcattacc ccatccgaga 360
aattctggag aaggaaaaga aggagaagag tttggctaaa acagaaggta ggccggagcc 420
tgcattatat ggaagcgagG acatccgccc ccttagcata gatgacttca aaAtctgccm 480
atgagcaggt gtgtgcgasc gtttcgtccg actcggcgaa catgaacgag ctcccttcaat 540
ggaacgacyt gtacgktgaa ggcgggtcaa ggaagaagaa agcgtgagc tacttcatgt 600
gatgtggtga gagcatagaa tccagaagga tcacagccgt ggcataagat cagaaggaac 660
acagagcggc catagtacca caccacacc cactatggcc ctaaattccag tcagggttttc 720
gctccttccc cctccctcag tagccgcccgc cgccccaccg ccgcctggtg taattagaac 780
tgtgtaccga gtcgagttgg tttgccagct gtttcgaggt tacagagttg agatttgaa 840
ttacaatggc gccattgccc tctccaacc ccccttttt cttcctctca taagttgcgg 900
tcactgtcct tcttgactc tctggccttt gttcttgtaa atgcgaaatg aagggatgtg 960
aaataagaac atcttcgtcc tgttgttg

(2) INFORMATION FOR SEQ ID NO:3268:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 amino acids
(B) TYPE: amino acid

Asp 1	Ser	Met	Leu	Gly 5	Arg	Arg	Glu	Asn 10	Pro	Gly	Glu	His	Glu	Ala 15	Met
Arg	Lys	Met	Lys	Asn 20	Glu	Phe	Met	Val 25	Asn	Trp	Asp	Gly	Leu 30	Arg	Thr
Lys	Asp	Lys	Glu	Arg 35	Val	Leu	Val 40	Leu	Gly	Ala	Thr	Asn 45	Arg	Pro	Phe
Asp	Leu	Asp	Glu	Ala 50	Val	Ile 55	Arg	Arg	Phe	Pro	Arg 60	Arg	Leu	Met	Val
Asn 65	Leu	Pro	Asp	Ala 70	Ser	Asn	Arg	Glu	Lys 75	Ile	Leu	Lys	Val	Ile 80	Leu
Ala	Lys	Glu	Glu	Leu 85	Gly	Ser	Asp	Val 90	Asp	Met	Asp	Ser	Leu 95	Ala	Asn
Met	Thr	Asp	Gly 100	Tyr	Ser	Gly	Ser 105	Asp	Leu	Lys	Asn	Leu 110	Cys	Xaa	Thr
Ala	Ala	His 115	Tyr	Pro	Ile	Arg	Glu 120	Ile	Leu	Glu	Lys	Glu 125	Lys	Lys	Glu
Lys	Ser	Leu	Ala	Lys 130	Thr	Glu	Gly 135	Arg	Pro	Glu	Pro 140	Ala	Leu	Tyr	Gly
Ser 145	Glu	Asp	Ile	Arg 150	Pro	Leu	Ser	Ile	Asp 155	Asp	Phe	Lys	Ile	Cys	Xaa 160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3269:

SEQUENCE DESCRIPTION: SEQ ID NO: 1																
Met	Leu	Gly	Arg	Arg	Glu	Asn	Pro	Gly	Glu	His	Glu	Ala	Met	Arg	Lys	
1				5					10					15		
Met	Lys	Asn	Glu	Phe	Met	Val	Asn	Trp	Asp	Gly	Leu	Arg	Thr	Lys	Asp	
			20					25					30			
Lys	Glu	Arg	Val	Leu	Val	Leu	Gly	Ala	Thr	Asn	Arg	Pro	Phe	Asp	Leu	
		35					40					45				
Asp	Glu	Ala	Val	Ile	Arg	Arg	Phe	Pro	Arg	Arg	Leu	Met	Val	Asn	Leu	
	50					55					60					
Pro	Asp	Ala	Ser	Asn	Arg	Glu	Lys	Ile	Leu	Lys	Val	Ile	Leu	Ala	Lys	
65				70						75					80	
Glu	Glu	Leu	Gly	Ser	Asp	Val	Asp	Met	Asp	Ser	Leu	Ala	Asn	Met	Thr	
			85						90					95		
Asp	Gly	Tyr	Ser	Gly	Ser	Asp	Leu	Lys	Asn	Leu	Cys	Xaa	Thr	Ala	Ala	
			100					105					110			
His	Tyr	Pro	Ile	Arg	Glu	Ile	Leu	Glu	Lys	Glu	Lys	Lys	Glu	Lys	Ser	
		115					120					125				
Leu	Ala	Lys	Thr	Glu	Gly	Arg	Pro	Glu	Pro	Ala	Leu	Tyr	Gly	Ser	Glu	
	130					135					140					
Asp	Ile	Arg	Pro	Leu	Ser	Ile	Asp	Asp	Phe	Lys	Ile	Cys	Xaa			

145 150 155

(2) INFORMATION FOR SEQ ID NO:3270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1576270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3270:

Met Arg Lys Met Lys Asn Glu Phe Met Val Asn Trp Asp Gly Leu Arg
1 5 10 15
Thr Lys Asp Lys Glu Arg Val Leu Val Leu Gly Ala Thr Asn Arg Pro
20 25 30
Phe Asp Leu Asp Glu Ala Val Ile Arg Arg Phe Pro Arg Arg Leu Met
35 40 45
Val Asn Leu Pro Asp Ala Ser Asn Arg Glu Lys Ile Leu Lys Val Ile
50 55 60
Leu Ala Lys Glu Glu Leu Gly Ser Asp Val Asp Met Asp Ser Leu Ala
65 70 75 80
Asn Met Thr Asp Gly Tyr Ser Gly Ser Asp Leu Lys Asn Leu Cys Xaa
85 90 95
Thr Ala Ala His Tyr Pro Ile Arg Glu Ile Leu Glu Lys Glu Lys Lys
100 105 110
Glu Lys Ser Leu Ala Lys Thr Glu Gly Arg Pro Glu Pro Ala Leu Tyr
115 120 125
Gly Ser Glu Asp Ile Arg Pro Leu Ser Ile Asp Asp Phe Lys Ile Cys
130 135 140
Xaa
145

(2) INFORMATION FOR SEQ ID NO:3271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 824 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..824

(D) OTHER INFORMATION: / Ceres Seq. ID 1576273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3271:

accagccacc gccaaagccgc attacaaaga acgcgaaccg ctgccagtcc aaaccctacg 60
gccgccgcca gcatcaagct ccccgaccaa accctactcg taccocgccc cgcgcgcagc 120
cgcagccgcg gccacaccag caagcagaac tagcagccat gccgcccaaa ttggaccctt 180
ctcaggtggt ggaggtcttc gtccgcgtga cgggagcgga ggtcggcgcg gcgtcgtcgc 240
tgcccccaaa gatcggcccg ctccgtctct ccccgaaaga gatcggcgag gacatcgcca 300
aggagaccgc caaggactgg aagggcctcc gcgtcaccgt caagctcacc gtgcagaacc 360
ggcaggccaa ggtctccgct gtcccctccg ccgcggcgct cgtcatcaag gcgctcaagg 420
aacccgagag ggacaggaag aaggtcaaga acatcaagca cagcGggcaa catcagcctc 480
gacgacgtca tcgagatcgc caagaCccat gcggaacagg tccatggcca aggagttggc 540
cgggaccgtc aaggagatcc tggggacctg cgtcaGcgtc ggggtgcaccg tcgatgggaa 600
ggaccccaag gacttgcagc aggagatcga tgatggtgag gtcgagatcc cctcagctta 660
aaggctatac aactagaaat catcggacac tattaagtgt tggtgttttg ttccaakksa 720
gttcctgcac ctcaatcgcc tattattgtc tgctttagtt ccttcaagtc ttgtgagaga 780
cctaatacgt accttgtgcc ttataaaatt acatcttccg attc

(2) INFORMATION FOR SEQ ID NO:3272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..219
(D) OTHER INFORMATION: / Ceres Seq. ID 1576274
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3272:
Pro Ala Thr Ala Lys Pro His Tyr Lys Glu Arg Glu Pro Leu Pro Val
1 5 10 15
Gln Thr Leu Arg Pro Pro Pro Ala Ser Ser Ser Pro Thr Lys Pro Tyr
20 25 30
Ser Tyr Pro Ala Ala Ala Ala Ala Ala Ala Thr Pro Ala Ser
35 40 45
Arg Thr Ser Ser His Ala Ala Gln Ile Gly Pro Leu Ser Gly Gly Gly
50 55 60
Gly Leu Arg Pro Arg Asp Gly Arg Arg Gly Arg Arg Gly Val Val Ala
65 70 75 80
Gly Pro Gln Asp Arg Pro Ala Arg Ser Leu Pro Glu Glu Asp Arg Arg
85 90 95
Gly His Arg Gln Gly Asp Arg Gln Gly Leu Glu Gly Pro Pro Arg His
100 105 110
Arg Gln Ala His Arg Ala Glu Pro Ala Gly Gln Gly Leu Arg Arg Pro
115 120 125
Leu Arg Arg Gly Ala Arg His Gln Gly Ala Gln Gly Thr Arg Glu Gly
130 135 140
Gln Glu Glu Gly Gln Glu His Gln Ala Gln Arg Ala Thr Ser Ala Ser
145 150 155 160
Thr Thr Ser Ser Arg Ser Pro Arg Pro Met Arg Asn Arg Ser Met Ala
165 170 175
Lys Glu Leu Ala Gly Thr Val Lys Glu Ile Leu Gly Thr Cys Val Ser
180 185 190
Val Gly Cys Thr Val Asp Gly Lys Asp Pro Lys Asp Leu Gln Gln Glu
195 200 205
Ile Asp Asp Gly Glu Val Glu Ile Pro Ser Ala
210 215

(2) INFORMATION FOR SEQ ID NO:3273:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..251
(D) OTHER INFORMATION: / Ceres Seq. ID 1576275
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3273:
Gln Pro Pro Pro Ser Arg Ile Thr Lys Asn Ala Asn Arg Cys Gln Ser
1 5 10 15
Lys Pro Tyr Gly Arg Arg Gln His Gln Ala Pro Arg Pro Asn Pro Thr
20 25 30
Arg Thr Pro Pro Pro Pro Gln Pro Gln Pro Arg Pro His Gln Gln Ala
35 40 45
Glu Leu Ala Ala Met Pro Pro Lys Leu Asp Pro Ser Gln Val Val Glu
50 55 60
Val Phe Val Arg Val Thr Gly Gly Glu Val Gly Ala Ala Ser Ser Leu
65 70 75 80
Ala Pro Lys Ile Gly Pro Leu Gly Leu Ser Pro Lys Lys Ile Gly Glu

85 90 95
Asp Ile Ala Lys Glu Thr Ala Lys Asp Trp Lys Gly Leu Arg Val Thr
100 105 110
Val Lys Leu Thr Val Gln Asn Arg Gln Ala Lys Val Ser Val Val Pro
115 120 125
Ser Ala Ala Ala Leu Val Ile Lys Ala Leu Lys Glu Pro Glu Arg Asp
130 135 140
Arg Lys Lys Val Lys Asn Ile Lys His Ser Gly Gln His Gln Pro Arg
145 150 155 160
Arg Arg His Arg Asp Arg Gln Asp Pro Cys Gly Thr Gly Pro Trp Pro
165 170 175
Arg Ser Trp Pro Gly Pro Ser Arg Arg Ser Trp Gly Pro Ala Ser Ala
180 185 190
Ser Gly Ala Pro Ser Met Gly Arg Thr Pro Arg Thr Cys Ser Arg Arg
195 200 205
Ser Met Met Val Arg Ser Arg Ser Pro Gln Leu Lys Gly Tyr Thr Thr
210 215 220
Arg Asn His Arg Thr Leu Leu Lys Cys Gly Val Leu Phe Gln Xaa Ser
225 230 235 240
Ser Cys Thr Ser Ile Ala Tyr Tyr Cys Leu Leu
245 250

(2) INFORMATION FOR SEQ ID NO:3274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..199

(D) OTHER INFORMATION: / Ceres Seq. ID 1576276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3274:

Met Pro Pro Lys Leu Asp Pro Ser Gln Val Val Glu Val Phe Val Arg
1 5 10 15
Val Thr Gly Gly Glu Val Gly Ala Ala Ser Ser Leu Ala Pro Lys Ile
20 25 30
Gly Pro Leu Gly Leu Ser Pro Lys Lys Ile Gly Glu Asp Ile Ala Lys
35 40 45
Glu Thr Ala Lys Asp Trp Lys Gly Leu Arg Val Thr Val Lys Leu Thr
50 55 60
Val Gln Asn Arg Gln Ala Lys Val Ser Val Val Pro Ser Ala Ala Ala
65 70 75 80
Leu Val Ile Lys Ala Leu Lys Glu Pro Glu Arg Asp Arg Lys Lys Val
85 90 95
Lys Asn Ile Lys His Ser Gly Gln His Gln Pro Arg Arg Arg His Arg
100 105 110
Asp Arg Gln Asp Pro Cys Gly Thr Gly Pro Trp Pro Arg Ser Trp Pro
115 120 125
Gly Pro Ser Arg Arg Ser Trp Gly Pro Ala Ser Ala Ser Gly Ala Pro
130 135 140
Ser Met Gly Arg Thr Pro Arg Thr Cys Ser Arg Arg Ser Met Met Val
145 150 155 160
Arg Ser Arg Ser Pro Gln Leu Lys Gly Tyr Thr Thr Arg Asn His Arg
165 170 175
Thr Leu Leu Lys Cys Gly Val Leu Phe Gln Xaa Ser Ser Cys Thr Ser
180 185 190
Ile Ala Tyr Tyr Cys Leu Leu
195

(2) INFORMATION FOR SEQ ID NO:3275:

(i) SEQUENCE CHARACTERISTICS:

acgaagcaca	caacaaacct	gcagatcccc	catggcaggc	tccacctccc	tcgtwccctc	60
tcccgctmcc	gcccctccat	ctcgccaccc	cttccacacg	tccacgtccg	catccccccg	120
ccacctgcgc	ccctcccctg	ctacacgcct	ccgcgctgcc	cggcgctggc	atcccgacgc	180
cgtcgttgtc	gtcccagatg	ccgcgccctg	ggtcggcgat	ctatcgggcg	ccgcgcggtc	240
ctaccgggac	ggaagtgagg	aggacgaaga	cgacgcagat	gaagatgagg	acgaagacga	300
ggaccgcagc	ctggacctac	tggcccggtt	cctgcactcc	gtattcagga	aggcctcacg	360
ccGcgcSgcg	ccgCgctgcc	aggtcctg	tgcgccttc	cgccccgc	gagctggtga	420
agttttcggt	caatggcgtg	cttgtcctga	cgttcttatg	gacctgaag	ggtcttctcg	480
aggtgcgtcg	cacatttgga	agcattgtgt	tgttgAattc	gattcaagaT	tactgtacgc	540
tgcacgctct	tggagaaaaa	aagttttcgg	tgc			

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1576316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3276:

Arg 1	Ser	Thr	Gln	Gln 5	Thr	Cys	Arg	Ser	Pro 10	Met	Ala	Gly	Ser	Thr 15	Ser
Leu	Xaa	Pro	Leu	Pro 20	Xaa	Pro	Ala	Pro 25	Pro	Ser	Arg	His	Arg 30	Phe	His
Thr	Ser	Thr 35	Ser	Ala	Ser	Pro	Arg 40	His	Leu	Arg	Pro	Ser 45	Pro	Ala	Thr
Arg	Leu 50	Arg	Ala	Ala	Arg	Arg 55	Arg	His	Pro	Asp	Ala 60	Val	Val	Val	Val
Pro 65	Asp	Ala	Arg	Pro	Trp 70	Val	Gly	Asp	Leu	Ser 75	Gly	Ala	Ala	Ala	Ser 80
Tyr	Arg	Asp	Gly	Ser 85	Glu	Glu	Asp	Glu 90	Asp	Asp	Ala	Asp	Glu 95	Asp	Glu
Asp	Glu	Asp	Glu 100	Asp	Arg	Ser	Leu	Asp 105	Leu	Leu	Ala	Arg	Phe 110	Leu	His
Ser	Val	Phe 115	Arg	Lys	Ala	Ser	Arg 120	Arg	Xaa	Ala	Pro	Arg 125	Cys	Gln	Val
Arg	Ala 130	Ala	Ala	Phe	Arg	Pro 135	Arg	Arg	Ala	Gly	Glu 140	Val	Phe	Gly	Gln
Trp 145	Arg	Ala	Cys	Pro	Asp 150	Val	Leu	Met	Asp	Pro 155	Glu	Gly	Ser	Ser	Arg 160
Gly	Gly	Leu	His	Ile 165	Trp	Lys	His	Gly 170	Val	Trp					

(2) INFORMATION FOR SEQ ID NO:3277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 190 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..190

(D) OTHER INFORMATION: / Ceres Seq. ID 1576317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3277:

Glu Ala His Asn Lys Pro Ala Asp Pro Pro Trp Gln Ala Pro Pro Pro
1 5 10 15
Ser Xaa Pro Phe Pro Xaa Pro Pro Leu His Leu Ala Thr Ala Ser Thr
20 25 30
Arg Pro Arg Pro His Pro Pro Ala Thr Cys Ala Pro Pro Leu Leu His
35 40 45
Ala Ser Ala Leu Pro Gly Val Gly Ile Pro Thr Pro Ser Leu Ser Ser
50 55 60
Gln Met Pro Ala Pro Gly Ser Ala Ile Tyr Arg Ala Pro Pro Arg Pro
65 70 75 80
Thr Gly Thr Glu Val Arg Arg Thr Lys Thr Thr Gln Met Lys Met Arg
85 90 95
Thr Lys Thr Arg Thr Ala Ala Trp Thr Tyr Trp Pro Gly Ser Cys Thr
100 105 110
Pro Tyr Ser Gly Arg Pro His Ala Ala Xaa Arg Arg Ala Ala Arg Ser
115 120 125
Val Leu Pro Pro Ser Val Pro Ala Glu Leu Val Lys Phe Ser Val Asn
130 135 140
Gly Val Leu Val Leu Thr Phe Leu Trp Ile Leu Lys Gly Leu Leu Glu
145 150 155 160
Val Val Cys Thr Phe Gly Ser Met Val Phe Gly Asn Ser Ile Gln Asp
165 170 175
Tyr Cys Thr Leu Pro Ala Leu Gly Glu Lys Arg Phe Ser Val
180 185 190

(2) INFORMATION FOR SEQ ID NO:3278:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1576318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3278:

Met Ala Gly Ser Thr Ser Leu Xaa Pro Leu Pro Xaa Pro Ala Pro Pro
1 5 10 15
Ser Arg His Arg Phe His Thr Ser Thr Ser Ala Ser Pro Arg His Leu
20 25 30
Arg Pro Ser Pro Ala Thr Arg Leu Arg Ala Ala Arg Arg His Pro
35 40 45
Asp Ala Val Val Val Val Pro Asp Ala Arg Pro Trp Val Gly Asp Leu
50 55 60
Ser Gly Ala Ala Ala Ser Tyr Arg Asp Gly Ser Glu Glu Asp Glu Asp
65 70 75 80
Asp Ala Asp Glu Asp Glu Asp Glu Asp Glu Asp Arg Ser Leu Asp Leu
85 90 95
Leu Ala Arg Phe Leu His Ser Val Phe Arg Lys Ala Ser Arg Arg Xaa
100 105 110
Ala Pro Arg Cys Gln Val Arg Ala Ala Phe Arg Pro Arg Arg Ala
115 120 125
Gly Glu Val Phe Gly Gln Trp Arg Ala Cys Pro Asp Val Leu Met Asp
130 135 140
Pro Glu Gly Ser Ser Arg Gly Gly Leu His Ile Trp Lys His Gly Val
145 150 155 160

SEQUENCE: 1576317

Trp

(2) INFORMATION FOR SEQ ID NO:3279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..447
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3279:

aagacctcct	cgcggtatg	gcgaaGcgtc	tgatcccgtc	gctgaaccgg	gttctggtgg	60
agaagctgct	gaagcccagc	aagagcgccg	gcggcatcct	cctcccggag	accaccaagc	120
agctgaacgc	cgctaaagtc	gttgctgttg	gccctggtga	tcgtgatagg	gatggcaagc	180
tgatccctgt	atctctgagc	gaaggcgaca	ctgttctgct	tccggagtac	ggtgggacag	240
aagtgaagct	tcagaaaaa	gagtaccttc	ttttcagaga	gcacgacata	ctggggaagc	300
tcgaggagta	gctctggact	gttaaaatgg	agttgtttga	aagtaggtat	gcaagagttt	360
tgccacggct	tatctttttt	ttttgtacgg	gggaacaaat	gagaaacaca	acccttgtga	420
gaatgcaata	acactgcctc	attcttg				

(2) INFORMATION FOR SEQ ID NO:3280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3280:

Asp	Leu	Leu	Ala	Ala	Met	Ala	Lys	Arg	Leu	Ile	Pro	Ser	Leu	Asn	Arg	
1			5					10						15		
Val	Leu	Val	Glu	Lys	Leu	Leu	Lys	Pro	Ser	Lys	Ser	Ala	Gly	Gly	Ile	
			20					25					30			
Leu	Leu	Pro	Glu	Thr	Thr	Lys	Gln	Leu	Asn	Ala	Ala	Lys	Val	Val	Ala	
			35				40						45			
Val	Gly	Pro	Gly	Asp	Arg	Asp	Arg	Asp	Gly	Lys	Leu	Ile	Pro	Val	Ser	
	50					55					60					
Leu	Ser	Glu	Gly	Asp	Thr	Val	Leu	Leu	Pro	Glu	Tyr	Gly	Gly	Thr	Glu	
	65				70				75					80		
Val	Lys	Leu	Ala	Glu	Lys	Glu	Tyr	Leu	Leu	Phe	Arg	Glu	His	Asp	Ile	
			85					90						95		
Leu	Gly	Lys	Leu	Glu	Glu											
			100													

(2) INFORMATION FOR SEQ ID NO:3281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3281:

Met Ala Lys Arg Leu Ile Pro Ser Leu Asn Arg Val Leu Val Glu Lys

1 5 10 15
Leu Leu Lys Pro Ser Lys Ser Ala Gly Gly Ile Leu Leu Pro Glu Thr
20 25 30
Thr Lys Gln Leu Asn Ala Ala Lys Val Val Ala Val Gly Pro Gly Asp
35 40 45
Arg Asp Arg Asp Gly Lys Leu Ile Pro Val Ser Leu Ser Glu Gly Asp
50 55 60
Thr Val Leu Leu Pro Glu Tyr Gly Gly Thr Glu Val Lys Leu Ala Glu
65 70 75 80
Lys Glu Tyr Leu Leu Phe Arg Glu His Asp Ile Leu Gly Lys Leu Glu
85 90 95
Glu

(2) INFORMATION FOR SEQ ID NO:3282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..798
(D) OTHER INFORMATION: / Ceres Seq. ID 1576334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3282:

gcaaaaccct aaccttgct tgtgcgcast cogctattaa agtctgcgta cagtccgccc 60
cggctaggcg accgcatccg catctccctt acgtcttctc gccggtcgcg cacgggcaaaa 120
gcagcgatgg ctacagcgac ggcagttggt ggacccgaca ggtggagact gcggcgctcgt 180
ccgcgggcggc agtgctggcc gtcgccgttg cctcgsagag tgtrctaggt ctgctcgctc 240
ttgcggttca aactgtaaat gttggagcag aaatatataa taaagatcag cgggcaatat 300
acaagtattt atctGggaag aatcaaatct gaaaatgtcc ctgaaaataa ggatgggtca 360
gacgacgacg atgatgacga cgacgatgaa gacaatgacg atgagggtgg tgacgacgat 420
gatgatgctg aggaggaatt ctctggagaa gaagatgggg gtgatgacga tgatgaagat 480
gatgatcctg aagctaattg tgaaggagga agtgacaacg acaatgatga cgacgaagat 540
ggtgatgatg atggcgatga ggacgatgaa ggtgatgagg acgacgaaga cgaggacgat 600
gatgaagatg acgaagacca gccaccttcc aagaagaaga aatgatttgc tcatccatgg 660
atttacctca gcttctccat gctgttagtt gtgttggtta gatcatggac agctttggga 720
tcaatgtagc ttgttgcttg tcatggtatc gtagtgtagg aaaatttgac atctgatgtt 780
aaatcactat cctgcttt

(2) INFORMATION FOR SEQ ID NO:3283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..128
(D) OTHER INFORMATION: / Ceres Seq. ID 1576335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3283:

Met Leu Glu Gln Lys Tyr Ile Ile Lys Ile Ser Gly Gln Tyr Thr Ser
1 5 10 15
Tyr Tyr Leu Gly Arg Ile Lys Ser Glu Asn Val Pro Glu Asn Lys Asp
20 25 30
Gly Ser Asp Asp Asp Asp Asp Asp Asp Asp Asp Glu Asp Asn Asp Asp
35 40 45
Glu Gly Gly Asp Asp Asp Asp Asp Ala Glu Glu Glu Phe Ser Gly Glu
50 55 60
Glu Asp Gly Gly Asp Asp Asp Asp Glu Asp Asp Asp Pro Glu Ala Asn
65 70 75 80

Gly Glu Gly Gly Ser Asp Asn Asp Asn Asp Asp Asp Glu Asp Gly Asp
85 90 95
Asp Asp Gly Asp Glu Asp Asp Glu Gly Asp Glu Asp Asp Glu Asp Glu
100 105 110
Asp Asp Asp Glu Asp Asp Glu Asp Gln Pro Pro Ser Lys Lys Lys Lys
115 120 125

(2) INFORMATION FOR SEQ ID NO:3284:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1576336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3284:

Met Ser Leu Lys Ile Arg Met Gly Gln Thr Thr Met Met Thr Thr
1 5 10 15
Thr Met Lys Thr Met Thr Met Arg Val Val Thr Thr Met Met Met Leu
20 25 30
Arg Arg Asn Ser Leu Glu Lys Lys Met Gly Val Met Thr Met Met Lys
35 40 45
Met Met Ile Leu Lys Leu Met Val Lys Glu Glu Val Thr Thr Thr Met
50 55 60
Met Thr Thr Lys Met Val Met Met Met Ala Met Arg Thr Met Lys Val
65 70 75 80
Met Arg Thr Thr Lys Thr Arg Thr Met Met Lys Met Thr Lys Thr Ser
85 90 95
His Leu Pro Arg Arg Arg Asn Asp Leu Leu Ile His Gly Phe Thr Ser
100 105 110
Ala Ser Pro Cys Cys
115

(2) INFORMATION FOR SEQ ID NO:3285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1576337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3285:

Met Gly Gln Thr Thr Thr Met Met Thr Thr Thr Met Lys Thr Met Thr
1 5 10 15
Met Arg Val Val Thr Thr Met Met Met Leu Arg Arg Asn Ser Leu Glu
20 25 30
Lys Lys Met Gly Val Met Thr Met Met Lys Met Met Ile Leu Lys Leu
35 40 45
Met Val Lys Glu Glu Val Thr Thr Thr Met Met Thr Thr Lys Met Val
50 55 60
Met Met Met Ala Met Arg Thr Met Lys Val Met Arg Thr Thr Lys Thr
65 70 75 80
Arg Thr Met Met Lys Met Thr Lys Thr Ser His Leu Pro Arg Arg Arg
85 90 95
Asn Asp Leu Leu Ile His Gly Phe Thr Ser Ala Ser Pro Cys Cys

100 105 110

(2) INFORMATION FOR SEQ ID NO:3286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 646 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..646

(D) OTHER INFORMATION: / Ceres Seq. ID 1576347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3286:

gacgggagaa aatctccaaa cgcagcaran mccctcgcgc cgccgacctc ttcagcctcg	60
cagcacaccg ccgccagccc gagtgaccgc tgcagcctag ggtttccgtc ggcgatggcg	120
ggtaargrag ggaagggtct gctggcggcc aagacgacgg cggccaagag caccgacaag	180
gacaaggaca ggaagaargc ccccggtgctg cgctcctccc gcgccggcct ccagttcccg	240
gtgggtcgca tccaccgcca gctcaagtcg cgtgcctctg cgcacggccg cgtcggcgcc	300
accgcccgcg tctattccgc cgccatcctc gagtacctca ccgccgaggt cctcgagctg	360
gGccggcaac gccagcaagg acctcaaggt caagcgcctc accccgcgcc acctgcagct	420
cgccatccgc ggggacgagg agctcgacac cctcatcaag ggaccatcg ccgggggccc	480
cgtcattccc cacatccaca agtcgctcat caacaagacc gccaggagt gaatcaaggc	540
cgtgctgctg cttctgcctg actacagtcc catctcgttc tgtacttggt caatctgagt	600
ttaagtgcag gttggcacag ttctagtaaa ctcctcctgt tcacct	

(2) INFORMATION FOR SEQ ID NO:3287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..186

(D) OTHER INFORMATION: / Ceres Seq. ID 1576348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3287:

Asp Gly Arg Lys Ser Pro Asn Ala Ala Xaa Xaa Leu Ala Pro Pro Thr	
1 5 10 15	
Ser Ser Ala Ser Gln His Thr Ala Ala Ser Pro Ser Asp Arg Cys Ser	
20 25 30	
Leu Gly Phe Pro Ser Ala Met Ala Gly Xaa Xaa Gly Lys Gly Leu Leu	
35 40 45	
Ala Ala Lys Thr Thr Ala Ala Lys Ser Thr Asp Lys Asp Lys Asp Arg	
50 55 60	
Lys Xaa Ala Pro Val Ser Arg Ser Ser Arg Ala Gly Leu Gln Phe Pro	
65 70 75 80	
Val Gly Arg Ile His Arg Gln Leu Lys Ser Arg Ala Ser Ala His Gly	
85 90 95	
Arg Val Gly Ala Thr Ala Ala Val Tyr Ser Ala Ala Ile Leu Glu Tyr	
100 105 110	
Leu Thr Ala Glu Val Leu Glu Leu Gly Arg Gln Arg Gln Gln Gly Pro	
115 120 125	
Gln Gly Gln Ala His His Pro Ala Pro Pro Ala Ala Arg His Pro Arg	
130 135 140	
Gly Arg Gly Ala Arg His Pro His Gln Gly His His Arg Arg Gly Arg	
145 150 155 160	
Arg His Pro Ala His Pro Gln Val Ala His Gln Gln Asp Arg Gln Gly	
165 170 175	
Val Asn Gln Gly Arg Ala Ala Ala Ser Ala	
180 185	

(2) INFORMATION FOR SEQ ID NO:3288:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 148 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..148
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576349
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3288:

Met Ala Gly Xaa Xaa Gly Lys Gly Leu Leu Ala Ala Lys Thr Thr Ala
1 5 10 15
Ala Lys Ser Thr Asp Lys Asp Lys Asp Arg Lys Xaa Ala Pro Val Ser
 20 25 30
Arg Ser Ser Arg Ala Gly Leu Gln Phe Pro Val Gly Arg Ile His Arg
 35 40 45
Gln Leu Lys Ser Arg Ala Ser Ala His Gly Arg Val Gly Ala Thr Ala
 50 55 60
Ala Val Tyr Ser Ala Ala Ile Leu Glu Tyr Leu Thr Ala Glu Val Leu
65 70 75 80
Glu Leu Gly Arg Gln Arg Gln Gln Gly Pro Gln Gly Gln Ala His His
 85 90 95
Pro Ala Pro Pro Ala Ala Arg His Pro Arg Gly Arg Gly Ala Arg His
 100 105 110
Pro His Gln Gly His His Arg Arg Gly Arg Arg His Pro Ala His Pro
 115 120 125
Gln Val Ala His Gln Gln Asp Arg Gln Gly Val Asn Gln Gly Arg Ala
130 135 140
Ala Ala Ser Ala
145

(2) INFORMATION FOR SEQ ID NO:3289:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 454 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..454
(D) OTHER INFORMATION: / Ceres Seq. ID 1576358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3289:

tatccaaatt caaatcag acaatgagt atgcagacaa gctagctgct ggcattgcag 60
cacctgtggg tggagtgatg acagagtgtg gtaccaatcc tcctgtcgaa catattctct 120
cagctgagga tgcagagtgc tgtatctgcc tatgccgta tgaagatggc gtggaactac 180
gtgagcttcc ttgcaaccac cattttcact gcagctgcat tgacaagtgg cttcacataa 240
atgctacatg ccattgtgc aagttcgaca tcatcaagag caaccgtgac atagaagagg 300
tctaggtcac taaggaaaaa acgccgcaaa acttttgtca tgtctctgct gtgttcttca 360
gtactaccgc taccacattt gcgatactga gttgtgatta ccggtccttt aggtgatgca 420
caaatggtac tcgGtgaata ttcttttat tagc

(2) INFORMATION FOR SEQ ID NO:3290:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1576359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3290:

Ser Lys Phe Lys Phe Gln Thr Met Ser Asp Ala Asp Lys Leu Ala Ala
1 5 10 15
Gly Ile Ala Ala Pro Val Gly Gly Val Met Thr Glu Cys Gly Thr Asn
20 25 30
Pro Pro Val Glu His Ile Leu Ser Ala Glu Asp Ala Glu Cys Cys Ile
35 40 45
Cys Leu Cys Pro Tyr Glu Asp Gly Val Glu Leu Arg Glu Leu Pro Cys
50 55 60
Asn His His Phe His Cys Ser Cys Ile Asp Lys Trp Leu His Ile Asn
65 70 75 80
Ala Thr Cys Pro Leu Cys Lys Phe Asp Ile Ile Lys Ser Asn Arg Asp
85 90 95
Ile Glu Glu Val
100

(2) INFORMATION FOR SEQ ID NO:3291:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1576360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3291:

Met Ser Asp Ala Asp Lys Leu Ala Ala Gly Ile Ala Ala Pro Val Gly
1 5 10 15
Gly Val Met Thr Glu Cys Gly Thr Asn Pro Pro Val Glu His Ile Leu
20 25 30
Ser Ala Glu Asp Ala Glu Cys Cys Ile Cys Leu Cys Pro Tyr Glu Asp
35 40 45
Gly Val Glu Leu Arg Glu Leu Pro Cys Asn His His Phe His Cys Ser
50 55 60
Cys Ile Asp Lys Trp Leu His Ile Asn Ala Thr Cys Pro Leu Cys Lys
65 70 75 80
Phe Asp Ile Ile Lys Ser Asn Arg Asp Ile Glu Glu Val
85 90

(2) INFORMATION FOR SEQ ID NO:3292:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1576361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3292:

Met Thr Glu Cys Gly Thr Asn Pro Pro Val Glu His Ile Leu Ser Ala
1 5 10 15
Glu Asp Ala Glu Cys Cys Ile Cys Leu Cys Pro Tyr Glu Asp Gly Val
20 25 30
Glu Leu Arg Glu Leu Pro Cys Asn His His Phe His Cys Ser Cys Ile
35 40 45
Asp Lys Trp Leu His Ile Asn Ala Thr Cys Pro Leu Cys Lys Phe Asp
50 55 60
Ile Ile Lys Ser Asn Arg Asp Ile Glu Glu Val

65

70

75

(2) INFORMATION FOR SEQ ID NO:3293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..339
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3293:

aacaacagcg aacacaNtct gCttcgcat ttttcccatc ccccttcgca acccaaacc	60
caacNtcgCt ccgcatcgat ggcgcccgaag gccgagaaga agcccgcggc gaagaagccg	120
gcggaggagg agcccgcggc tgagaaggcg cccgccggga agaagcagag gtgggggttg	180
ttcattgccca ccaagtgatt tggcctggca gcaggagggc ttttcggaat aagaatggat	240
gtggctgtaa ctctgcttct agaccgtga tggttcagct tagaagcagg ggatcttcat	300
catcagaata aaaacgtgtg ctgtgtgtt gctgtgtcc	

(2) INFORMATION FOR SEQ ID NO:3294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3294:

Asn Asn Ser Glu His Xaa Leu Leu Arg Ile Ser Ser His Pro Pro Ser	
1 5 10 15	
Gln Pro Lys Pro Gln Xaa Arg Ser Ala Ser Met Ala Pro Lys Ala Glu	
20 25 30	
Lys Lys Pro Ala Ala Lys Lys Pro Ala Glu Glu Glu Pro Ala Ala Glu	
35 40 45	
Lys Ala Pro Ala Gly Lys Lys Gln Arg Trp Gly Leu Phe Ile Ala Thr	
50 55 60	
Lys	

65

(2) INFORMATION FOR SEQ ID NO:3295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3295:

Thr Thr Ala Asn Thr Xaa Cys Phe Ala Phe Leu Pro Ile Pro Leu Arg	
1 5 10 15	
Asn Pro Asn Pro Asn Xaa Ala Pro His Arg Trp Arg Pro Arg Pro Arg	
20 25 30	
Arg Ser Pro Arg Arg Arg Ser Arg Arg Arg Arg Ser Pro Arg Leu Arg	
35 40 45	
Arg Arg Pro Pro Gly Arg Ser Arg Gly Gly Gly Cys Ser Leu Pro Pro	
50 55 60	

Ser Asp Leu Ala Trp Gln Gln Glu Gly Ser Ser Glu
65 70 75

(2) INFORMATION FOR SEQ ID NO:3296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3296:

Gln Gln Arg Thr Xaa Ser Ala Ser His Phe Phe Pro Ser Pro Phe Ala
1 5 10 15
Thr Gln Thr Pro Xaa Ser Leu Arg Ile Asp Gly Ala Gln Gly Arg Glu
20 25 30
Glu Ala Arg Gly Glu Glu Ala Gly Gly Gly Gly Ala Arg Gly
35 40 45

(2) INFORMATION FOR SEQ ID NO:3297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..634
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3297:

acccaagtcc aagcaccttc ccaaaaaaat cccccatttt cttcgaggcg aggagagcgt 60
gaaagacagg gcaccggcag cgacgatgtc ggggcgcggc aagggcggca aaggtctggs 120
caaggcgga Gcaaagcgcc accgtaaggT gctccgtgac aacatccagg gcatcaccaa 180
gcccgcgatc cgtaggctgg ctccggagggg cggcgtgaag cgcatttcgg ggcttatcta 240
cgaggagggt aagactgtgg acctctatgt ccccaggaag tgctcggcca caaacaggat 300
catcactgcc aaggaccatg cctctgtcca gatcaacatt ggccacttgg atgcgaatgg 360
cctgtatgat ggtcacttca caacgtttgc tctctctggg tttgtccgtg ctcagggtga 420
cgcagacagc tccttggaca ggctgtggca aaagaagaag gctgatatca agcagtagat 480
tttacatcta gtttaccaag aattggacac cgccttagct atgttttgaa ttcattgtcac 540
tatatgcAat gttgtgattt cagctgggtac cttaaactctg aagatttagt atctttgttg 600
ggttccttct gagtttgatg tgtggtgttc gttt

(2) INFORMATION FOR SEQ ID NO:3298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3298:

Pro Lys Ser Lys His Leu Pro Lys Lys Ile Pro His Phe Leu Arg Gly
1 5 10 15
Glu Glu Ser Val Lys Asp Arg Ala Pro Ala Ala Thr Met Ser Gly Arg
20 25 30
Gly Lys Gly Gly Lys Gly Leu Xaa Lys Gly Gly Ala Lys Arg His Arg
35 40 45

Lys Val Leu Arg Asp Asn Ile Gln Gly Ile Thr Lys Pro Ala Ile Arg
50 55 60
Arg Leu Ala Arg Arg Gly Gly Val Lys Arg Ile Ser Gly Leu Ile Tyr
65 70 75 80
Glu Glu Gly Lys Thr Val Asp Leu Tyr Val Pro Arg Lys Cys Ser Ala
85 90 95
Thr Asn Arg Ile Ile Thr Ala Lys Asp His Ala Ser Val Gln Ile Asn
100 105 110
Ile Gly His Leu Asp Ala Asn Gly Leu Tyr Asp Gly His Phe Thr Thr
115 120 125
Phe Ala Leu Ser Gly Phe Val Arg Ala Gln Gly Asp Ala Asp Ser Ser
130 135 140
Leu Asp Arg Leu Trp Gln Lys Lys Lys Ala Asp Ile Lys Gln
145 150 155

(2) INFORMATION FOR SEQ ID NO:3299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3299:

Met Ser Gly Arg Gly Lys Gly Gly Lys Gly Leu Xaa Lys Gly Gly Ala
1 5 10 15
Lys Arg His Arg Lys Val Leu Arg Asp Asn Ile Gln Gly Ile Thr Lys
20 25 30
Pro Ala Ile Arg Arg Leu Ala Arg Arg Gly Gly Val Lys Arg Ile Ser
35 40 45
Gly Leu Ile Tyr Glu Glu Gly Lys Thr Val Asp Leu Tyr Val Pro Arg
50 55 60
Lys Cys Ser Ala Thr Asn Arg Ile Ile Thr Ala Lys Asp His Ala Ser
65 70 75 80
Val Gln Ile Asn Ile Gly His Leu Asp Ala Asn Gly Leu Tyr Asp Gly
85 90 95
His Phe Thr Thr Phe Ala Leu Ser Gly Phe Val Arg Ala Gln Gly Asp
100 105 110
Ala Asp Ser Ser Leu Asp Arg Leu Trp Gln Lys Lys Lys Ala Asp Ile
115 120 125
Lys Gln
130

(2) INFORMATION FOR SEQ ID NO:3300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..847
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3300:

acaaaatgaa gatgaagatg aagaagttga tgaaagtga gaagctgcag atgattcacg	60
caagcctgca acatcaattg gctcagcata cagactgctt actccatcag taaaggtcca	120
gttggttgata tacttcatgc tgaaatacgc aatggagatt ttgctttcag agtctagtgt	180
tatcactaat cactatttca gttggaacac aagcgcagtg gncaattttt ctagcaatcc	240
ttgggttgac ggtgcttcct gttaatgctg ttgttggaac atacatcagc aatatgtttg	300

aggacaggca actgctcatg gtctctcaaa ttacgttgct agtaggcatt atcttcagct 360
tcaaggttac gagtacatac tctgttgctc agtatgttgt ctcagcactt gtcacatttg 420
tttctgcaga agttcttgaa ggtgtgaacc ttccctcct atcaagcgtg atgtcatctc 480
gcctctcccg tggcacatac aacggtggcc tcctctcgac ggaggccVgg gaccctggcg 540
aggggtggctg ctgactgcac catcactgcg gcggggtacc tgggcgtggg gaagcttctc 600
aacgtcaccc tgctaccatc cctggtgata tgtgttgctg ccattgcctg caccttcctg 660
acataatact cgcttttctg atggagcttc acaatgtatt tgtgtcatca tgattcgttc 720
catattagcg caaatcaagg cagctgggag accgccattg ccattgcccg aaggggctat 780
tgtattacta ttattatatg ttogtcgatt tgattgctat aaattgattg ataaaatgat 840
tgtagcg

(2) INFORMATION FOR SEQ ID NO:3301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3301:

Gln Asn Glu Asp Glu Asp Glu Glu Val Asp Glu Ser Glu Glu Ala Ala
1 5 10 15
Asp Asp Ser Arg Lys Pro Ala Thr Ser Ile Gly Ser Ala Tyr Arg Leu
20 25 30
Leu Thr Pro Ser Val Lys Val Gln Leu Leu Ile Tyr Phe Met Leu Lys
35 40 45
Tyr Ala Met Glu Ile Leu Leu Ser Glu Ser Ser Val Ile Thr Asn His
50 55 60
Tyr Phe Ser Trp Asn Thr Ser Ala Val Xaa Asn Phe Ser Ser Asn Pro
65 70 75 80
Trp Val Asp Gly Ala Ser Cys
85

(2) INFORMATION FOR SEQ ID NO:3302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3302:

Met Phe Glu Asp Arg Gln Leu Leu Met Val Ser Gln Ile Thr Leu Leu
1 5 10 15
Val Gly Ile Ile Phe Ser Phe Lys Val Thr Ser Thr Tyr Ser Val Val
20 25 30
Gln Tyr Val Val Ser Ala Leu Val Thr Phe Val Ser Ala Glu Val Leu
35 40 45
Glu Gly Val Asn Leu Ser Leu Leu Ser Ser Val Met Ser Ser Arg Leu
50 55 60
Ser Arg Gly Thr Tyr Asn Gly Gly Leu Leu Ser Thr Glu Ala Xaa Asp
65 70 75 80
Pro Gly Glu Gly Gly Arg
85

(2) INFORMATION FOR SEQ ID NO:3303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids

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- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..78
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3303:

```
Met Val Ser Gln Ile Thr Leu Leu Val Gly Ile Ile Phe Ser Phe Lys
1           5           10           15
Val Thr Ser Thr Tyr Ser Val Val Gln Tyr Val Val Ser Ala Leu Val
          20           25           30
Thr Phe Val Ser Ala Glu Val Leu Glu Gly Val Asn Leu Ser Leu Leu
          35           40           45
Ser Ser Val Met Ser Ser Arg Leu Ser Arg Gly Thr Tyr Asn Gly Gly
          50           55           60
Leu Leu Ser Thr Glu Ala Xaa Asp Pro Gly Glu Gly Gly Arg
65           70           75
```

(2) INFORMATION FOR SEQ ID NO:3304:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 688 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..688
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3304:

```
ccacccaccc ccacacccac gagcccgcg gcggtgtctc tgctgtctgc tctgcaccca      60
ggaccttcgg ccacaggagc tcagccctat ccctcgacgg tgctcgcggc cggcgcgcg      120
cggtcgcacc ctccccatc tccagctcca cgccgtctcc accgcctgga atccagggcc      180
tccgacgcca cccacctcc accgcctgga atcgaggacc gtcggcgtcc ttcagatcag      240
cggcgagcgc aacaaggagc aggaggagaa gacggacacc tggcaccgcg tggagcggag      300
cagcgggaga ttctgcgca ggttccgact gcccgagAAC gccaagacgg agcagatcag      360
ggccgccatg gagaacggcg tgcttacagt cactgtgcc aaggaggacg ccaagaagcc      420
CCtgaagtga agtccattca gatctccggc tagacctgg tctgcggtcg tctgtacctgc      480
gtggtttgag gaacggcagt tcgcctcggt cggtctgtga aataaaattg gggtacaaga      540
attatggcgt ttgtcaatat gatcgtaatg tcgtaggatg gtggaatgtg gtcacaaact      600
ttgcgtatgt tgggtctact ggtggtgtct actctgaatc tatgtatgga tgtcatgagt      660
tccagttcct gtggtgttcg tatgatgc
```

(2) INFORMATION FOR SEQ ID NO:3305:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..150
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3305:

```
Pro Pro Thr Pro Thr Pro Thr Ser Pro Ala Ala Cys Ser Leu Leu Ser
1           5           10           15
Ala Leu His Pro Gly Pro Ser Ala Thr Gly Ala Gln Pro Tyr Pro Ser
          20           25           30
Thr Val Leu Ala Ala Gly Ala Arg Arg Leu Asp Pro Ser Pro Ser Pro
          35           40           45
```

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Ala Pro Arg Arg Leu His Arg Leu Glu Ser Arg Ala Ser Asp Ala Thr
50 55 60
Pro Pro Pro Pro Pro Gly Ile Glu Asp Arg Arg Arg Pro Ser Asp Gln
65 70 75 80
Arg Arg Ala Gln Gln Gly Ala Gly Gly Glu Asp Gly His Leu Ala Pro
85 90 95
Arg Gly Ala Glu Gln Arg Glu Ile Pro Ala Gln Val Pro Thr Ala Arg
100 105 110
Glu Arg Gln Asp Gly Ala Asp Gln Gly Arg His Gly Glu Arg Arg Ala
115 120 125
Tyr Ser His Cys Ala Gln Gly Arg Gln Glu Ala Pro Glu Val Lys
130 135 140
Ser Ile Gln Ile Ser Gly
145 150

(2) INFORMATION FOR SEQ ID NO:3306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3306:

His Pro Pro Pro His Pro Arg Ala Arg Arg Ala Leu Cys Cys Leu
1 5 10 15
Leu Cys Thr Gln Asp Leu Arg Pro Gln Glu Leu Ser Pro Ile Pro Arg
20 25 30
Arg Cys Ser Arg Pro Ala Arg Gly Gly Ser Thr Leu Pro His Leu Gln
35 40 45
Leu His Ala Val Ser Thr Ala Trp Asn Pro Gly Pro Pro Thr Pro Pro
50 55 60
His Leu His Arg Leu Glu Ser Arg Thr Val Gly Val Leu Gln Ile Ser
65 70 75 80
Gly Glu Arg Asn Lys Glu Gln Glu Glu Lys Thr Asp Thr Trp His Arg
85 90 95
Val Glu Arg Ser Ser Gly Arg Phe Leu Arg Arg Phe Arg Leu Pro Glu
100 105 110
Asn Ala Lys Thr Glu Gln Ile Arg Ala Ala Met Glu Asn Gly Val Leu
115 120 125
Thr Val Thr Val Pro Lys Glu Asp Ala Lys Lys Pro Leu Lys
130 135 140

(2) INFORMATION FOR SEQ ID NO:3307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3307:

Thr His Pro His Thr His Glu Pro Gly Gly Val Leu Ser Ala Val Cys
1 5 10 15
Ser Ala Pro Arg Thr Phe Gly His Arg Ser Ser Ala Leu Ser Leu Asp
20 25 30
Gly Ala Arg Gly Arg Arg Ala Ala Ala Arg Pro Phe Pro Ile Ser Ser

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35	40	45
Ser Thr Pro Ser Pro Pro Pro Gly Ile Gln Gly Leu Arg Arg His Pro		
50	55	60
Thr Ser Thr Ala Trp Asn Arg Gly Pro Ser Ala Ser Phe Arg Ser Ala		
65	70	75
Ala Ser Ala Thr Arg Ser Arg Arg Arg Arg Arg Thr Pro Gly Thr Ala		
85	90	95
Trp Ser Gly Ala Ala Gly Asp Ser Cys Ala Gly Ser Asp Cys Pro Arg		
100	105	110
Thr Pro Arg Arg Ser Arg Ser Gly Pro Pro Trp Arg Thr Ala Cys Leu		
115	120	125
Gln Ser Leu Cys Pro Arg Arg Thr Pro Arg Ser Pro		
130	135	140

(2) INFORMATION FOR SEQ ID NO:3308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..425
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3308:

atccagttac agtccggagt ctggttagta ctccgcatgt tcgttctttt tacgccgacg	60
gaaatcaacc tgcgcogctg ccttctccgt tctcgccgtc gcctccgcct ccgctgccgc	120
cgcgccaggtc agggtcattgt cgatcttcga gtacaacggg agcgccgtgg tggcgatggt	180
ggggaagaac tgCttcgcca tcgccagcga ccgccgcctc ggcgtgcagc tgcagacgat	240
cgccaccgac ttccgacggg tgttcaaggt ccacgacaag ctctacatcg ggctctcggg	300
gctcgccacc gacgccaga cgctgtatca gcgctggtg ttcaggcaca agttgtacca	360
gctgagggag gagagggaca tgaagccga agcctttgcc agccttgttt cagccctcct	420
ctatg	

(2) INFORMATION FOR SEQ ID NO:3309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3309:

Ile Gln Leu Gln Ser Gly Val Trp Leu Val Leu Arg Met Phe Val Leu	
1	5
Phe Thr Pro Thr Glu Ile Asn Leu Arg Arg Cys Leu Leu Arg Ser Arg	10
20	25
Arg Arg Leu Arg Leu Arg Cys Arg Arg Ala Gly Gln Gly His Val Asp	30
35	40
Leu Arg Val Gln Arg Glu Arg Arg Gly Gly Asp Gly Gly Glu Glu Leu	45
50	55
Leu Arg Asp Arg Gln Arg Pro Pro Pro Arg Arg Ala Ala Ala Asp Asp	60
65	70
Arg His Arg Leu Pro Thr Gly Val Gln Gly Pro Arg Gln Ala Leu His	75
85	90
Arg Ala Leu Gly Ala Arg His Arg Arg Pro Asp Ala Val Ser Ala Ala	95
100	105
Gly Val Gln Ala Gln Val Val Pro Ala Glu Gly Gly Glu Gly His Glu	110
115	120

Ala Arg Ser Leu Cys Gln Pro Cys Phe Ser Pro Pro Leu
130 135 140

(2) INFORMATION FOR SEQ ID NO:3310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1576407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3310:

Pro Val Thr Val Arg Ser Leu Val Ser Thr Pro His Val Arg Ser Phe
1 5 10 15
Tyr Ala Asp Gly Asn Gln Pro Ala Pro Leu Pro Ser Pro Phe Ser Pro
20 25 30
Ser Pro Pro Pro Leu Pro Pro Arg Arg Ser Gly Ser Cys Arg Ser
35 40 45
Ser Ser Thr Thr Gly Ala Pro Trp Trp Arg Trp Trp Gly Arg Thr Ala
50 55 60
Ser Arg Ser Pro Ala Thr Ala Ala Ser Ala Cys Ser Cys Arg Arg Ser
65 70 75 80
Pro Pro Thr Ser Asp Gly Cys Ser Arg Ser Thr Thr Ser Ser Thr Ser
85 90 95
Gly Ser Arg Gly Ser Pro Pro Thr Pro Arg Arg Cys Ile Ser Gly Trp
100 105 110
Cys Ser Gly Thr Ser Cys Thr Ser
115 120

(2) INFORMATION FOR SEQ ID NO:3311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1576408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3311:

Met Phe Val Leu Phe Thr Pro Thr Glu Ile Asn Leu Arg Arg Cys Leu
1 5 10 15
Leu Arg Ser Arg Arg Arg Leu Arg Leu Arg Cys Arg Arg Ala Gly Gln
20 25 30
Gly His Val Asp Leu Arg Val Gln Arg Glu Arg Arg Gly Gly Asp Gly
35 40 45
Gly Glu Glu Leu Leu Arg Asp Arg Gln Arg Pro Pro Pro Arg Arg Ala
50 55 60
Ala Ala Asp Asp Arg His Arg Leu Pro Thr Gly Val Gln Gly Pro Arg
65 70 75 80
Gln Ala Leu His Arg Ala Leu Gly Ala Arg His Arg Arg Pro Asp Ala
85 90 95
Val Ser Ala Ala Gly Val Gln Ala Gln Val Val Pro Ala Glu Gly Gly
100 105 110
Glu Gly His Glu Ala Arg Ser Leu Cys Gln Pro Cys Phe Ser Pro Pro
115 120 125
Leu

(2) INFORMATION FOR SEQ ID NO:3312:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 986 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..986
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576429
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3312:

aacgctgcct tcccgcggtt atcctttccc acgactcctc tccccgcggt gagaacatgc 60
cccgcgtcct tgtccaggca ccattgcgcg cggccgctgc ctcccttgca ccatcggcct 120
ctacagatga agctcaaagg aagtgaactc aaattatcac tcaagaatct caagagcatt 180
tggtgaagag tgtttctctg attttgtgaa tgtccagtat gcagtgaact tctagaagtt 240
tttatttatg tatgcatgtt ttaaatactt tgatcaatgg atgcttataa agattctatg 300
gaatttctgg aggagttatc tgtctttgat cttcatctgt ggaggccgtg gtggccggtt 360
cggcggcggg ttccgcgcagc agggcccgcg cgcagaggtc gtcgaggtgt cgacgttcgt 420
gcacgcgtgc gagggagacg cggtgacgaa actcaccaac gagaaGgtgc cctacttcaa 480
cgcgcccata tacctgcaga acaagactca ggtcggcaag gtcgacgaga tcttcggccc 540
catcaacgaa tcctatttct ctgtgaagat gatggaagg atcattgcaa catcgtacaa 600
ggaaggcgac aagttctata tcgaccccat gaaattgctg cctctttcgc gcttcctgcc 660
gcaaccaag ggacaatctc aaggagcacc tagaggtggt ggccgtgtgg aaggggtggt 720
ggccgaggcc gtggtggttc gttccggggt ggaagaggac caccaagggg tgggtggcca 780
ggtccaaggg gtggaagccg tgggtggttt agagggcgag gaaggttcta ggtgtagttt 840
gagtttgatg atgttttttt ttgttgaggc atcatagcta cccaattgga aacttccatg 900
ttcttgtaac ctgatatgtt taaggtagca gaacactttg tttgtggaac ttggattctc 960
aattgaaaca aagggtttgt acctgt

(2) INFORMATION FOR SEQ ID NO:3313:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..209
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576430
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3313:

Met Tyr Ala Cys Phe Lys Tyr Phe Asp Gln Trp Met Leu Ile Lys Ile
1 5 10 15
Leu Trp Asn Phe Trp Arg Ser Tyr Leu Ser Leu Ile Phe Ile Cys Gly
20 25 30
Gly Arg Gly Gly Arg Phe Gly Gly Phe Arg Asp Glu Gly Pro Pro
35 40 45
Ala Glu Val Val Glu Val Ser Thr Phe Val His Ala Cys Glu Gly Asp
50 55 60
Ala Val Thr Lys Leu Thr Asn Glu Lys Val Pro Tyr Phe Asn Ala Pro
65 70 75 80
Ile Tyr Leu Gln Asn Lys Thr Gln Val Gly Lys Val Asp Glu Ile Phe
85 90 95
Gly Pro Ile Asn Glu Ser Tyr Phe Ser Val Lys Met Met Glu Gly Ile
100 105 110
Ile Ala Thr Ser Tyr Lys Glu Gly Asp Lys Phe Tyr Ile Asp Pro Met
115 120 125
Lys Leu Leu Pro Leu Ser Arg Phe Leu Pro Gln Pro Lys Gly Gln Ser
130 135 140
Gln Gly Ala Pro Arg Gly Gly Gly Arg Val Glu Gly Val Val Ala Glu
145 150 155 160
Ala Val Val Val Arg Ser Gly Val Glu Glu Asp His Gln Gly Val Val

	165		170		175										
Ala	Glu	Val	Gln	Gly	Val	Glu	Ala	Val	Val	Val	Leu	Glu	Gly	Glu	Glu
	180						185						190		
Gly	Ser	Arg	Cys	Ser	Leu	Ser	Leu	Met	Met	Phe	Phe	Phe	Val	Glu	Ala
	195						200						205		
Ser															

(2) INFORMATION FOR SEQ ID NO:3314:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1576431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3314:

Met	Asp	Ala	Tyr	Lys	Asp	Ser	Met	Glu	Phe	Leu	Glu	Glu	Leu	Ser	Val
1			5					10						15	
Phe	Asp	Leu	His	Leu	Trp	Arg	Pro	Trp	Trp	Pro	Val	Arg	Arg	Arg	Val
		20					25						30		
Pro	Arg	Arg	Gly	Pro	Ala	Arg	Arg	Gly	Arg	Arg	Gly	Val	Asp	Val	Arg
		35				40						45			
Ala	Arg	Val	Arg	Gly	Arg	Arg	Gly	Asp	Glu	Thr	His	Gln	Arg	Glu	Gly
		50				55					60				
Ala	Leu	Leu	Gln	Arg	Ala	His	Ile	Pro	Ala	Glu	Gln	Asp	Ser	Gly	Arg
65			70						75					80	
Gln	Gly	Arg	Arg	Asp	Leu	Arg	Pro	His	Gln	Arg	Ile	Leu	Phe	Leu	Cys
		85						90						95	
Glu	Asp	Asp	Gly	Arg	Asp	His	Cys	Asn	Ile	Val	Gln	Gly	Arg	Arg	Gln
		100					105						110		
Val	Leu	Tyr	Arg	Pro	His	Glu	Ile	Ala	Ala	Ser	Phe	Ala	Leu	Pro	Ala
		115				120						125			
Ala	Thr	Lys	Gly	Thr	Ile	Ser	Arg	Ser	Thr						
		130				135									

(2) INFORMATION FOR SEQ ID NO:3315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..198

(D) OTHER INFORMATION: / Ceres Seq. ID 1576432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3315:

Met	Leu	Ile	Lys	Ile	Leu	Trp	Asn	Phe	Trp	Arg	Ser	Tyr	Leu	Ser	Leu
1			5					10						15	
Ile	Phe	Ile	Cys	Gly	Gly	Arg	Gly	Gly	Arg	Phe	Gly	Gly	Gly	Phe	Arg
		20					25						30		
Asp	Glu	Gly	Pro	Pro	Ala	Glu	Val	Glu	Val	Ser	Thr	Phe	Val	His	
		35				40					45				
Ala	Cys	Glu	Gly	Asp	Ala	Val	Thr	Lys	Leu	Thr	Asn	Glu	Lys	Val	Pro
		50				55				60					
Tyr	Phe	Asn	Ala	Pro	Ile	Tyr	Leu	Gln	Asn	Lys	Thr	Gln	Val	Gly	Lys
65			70						75					80	
Val	Asp	Glu	Ile	Phe	Gly	Pro	Ile	Asn	Glu	Ser	Tyr	Phe	Ser	Val	Lys
		85						90						95	

Met Met Glu Gly Ile Ile Ala Thr Ser Tyr Lys Glu Gly Asp Lys Phe
100 105 110
Tyr Ile Asp Pro Met Lys Leu Leu Pro Leu Ser Arg Phe Leu Pro Gln
115 120 125
Pro Lys Gly Gln Ser Gln Gly Ala Pro Arg Gly Gly Gly Arg Val Glu
130 135 140
Gly Val Val Ala Glu Ala Val Val Val Arg Ser Gly Val Glu Glu Asp
145 150 155 160
His Gln Gly Val Val Ala Glu Val Gln Gly Val Glu Ala Val Val Val
165 170 175
Leu Glu Gly Glu Gly Ser Arg Cys Ser Leu Ser Leu Met Met Phe
180 185 190
Phe Phe Val Glu Ala Ser
195

(2) INFORMATION FOR SEQ ID NO:3316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..582
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3316:

atccaggcgt	acagccctcc	gcctcgtgaa	ggcaaagcac	gcgcaaagcc	accacagcgt	60
cgctcctctt	gtctccagtc	caagcaagcg	aagagcaccc	ctcgagatct	ctccctcccc	120
gcgcgcccat	ggacgcagtt	gactcggtag	tcgacccgct	ccgggagttc	gccaaggaca	180
gcatccgcct	cgtaagcgc	tgccacaagc	cggaccgcaa	ggagttcacc	aaggtcgccg	240
cgcggactgc	gacgggttc	gtcgtcatgg	gattcgtcgg	cttctttgtc	aagctcatct	300
tcatccctat	caacaacatc	atcgtcggct	ccggctgata	cgttcacctc	aggctagtgg	360
ctgcaggagt	ggacaatggc	gtcactacct	tggaggcagc	accgttttca	gctctgattt	420
ccgcaaagca	attcctttag	gacttggtgt	gttaaagggc	aactccctta	tcttttcctc	480
tcttgaggtc	gtgtggtaga	tctggaactc	ttttgtacct	ggtgccgaat	agtcttttgg	540
ggatcagcgg	gtgacaaaat	tTaaatggtt	actgtcttgg	gg		

(2) INFORMATION FOR SEQ ID NO:3317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3317:

Ile Gln Ala Tyr Ser Pro Pro Pro Arg Glu Gly Lys Ala Arg Ala Lys
1 5 10 15
Pro Pro Gln Arg Arg Pro Leu Arg Leu Gln Ser Lys Gln Ala Lys Ser
20 25 30
Thr Pro Arg Asp Leu Ser Leu Pro Ala Pro Pro Trp Thr Gln Leu Thr
35 40 45
Arg

(2) INFORMATION FOR SEQ ID NO:3318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..46
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576435
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3318:

```
Ser Arg Arg Thr Ala Leu Arg Leu Val Lys Ala Lys His Ala Gln Ser
1           5           10           15
His His Ser Val Val Leu Phe Val Ser Ser Pro Ser Lys Arg Arg Ala
20           25           30
Pro Leu Glu Ile Ser Pro Ser Pro Arg Arg His Gly Arg Ser
35           40           45
```

(2) INFORMATION FOR SEQ ID NO:3319:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..69
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576436
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3319:

```
Met Asp Ala Val Asp Ser Val Val Asp Pro Leu Arg Glu Phe Ala Lys
1           5           10           15
Asp Ser Ile Arg Leu Val Lys Arg Cys His Lys Pro Asp Arg Lys Glu
20           25           30
Phe Thr Lys Val Ala Ala Arg Thr Ala Ile Gly Phe Val Val Met Gly
35           40           45
Phe Val Gly Phe Phe Val Lys Leu Ile Phe Ile Pro Ile Asn Asn Ile
50           55           60
Ile Val Gly Ser Gly
65
```

(2) INFORMATION FOR SEQ ID NO:3320:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 810 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..810
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576437
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3320:

```
aacgacccaa gtcccaacgg aacttagctg ccgagcgccc aaagcccccac cgccgctccc      60
atcaagcggc gctaaagggt tcctcgcccc caacgcgatg ccgaagaaca agggaaaggg      120
aggcaagaac cggaagcggg gcaagaacga rgcggacgac gagaagcggg agctggntgt      180
tcaaggagga cgggcaggag tacgcgcagg tgacgcggat gctgggcaac ggccgctgcg      240
aggcgctctg catcgacggc accaagcgcc tctgccacat ccggggcaag atgcacaaga      300
aggtgtggat cgccgccggg gacatcgtgc tcgtcggcct gcgcgactac caGggacgac      360
aaggcggacg tcatcctcaa gtacatgaac gacgaggccc gcctgctcaa gGCctacggc      420
gagatccccg acaacgtcag gctcaacgag ggcgtcgttg atgaggagga agccggcgcg      480
caggatgact atatacagtt cgaggacgag gacatcgaca agatctgatg atgcctctt      540
ccacacggtc cctttccatg gtaaaactaaa cgtatgcaaa acaattgtat ccttctgttt      600
tgtggtggct accatgactg aagaatggta gtcgtgggtg ttgtataatg atttgggcgg      660
agagtactgt gtataatgat ttgggggcac ttgttgtgcc caataacccc atatggtgat      720
atagcaagta tgggactgaa cgaaccgttc ctctcccttt ctgttaatat gatatatattg      780
gttgggcatg atccaatttt ttttttttct
```


(2) INFORMATION FOR SEQ ID NO:3321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1576438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3321:

Thr Thr Gln Val Thr Glu Leu Ser Cys Arg Ala Pro Lys Ala Pro
1 5 10 15
Pro Pro Leu Pro Ser Ser Gly Ala Lys Gly Phe Leu Ala Arg Asn Ala
20 25 30
Met Pro Lys Asn Lys Gly Lys Gly Gly Lys Asn Arg Lys Arg Gly Lys
35 40 45
Asn Xaa Ala Asp Asp Glu Lys Arg Glu Leu Xaa Val Gln Gly Gly Arg
50 55 60
Ala Gly Val Arg Ala Gly Asp Ala Asp Ala Gly Gln Arg Pro Leu Arg
65 70 75 80
Gly Ala Leu His Arg Arg His Gln Ala Pro Leu Pro His Pro Gly Gln
85 90 95
Asp Ala Gln Glu Gly Val Asp Arg Arg Arg Gly His Arg Ala Arg Arg
100 105 110
Pro Ala Arg Leu Pro Gly Thr Thr Arg Arg Thr Ser Ser Ser Ser Thr
115 120 125

(2) INFORMATION FOR SEQ ID NO:3322:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1576439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3322:

Arg Pro Lys Ser Gln Arg Asn Leu Ala Ala Glu Arg Pro Lys Pro His
1 5 10 15
Arg Arg Ser His Gln Ala Ala Leu Lys Val Ser Ser Pro Ala Thr Arg
20 25 30
Cys Arg Arg Thr Arg Glu Arg Glu Ala Arg Thr Gly Ser Gly Ala Arg
35 40 45
Thr Xaa Arg Thr Thr Arg Ser Gly Ser Trp Xaa Phe Lys Glu Asp Gly
50 55 60
Gln Glu Tyr Ala Gln Val Thr Arg Met Leu Gly Asn Gly Arg Cys Glu
65 70 75 80
Ala Leu Cys Ile Asp Gly Thr Lys Arg Leu Cys His Ile Arg Gly Lys
85 90 95
Met His Lys Lys Val Trp Ile Ala Ala Gly Asp Ile Val Leu Val Gly
100 105 110
Leu Arg Asp Tyr Gln Gly Arg Gln Gly Gly Arg His Pro Gln Val His
115 120 125
Glu Arg Arg Gly Pro Pro Ala Gln Gly Leu Arg Arg Asp Pro Arg Gln
130 135 140
Arg Gln Ala Gln Arg Gly Arg Arg

145 150

(2) INFORMATION FOR SEQ ID NO:3323:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1576440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3323:

Met	Pro	Lys	Asn	Lys	Gly	Lys	Gly	Gly	Lys	Asn	Arg	Lys	Arg	Gly	Lys
1			5						10					15	
Asn	Xaa	Ala	Asp	Asp	Glu	Lys	Arg	Glu	Leu	Xaa	Val	Gln	Gly	Gly	Arg
			20					25					30		
Ala	Gly	Val	Arg	Ala	Gly	Asp	Ala	Asp	Ala	Gly	Gln	Arg	Pro	Leu	Arg
		35				40					45				
Gly	Ala	Leu	His	Arg	Arg	His	Gln	Ala	Pro	Leu	Pro	His	Pro	Gly	Gln
	50					55				60					
Asp	Ala	Gln	Glu	Gly	Val	Asp	Arg	Arg	Arg	Gly	His	Arg	Ala	Arg	Arg
65					70				75					80	
Pro	Ala	Arg	Leu	Pro	Gly	Thr	Thr	Arg	Arg	Thr	Ser	Ser	Ser	Ser	Thr
			85					90						95	

(2) INFORMATION FOR SEQ ID NO:3324:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1030 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1030

(D) OTHER INFORMATION: / Ceres Seq. ID 1576441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3324:

gtcggtaggt	gtccctccct	ttactccctc	cgccctccca	cagtcaccact	gcccttctctc	60
tcgggtccatc	gcaagctcct	gcgggtccctgc	ctacggcgct	acggcgggcat	ccacccttct	120
gccgcatcgt	ctttctcaag	acgctgcccc	aggtccatcg	cgcctaggggt	tcgccgagtc	180
cggcgggcgct	aagataatga	gtggggcaccg	aaacagtcot	ggaaagcgct	actctgatta	240
tactgaaact	ggaggcggtg	agagaagaaa	tcctgggtgat	gatacctatg	cccctgggtcc	300
tgatgacact	gtgtatcgct	acctctgcgc	ctctagaaaa	atTgggagta	tcattggcag	360
gggtggagaa	atTgcaaagc	agttgaggac	tgagacccaa	gctaAgatca	ggattgggtga	420
gagtgtccct	ggatgtgaag	agcgagttat	taccatat	agctcaagtc	gaagaactaa	480
taccatcgat	gatgctgaag	ataaggtttg	ccctgctcag	gatgccctct	ttagagttca	540
tgagaggctt	gccactgatg	agagtttttg	taacgaagac	agcgaagaaa	tttcacctca	600
agttactgtt	cgctgcttg	tgccatcaga	ccagattgga	tgcatctctg	gaaaagggtg	660
gcacatcatc	caaggaatcc	gcagtgcgac	tggtgcgcaa	atacgcgtgc	ttagtaagga	720
tcatatccct	gcattgtgcca	ttagtggcga	tgaacttctc	cagatatctg	gggacatggt	780
agttgtcaaa	aaggctcttt	gtcaagtgtc	atctcgccctc	cataacaacc	catccaagtc	840
acagcatctt	cttgcattcca	gcttgaccca	accgtatcca	gggggtaccc	accttgggtg	900
ttctctctgt	gcacctgttg	tagggatcac	tccagtaatt	cctccttatg	gaggctacaa	960
aggtgacgtg	gcaggagatt	ggccctcttt	ataccaaccc	cgacgggatg	agagctctgc	1020
aaaggagttt						

(2) INFORMATION FOR SEQ ID NO:3325:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 343 amino acids

(B) TYPE: amino acid

[illegible]

(A) NAME/KEY: peptide

[illegible]

(B) LOCATION: 1..278

(D) OTHER INFORMATION: / Ceres Seq. ID 1576443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3326:

Met Ser Gly His Arg Asn Ser His Gly Lys Arg Tyr Ser Asp Tyr Thr
1 5 10 15
Glu Thr Gly Gly Gly Lys Arg Arg Asn Pro Gly Asp Asp Thr Tyr Ala
20 25 30
Pro Gly Pro Asp Asp Thr Val Tyr Arg Tyr Leu Cys Ala Ser Arg Lys
35 40 45
Ile Gly Ser Ile Ile Gly Arg Gly Gly Glu Ile Ala Lys Gln Leu Arg
50 55 60
Thr Glu Thr Gln Ala Lys Ile Arg Ile Gly Glu Ser Val Pro Gly Cys
65 70 75 80
Glu Glu Arg Val Ile Thr Ile Phe Ser Ser Ser Arg Arg Thr Asn Thr
85 90 95
Ile Asp Asp Ala Glu Asp Lys Val Cys Pro Ala Gln Asp Ala Leu Phe
100 105 110
Arg Val His Glu Arg Leu Ala Thr Asp Glu Ser Phe Gly Asn Glu Asp
115 120 125
Ser Glu Glu Ile Ser Pro Gln Val Thr Val Arg Leu Leu Val Pro Ser
130 135 140
Asp Gln Ile Gly Cys Ile Leu Gly Lys Gly Gly His Ile Ile Gln Gly
145 150 155 160
Ile Arg Ser Glu Thr Gly Ala Gln Ile Arg Val Leu Ser Lys Asp His
165 170 175
Ile Pro Ala Cys Ala Ile Ser Gly Asp Glu Leu Leu Gln Ile Ser Gly
180 185 190
Asp Met Val Val Val Lys Lys Ala Leu Cys Gln Val Ser Ser Arg Leu
195 200 205
His Asn Asn Pro Ser Lys Ser Gln His Leu Leu Ala Ser Ser Leu Thr
210 215 220
Gln Pro Tyr Pro Gly Gly Thr His Leu Gly Gly Ser Ser Ala Ala Pro
225 230 235 240
Val Val Gly Ile Thr Pro Val Ile Pro Pro Tyr Gly Gly Tyr Lys Gly
245 250 255
Asp Val Ala Gly Asp Trp Pro Ser Leu Tyr Gln Pro Arg Arg Asp Glu
260 265 270
Ser Ser Ala Lys Glu Phe
275

(2) INFORMATION FOR SEQ ID NO:3327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 713 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..713

(D) OTHER INFORMATION: / Ceres Seq. ID 1576444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3327:

taggataatt	cttgggtgctg	ctgcaacaga	aatagagctg	gcaaagagat	tgaaggagtt	60
ctctttgaag	gaaacaggtt	tggaccagta	tgctgttgcg	aaatttgctg	aaastttgaa	120
atggttccaa	gaaccctggc	agaaaatgcc	ggacttagcg	caatggatgt	aatatcctct	180
ctttatgctg	agcatgctag	tggcaatgtg	aaagttggca	ttgacctgga	ggaagggtgcc	240
tgcaaggaca	tcacgacctt	gaaaatatgg	gacctttatg	tcacaaaagt	ctttgcccta	300
aaatattctg	ccgatgccgc	atgcaccgtg	ctgcgggttg	accagatcat	tatggcgaaG	360
csggcaggag	gtccaagaag	agatgcccg	cttgggtggcg	ggatggacga	ggactagttt	420
gactgtgatt	gttctctttg	tgtatcacgt	acgcaagggt	tcagagcagg	gaacatcatg	480
tcttatttag	ggtttgggtc	tgtagaaggt	tttgggtgct	gtagttcacg	tttggaaaggg	540
ttgcacggct	gtgctggtat	cgtatgggga	atttgcttgt	tctttcctgg	tgtattattg	600

cagtgccgat gtattattca ttcgagggtt ctttccttca gttcatcaca ccgactgagc 660
tcatatgagt sytacttcag tttttttatt atagaagcaa aaatgttaca gcc

(2) INFORMATION FOR SEQ ID NO:3328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3328:

Met	Val	Pro	Arg	Thr	Leu	Ala	Glu	Asn	Ala	Gly	Leu	Ser	Ala	Met	Asp
1				5					10					15	
Val	Ile	Ser	Ser	Leu	Tyr	Ala	Glu	His	Ala	Ser	Gly	Asn	Val	Lys	Val
			20					25					30		
Gly	Ile	Asp	Leu	Glu	Glu	Gly	Ala	Cys	Lys	Asp	Ile	Thr	Thr	Leu	Lys
		35					40					45			
Ile	Trp	Asp	Leu	Tyr	Val	Thr	Lys	Phe	Phe	Ala	Leu	Lys	Tyr	Ser	Ala
	50					55					60				
Asp	Ala	Ala	Cys	Thr	Val	Leu	Arg	Val	Asp	Gln	Ile	Ile	Met	Ala	Lys
65					70				75					80	
Xaa	Ala	Gly	Gly	Pro	Arg	Arg	Asp	Ala	Gln	Pro	Gly	Gly	Gly	Met	Asp
				85				90						95	

Glu Asp

(2) INFORMATION FOR SEQ ID NO:3329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3329:

Met	Asp	Val	Ile	Ser	Ser	Leu	Tyr	Ala	Glu	His	Ala	Ser	Gly	Asn	Val
1				5					10					15	
Lys	Val	Gly	Ile	Asp	Leu	Glu	Glu	Gly	Ala	Cys	Lys	Asp	Ile	Thr	Thr
			20					25					30		
Leu	Lys	Ile	Trp	Asp	Leu	Tyr	Val	Thr	Lys	Phe	Phe	Ala	Leu	Lys	Tyr
		35				40						45			
Ser	Ala	Asp	Ala	Ala	Cys	Thr	Val	Leu	Arg	Val	Asp	Gln	Ile	Ile	Met
	50					55					60				
Ala	Lys	Xaa	Ala	Gly	Gly	Pro	Arg	Arg	Asp	Ala	Gln	Pro	Gly	Gly	Gly
65					70				75					80	

Met Asp Glu Asp

(2) INFORMATION FOR SEQ ID NO:3330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1576447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3330:

```
Met Ser Tyr Leu Gly Phe Gly Ser Val Glu Gly Phe Gly Ala Cys Ser
1           5           10           15
Ser Arg Leu Glu Gly Leu His Gly Cys Ala Gly Ile Val Trp Gly Ile
          20          25          30
Cys Leu Phe Phe Pro Gly Val Leu Leu Gln Cys Arg Cys Ile Ile His
          35          40          45
Ser Arg Val Leu Ser Phe Ser Ser Ser His Arg Leu Ser Ser Tyr Glu
          50          55          60
Xaa Tyr Phe Ser Phe Phe Ile Ile Glu Ala Lys Met Leu Gln
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:3331:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..927

(D) OTHER INFORMATION: / Ceres Seq. ID 1576470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3331:

```
atttgcatct gagttcctga ttgttgatt ccagtttctt ctgtgagttt tgtgggater 60
craggaagaa ctagaaggat gtcgtgctgc rgargcaact rcrggtvcvg cgccggctgc 120
aagtrcggca rcggctgcgg aggggtgcaag atgtaccggg acatggctga rcaggtgacc 180
accactaccc agactctcat catgggtgtw gcacctctct rmccgcccgc ccgctcccgc 240
tcccagctcg tgttccgctt cttgcagccg tcgccgcgaa gctccagaga acttccgtca 300
acatggggaa racacgtggt atggrarccg ggcgcaagct caagaccac cgcagaacca 360
gcggtgggct gacaaggcat acaagaagag ccatttgggS caatgagtgg aagaaaccct 420
tcgctgggtc atcccatgcc aagggcattg ycctggagaa gatttggtatt gaggccaagc 480
agcccaactc cgctatccgt aagtgtgtct gtgttcagct tgtaagaat ggcaagaaga 540
ttgctgcctt cgtgccaaat gacggttggt tgaactacat tgaggaaaat gatgaggtct 600
tgattgctgg atttggtcgt aagggccacg ctgtgggaga tattcctggt gtccggttca 660
agtgctcaa ggtttccggt gtgtctctgc ttgccctttt caaggagaag aaagagaagc 720
caagtccta gattgctctt gctaccaaa tcagcaagcg tggagttgaa acgggagggc 780
gttagatgat taagaagaat ggttgcttgc tatgtttgca gtgcattcgt gcaattgtta 840
acctaagatt ttgttggtga aaacgatttc ttttcagact tgcttctggt gagtgcctatc 900
attccatata aatgtacttc ctcttct
```

(2) INFORMATION FOR SEQ ID NO:3332:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1576471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3332:

```
Met Ser Cys Cys Xaa Xaa Asn Xaa Xaa Xaa Ala Gly Cys Lys Xaa
1           5           10           15
Gly Xaa Gly Cys Gly Gly Cys Lys Met Tyr Pro Asp Met Ala Xaa Gln
          20          25          30
Val Thr Thr Thr Thr Gln Thr Leu Ile Met Gly Xaa Ala Pro Ser Xaa
          35          40          45
Arg Arg Arg Arg Ser Arg Ser Gln Leu Val Phe Arg Phe Leu Gln Pro
          50          55          60
```

Ser Pro Arg Ser Ser Arg Glu Leu Pro Ser Thr Trp Gly Xaa His Val
65 70 75 80
Val Trp Xaa Pro Gly Ala Ser Ser Arg Pro Thr Ala Glu Pro Ala Val
85 90 95
Gly

(2) INFORMATION FOR SEQ ID NO:3333:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1576472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3333:

Met Gly Xaa Thr Arg Gly Met Xaa Xaa Gly Arg Lys Leu Lys Thr His
1 5 10 15
Arg Arg Thr Ser Gly Gly Leu Thr Arg His Thr Arg Arg Ala Ile Trp
20 25 30
Xaa Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser Ser His Ala Lys Gly
35 40 45
Ile Xaa Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala
50 55 60
Ile Arg Lys Cys Ala Arg Val Gln Leu Val Lys Asn Gly Lys Lys Ile
65 70 75 80
Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Tyr Ile Glu Glu Asn
85 90 95
Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His Ala Val Gly
100 105 110
Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser Gly Val Ser
115 120 125
Leu Leu Ala Leu Phe Lys Glu Lys Lys Glu Lys Pro Arg Ser
130 135 140

(2) INFORMATION FOR SEQ ID NO:3334:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1576473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3334:

Met Xaa Xaa Gly Arg Lys Leu Lys Thr His Arg Arg Thr Ser Gly Gly
1 5 10 15
Leu Thr Arg His Thr Arg Arg Ala Ile Trp Xaa Asn Glu Trp Lys Lys
20 25 30
Pro Phe Ala Gly Ser Ser His Ala Lys Gly Ile Xaa Leu Glu Lys Ile
35 40 45
Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala Ile Arg Lys Cys Ala Arg
50 55 60
Val Gln Leu Val Lys Asn Gly Lys Lys Ile Ala Ala Phe Val Pro Asn
65 70 75 80
Asp Gly Cys Leu Asn Tyr Ile Glu Glu Asn Asp Glu Val Leu Ile Ala
85 90 95
Gly Phe Gly Arg Lys Gly His Ala Val Gly Asp Ile Pro Gly Val Arg

100 105 110
Phe Lys Val Val Lys Val Ser Gly Val Ser Leu Leu Ala Leu Phe Lys
115 120 125
Glu Lys Lys Glu Lys Pro Arg Ser
130 135

(2) INFORMATION FOR SEQ ID NO:3335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..440
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3335:

aaaccctagc cgccgccaga ccattcggtt ctcgcgagcc atcgcttctg taattctcag 60
gcattccggaa gaaatggcca agtcgaagaa ccacacggcg cacaaccagt cgttcaaggc 120
gcacaagaac ggcattaaga aacccaagcg ccaccgccag acctccacca aggggatgga 180
ccccaaagttc ctgaggaacc tgaggtattc taggaaggcg aacaaaaaga gtggtgaggc 240
tgaagctgag gactaggaag gaaagcatgg ctttggttcc tctgttttta gtcagttcc 300
accttttaga cctgggggtt tgctaaagat ggGaacttaa gtggtgttac tgtatgatgg 360
caaggacctt ttgctgccga agGttatgtt ttgaagttca tgctacctt taaagtacgg 420
attacctgtt gcctatgttc

(2) INFORMATION FOR SEQ ID NO:3336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3336:

Asn Pro Ser Arg Gln Thr Ile Arg Phe Ser Arg Ala Ile Ala Ser
1 5 10 15
Val Ile Leu Arg His Pro Glu Glu Met Ala Lys Ser Lys Asn His Thr
20 25 30
Ala His Asn Gln Ser Phe Lys Ala His Lys Asn Gly Ile Lys Lys Pro
35 40 45
Lys Arg His Arg Gln Thr Ser Thr Lys Gly Met Asp Pro Lys Phe Leu
50 55 60
Arg Asn Leu Arg Tyr Ser Arg Lys Gly Asn Lys Lys Ser Gly Glu Ala
65 70 75 80
Glu Ala Glu Glu

(2) INFORMATION FOR SEQ ID NO:3337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3337:

Met Ala Lys Ser Lys Asn His Thr Ala His Asn Gln Ser Phe Lys Ala
1 5 10 15
His Lys Asn Gly Ile Lys Lys Pro Lys Arg His Arg Gln Thr Ser Thr
20 25 30
Lys Gly Met Asp Pro Lys Phe Leu Arg Asn Leu Arg Tyr Ser Arg Lys
35 40 45
Gly Asn Lys Lys Ser Gly Glu Ala Glu Ala Glu Glu
50 55 60

(2) INFORMATION FOR SEQ ID NO:3338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..577
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3338:

gagccgaact caacccaact tctctccctc tccctcgctt gcctgccgtt ccgcgtttga 60
ccaactcccc cgcaccgtaa ccctagcagc agatcgccca tggagagctg ggcgacctgg 120
gtggggacaa gcgtcacctc cgccttcttc gcctccctcg agcgtctgtc ctgcatcaac 180
ctctccaccg acgacgacga cgacgacgag gaccacgacg aggccaaagga ccggccccctc 240
atcctcgccg ccgccccacg ccacgactcc gccgccaagc ccgatccaga ctccgcgcgc 300
gaggaccagg acgaccagaa gcaagagcag ccgccMgctg ccgccgtatg aatcaaacc 360
gattccttgc ttgtactagc tgctactgct gttatgtcgc caaataaagt cgtgtgtgcg 420
tgtgcagtca gtactactgc tctgctgcta ctatcctagt cctagtatat tagtatatta 480
tacagtccctc tctgtgaaat ttgaatcgac tcgaaaatca aacccccacca atatgagctt 540
gttaatatatt gtctcccgga atcaaccagc gcttggt

(2) INFORMATION FOR SEQ ID NO:3339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3339:

Ser Arg Thr Gln Pro Asn Phe Ser Pro Ser Pro Ser Pro Ala Cys Arg
1 5 10 15
Ser Ala Phe Asp Gln Leu Pro Arg Thr Val Thr Leu Ala Ala Asp Arg
20 25 30
Pro Trp Arg Ala Gly Arg Pro Gly Trp Gly Gln Ala Ser Pro Pro Pro
35 40 45
Ser Ser Pro Pro Ser Ser Ala Ala Pro Ala Ser Thr Ser Pro Pro Thr
50 55 60
Thr Thr Thr Thr Thr Arg Thr Thr Thr Arg Pro Arg Thr Gly Pro Ser
65 70 75 80
Ser Ser Pro Pro Pro His Ala Thr Thr Pro Pro Pro Ser Pro Ile Gln
85 90 95
Thr Pro Pro Pro Arg Thr Arg Thr Thr Arg Ser Lys Ser Ser Arg Xaa
100 105 110
Leu Pro Pro Tyr Glu Ser Asn Pro Ile Pro Cys Leu Tyr
115 120 125

(2) INFORMATION FOR SEQ ID NO:3340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids

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- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..83
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576493
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3340:

Met Glu Ser Trp Ala Thr Trp Val Gly Thr Ser Val Thr Ser Ala Phe
1 5 10 15
Phe Ala Ser Leu Glu Arg Cys Ser Cys Ile Asn Leu Ser Thr Asp Asp
20 25 30
Asp Asp Asp Asp Glu Asp His Asp Glu Ala Lys Asp Arg Pro Leu Ile
35 40 45
Leu Ala Ala Ala Pro Arg His Asp Ser Ala Ala Lys Pro Asp Pro Asp
50 55 60
Ser Ala Ala Glu Asp Gln Asp Asp Gln Lys Gln Glu Gln Pro Xaa Ala
65 70 75 80
Ala Ala Val

- (2) INFORMATION FOR SEQ ID NO:3341:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 618 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..618
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576494
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3341:

agccgactga atcttccacc tcgcttcgcg cctccggctc cgcgccgggc ccgcataatc 60
tgtgctcggg atcgctctt cccgcggcaa atgggggccc actccgagga cgccgtcaag 120
cagctcagcc tcctcatgga gcaagtdgag gccccgctga agagatcgtt tcagaatatg 180
caccagggct atcctaaaga aacactgggt cgtttcctta aggctagaga gtggaatgta 240
gcaaaggctc ataaaatgat tgtagaatgt ttgaattgga ggattcaaaa tgaaattgat 300
agtgtgctag agaggcctat agtcccagta gatttataca ggtcaatacg tgattcacaa 360
cttattggcc tgtcaggata cacaaaggag ggtctcccaa tttttggcat tgggtgttggg 420
catagcacat atgacaaagc ttcgggtccac tactatgtgc aatctcatat ccagattaac 480
gagtaccgtg atcgataat tttgcctagg ctgacacaac agtttgggcg gcctgttacc 540
agctgtataa aagtgtctgga tatgactggt ttgaagctat cagcactaag ccaaataaag 600
atgttgactT ccatatcg

- (2) INFORMATION FOR SEQ ID NO:3342:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 206 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..206
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576495
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3342:

Ser Arg Leu Asn Leu Pro Pro Arg Phe Ala Pro Pro Ala Pro Arg Arg
1 5 10 15
Ala Arg Ile Ile Cys Ala Arg Asp Arg Leu Phe Pro Arg Gln Met Gly
20 25 30
Ala Asp Ser Glu Asp Ala Val Lys Gln Leu Ser Leu Leu Met Glu Gln

35 40 45
Xaa Glu Ala Pro Leu Lys Arg Ser Phe Gln Asn Met His Gln Gly Tyr
50 55 60
Pro Lys Glu Thr Leu Val Arg Phe Leu Lys Ala Arg Glu Trp Asn Val
65 70 75 80
Ala Lys Ala His Lys Met Ile Val Glu Cys Leu Asn Trp Arg Ile Gln
85 90 95
Asn Glu Ile Asp Ser Val Leu Glu Arg Pro Ile Val Pro Val Asp Leu
100 105 110
Tyr Arg Ser Ile Arg Asp Ser Gln Leu Ile Gly Leu Ser Gly Tyr Thr
115 120 125
Lys Glu Gly Leu Pro Ile Phe Gly Ile Gly Val Gly His Ser Thr Tyr
130 135 140
Asp Lys Ala Ser Val His Tyr Tyr Val Gln Ser His Ile Gln Ile Asn
145 150 155 160
Glu Tyr Arg Asp Arg Ile Ile Leu Pro Arg Leu Thr Gln Gln Phe Gly
165 170 175
Arg Pro Val Thr Ser Cys Ile Lys Val Leu Asp Met Thr Gly Leu Lys
180 185 190
Leu Ser Ala Leu Ser Gln Ile Lys Met Leu Thr Ser Ile Ser
195 200 205

(2) INFORMATION FOR SEQ ID NO:3343:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1576496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3343:

Met Gly Ala Asp Ser Glu Asp Ala Val Lys Gln Leu Ser Leu Leu Met
1 5 10 15
Glu Gln Xaa Glu Ala Pro Leu Lys Arg Ser Phe Gln Asn Met His Gln
20 25 30
Gly Tyr Pro Lys Glu Thr Leu Val Arg Phe Leu Lys Ala Arg Glu Trp
35 40 45
Asn Val Ala Lys Ala His Lys Met Ile Val Glu Cys Leu Asn Trp Arg
50 55 60
Ile Gln Asn Glu Ile Asp Ser Val Leu Glu Arg Pro Ile Val Pro Val
65 70 75 80
Asp Leu Tyr Arg Ser Ile Arg Asp Ser Gln Leu Ile Gly Leu Ser Gly
85 90 95
Tyr Thr Lys Glu Gly Leu Pro Ile Phe Gly Ile Gly Val Gly His Ser
100 105 110
Thr Tyr Asp Lys Ala Ser Val His Tyr Tyr Val Gln Ser His Ile Gln
115 120 125
Ile Asn Glu Tyr Arg Asp Arg Ile Ile Leu Pro Arg Leu Thr Gln Gln
130 135 140
Phe Gly Arg Pro Val Thr Ser Cys Ile Lys Val Leu Asp Met Thr Gly
145 150 155 160
Leu Lys Leu Ser Ala Leu Ser Gln Ile Lys Met Leu Thr Ser Ile Ser
165 170 175

(2) INFORMATION FOR SEQ ID NO:3344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..161
(D) OTHER INFORMATION: / Ceres Seq. ID 1576497
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3344:

Met Glu Gln Xaa Glu Ala Pro Leu Lys Arg Ser Phe Gln Asn Met His
1 5 10 15
Gln Gly Tyr Pro Lys Glu Thr Leu Val Arg Phe Leu Lys Ala Arg Glu
20 25 30
Trp Asn Val Ala Lys Ala His Lys Met Ile Val Glu Cys Leu Asn Trp
35 40 45
Arg Ile Gln Asn Glu Ile Asp Ser Val Leu Glu Arg Pro Ile Val Pro
50 55 60
Val Asp Leu Tyr Arg Ser Ile Arg Asp Ser Gln Leu Ile Gly Leu Ser
65 70 75 80
Gly Tyr Thr Lys Glu Gly Leu Pro Ile Phe Gly Ile Gly Val Gly His
85 90 95
Ser Thr Tyr Asp Lys Ala Ser Val His Tyr Tyr Val Gln Ser His Ile
100 105 110
Gln Ile Asn Glu Tyr Arg Asp Arg Ile Ile Leu Pro Arg Leu Thr Gln
115 120 125
Gln Phe Gly Arg Pro Val Thr Ser Cys Ile Lys Val Leu Asp Met Thr
130 135 140
Gly Leu Lys Leu Ser Ala Leu Ser Gln Ile Lys Met Leu Thr Ser Ile
145 150 155 160
Ser

- (2) INFORMATION FOR SEQ ID NO:3345:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 768 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..768
(D) OTHER INFORMATION: / Ceres Seq. ID 1576508
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3345:

ttccttcctg attgccacag ccacacccgg cgcctctctc tccctccctcg gacagggaga 60
gaccctttcc atccaagcta gccaaaccct agccacccgc gggtccaatc tgccaacgctc 120
tcgtccgctg gttggtggct cggcgccatg gcctcgtccg cctacgccgc ttgggacgcc 180
gcggaggagg cggacatcga cgcctccgca tcgcaggagg agctcatcgg ccgcgcccgc 240
ttcatctccc gtgacaatga ggaggagggg gagggggagg gggaggagga ggaggaggtc 300
gagtggttca gcacgccgcc tctcacgcat caggaccgcg agagtcaggg ggaagaagtc 360
atcgatcatgt gctccatccc cttcacccag cctgacccca cccctcccm cgCtcccgt 420
ccctccctc cctcggacag taagagtcgc cgtccggagc ggggtcaaatt gaagccgcgg 480
aagaaggtct gcaagaggaa gaggggtctgc aagaggaagg tgagaagagc caacaagatc 540
aggtctccga ctccgagccg cagccccgaa ctggaccytc tcgccagggc cgtgctcatg 600
atcccaaccg ctctttctac aatcacccgt ggtgaggata tccctcgagg tgctcgcagc 660
cgcgcatct tctagatcta ctagttgcct gtgtattttg tgcatgtag cgtagtcct 720
tgtgtttctg ccgatcaatc catatgctat ggcctggctg gattttgt

- (2) INFORMATION FOR SEQ ID NO:3346:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:3348:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..102
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576511
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3348:
Met Cys Ser Ile Pro Phe Thr Gln Pro Asp Pro Thr Pro Pro Xaa Ala
1 5 10 15
Pro Ala Pro Ser Pro Pro Ser Asp Ser Lys Ser Arg Arg Pro Glu Arg
 20 25 30
Val Lys Leu Lys Pro Arg Lys Lys Val Cys Lys Arg Lys Arg Val Cys
 35 40 45
Lys Arg Lys Val Arg Arg Ala Asn Lys Ile Arg Ser Pro Thr Pro Ser
50 55 60
Arg Ser Pro Glu Leu Asp Xaa Leu Ala Arg Ala Val Leu Met Ile Pro
65 70 75 80
Thr Ala Pro Ser Thr Ile Thr Gly Gly Glu Asp Ile Leu Glu Val Ala
 85 90 95
Arg Ser Arg Gly Ile Phe
 100

(2) INFORMATION FOR SEQ ID NO:3349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..663

(D) OTHER INFORMATION: / Ceres Seq. ID 1576523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3349:

```
aggtgtgtct agtctctagt ctagctaggc actactctag ctccaagtg gccaaagtata      60
ctcgccagag tacgtagagt gtaGbtgagc gtcgtcgaag gatggcgtGg acytcccgcc      120
gcatgggtcgc gtcgcgcgtc gtcttctctgc tgatgctgct cgccgcctca gagatgggga      180
cgacgaggkt ggcggaggcg aggcactgca cgtcgcagag ccaccggttc gtcggcgcct      240
gcatgagcaa gagcaactgc gagaacgtct gcaggacgga gggcttccc tggggcgagt      300
gcaggtggca cggcatagag cgcaagtgcc actgcaagcg gatctgctag taattaacta      360
gccggctggc cagcgcgatgc atgcacgacg accgacctac ctgctgctgg tccgttttgcg      420
tttgtttctt gtccttttggg ccttgctgtg gcgcgcagtc ttgcgtacgt gcgtgtgcgt      480
gtgtcttttc agttactctc aattagtcac agcagacgtg cgtgggtgcg agcgtgtgtc      540
tcgttgcaatt gatgaaccgg cttcacgtgc tgtggtttta cagtttctga tgtgttttag      600
ctaactctga ataataaata ataaggcccc gtcttcacgc agttgcgtac tgggtgctta      660
cgt
```

(2) INFORMATION FOR SEQ ID NO:3350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1576524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3350:

Met Ala Trp Xaa Ser Arg Arg Met Val Ala Ser Ala Leu Val Phe Leu
1 5 10 15
Leu Met Leu Leu Ala Ala Ser Glu Met Gly Thr Thr Arg Xaa Ala Glu
20 25 30
Ala Arg His Cys Thr Ser Gln Ser His Arg Phe Val Gly Ala Cys Met
35 40 45
Ser Lys Ser Asn Cys Glu Asn Val Cys Arg Thr Glu Gly Phe Pro Trp
50 55 60
Gly Glu Cys Arg Trp His Gly Ile Glu Arg Lys Cys His Cys Lys Arg
65 70 75 80
Ile Cys

(2) INFORMATION FOR SEQ ID NO:3351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3351:

Met Val Ala Ser Ala Leu Val Phe Leu Leu Met Leu Leu Ala Ala Ser
1 5 10 15
Glu Met Gly Thr Thr Arg Xaa Ala Glu Ala Arg His Cys Thr Ser Gln
20 25 30
Ser His Arg Phe Val Gly Ala Cys Met Ser Lys Ser Asn Cys Glu Asn
35 40 45
Val Cys Arg Thr Glu Gly Phe Pro Trp Gly Glu Cys Arg Trp His Gly
50 55 60
Ile Glu Arg Lys Cys His Cys Lys Arg Ile Cys
65 70 75

(2) INFORMATION FOR SEQ ID NO:3352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3352:

Met His Ala Arg Arg Pro Thr Tyr Leu Leu Val Arg Leu Arg Leu
1 5 10 15
Phe Leu Val Leu Trp Ala Leu Leu Trp Arg Ala Val Leu Arg Thr Cys
20 25 30
Val Cys Val Cys Leu Phe Ser Tyr Ser Gln Leu Val Ile Ala Asp Val
35 40 45
Arg Gly Cys Glu Arg Val Ser Arg Cys Ile Asp Glu Pro Ala Ser Arg
50 55 60
Ala Val Val Leu Gln Phe Leu Met Cys Phe Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:3353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3353:

(2) INFORMATION FOR SEQ ID NO:3354:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..203

(D) OTHER INFORMATION: / Ceres Seq. ID 1576536

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3354:

Met	Lys	Phe	Asn	Ile	Ala	Asn	Pro	Ser	Thr	Gly	Cys	Gln	Lys	Lys	Leu
1				5					10					15	
Glu	Ile	Asp	Asp	Asp	Gln	Lys	Leu	Arg	Ala	Phe	Tyr	Asp	Arg	Arg	Ser
			20					25					30		
Pro	Arg	Arg	Ser	Val	Val	Met	Leu	Trp	Val	Arg	Ser	Leu	Arg	Val	Met
			35				40					45			
Ser	Ser	Arg	Ser	Trp	Val	Asp	Val	Ser	Gln	Asp	Leu	Ser	Val	Ile	Asn
	50					55					60				
Leu	Val	Ile	Val	Lys	Lys	Gly	Glu	Asn	Asp	Leu	Pro	Gly	Leu	Thr	Asp
65					70					75					80
Thr	Glu	Lys	Pro	Arg	Met	Arg	Gly	Pro	Lys	Arg	Ala	Ser	Lys	Ile	Arg
				85					90					95	
Lys	Leu	Phe	Asn	Leu	Ala	Lys	Asp	Asp	Asp	Val	Arg	Lys	Tyr	Val	Asn
			100					105					110		
Thr	Tyr	Arg	Arg	Thr	Phe	Thr	Thr	Lys	Asn	Gly	Lys	Lys	Val	Ser	Lys
		115					120					125			
Ala	Pro	Lys	Ile	Gln	Arg	Leu	Val	Thr	Pro	Leu	Thr	Leu	Gln	Arg	Lys
		130				135					140				
Arg	Ala	Arg	Ile	Ala	Asp	Lys	Lys	Lys	Arg	Ile	Ala	Lys	Lys	Lys	Ser
145				150						155				160	
Glu	Ala	Ala	Glu	Tyr	Gln	Lys	Leu	Leu	Ala	Gln	Arg	Leu	Lys	Glu	Gln
			165						170					175	
Arg	Asp	Arg	Arg	Ser	Glu	Ser	Leu	Ala	Lys	Arg	Arg	Ser	Lys	Leu	Ser
			180					185					190		
Ala	Ala	Ala	Lys	Ala	Ser	Ala	Ala	Thr	Ser	Ala					
		195					200								

(2) INFORMATION FOR SEQ ID NO:3355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1576537

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3355:

Met Leu Trp Val Arg Ser Leu Arg Val Met Ser Ser Arg Ser Trp Val
1 5 10 15
Asp Val Ser Gln Asp Leu Ser Val Ile Asn Leu Val Ile Val Lys Lys
20 25 30
Gly Glu Asn Asp Leu Pro Gly Leu Thr Asp Thr Glu Lys Pro Arg Met
35 40 45
Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg Lys Leu Phe Asn Leu Ala
50 55 60
Lys Asp Asp Asp Val Arg Lys Tyr Val Asn Thr Tyr Arg Arg Thr Phe
65 70 75 80
Thr Thr Lys Asn Gly Lys Lys Val Ser Lys Ala Pro Lys Ile Gln Arg
85 90 95
Leu Val Thr Pro Leu Thr Leu Gln Arg Lys Arg Ala Arg Ile Ala Asp
100 105 110
Lys Lys Lys Arg Ile Ala Lys Lys Lys Ser Glu Ala Ala Glu Tyr Gln
115 120 125
Lys Leu Leu Ala Gln Arg Leu Lys Glu Gln Arg Asp Arg Arg Ser Glu
130 135 140
Ser Leu Ala Lys Arg Arg Ser Lys Leu Ser Ala Ala Ala Lys Ala Ser
145 150 155 160
Ala Ala Thr Ser Ala
165

(2) INFORMATION FOR SEQ ID NO:3356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1576538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3356:

Met Ser Ser Arg Ser Trp Val Asp Val Ser Gln Asp Leu Ser Val Ile
1 5 10 15
Asn Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr
20 25 30
Asp Thr Glu Lys Pro Arg Met Arg Gly Pro Lys Arg Ala Ser Lys Ile
35 40 45
Arg Lys Leu Phe Asn Leu Ala Lys Asp Asp Asp Val Arg Lys Tyr Val
50 55 60
Asn Thr Tyr Arg Arg Thr Phe Thr Thr Lys Asn Gly Lys Lys Val Ser
65 70 75 80
Lys Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg
85 90 95
Lys Arg Ala Arg Ile Ala Asp Lys Lys Lys Arg Ile Ala Lys Lys Lys
100 105 110
Ser Glu Ala Ala Glu Tyr Gln Lys Leu Leu Ala Gln Arg Leu Lys Glu

115 120 125
Gln Arg Asp Arg Arg Ser Glu Ser Leu Ala Lys Arg Arg Ser Lys Leu
130 135 140
Ser Ala Ala Ala Lys Ala Ser Ala Ala Thr Ser Ala
145 150 155

(2) INFORMATION FOR SEQ ID NO:3357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..782
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3357:

agtgggtcgt	ccactgtgac	gtgaagccgg	agaacatact	tctgaccg	gatttcgatg	60
ccaagatagc	agactttggg	ctggccaagc	tcgcgaacaa	gggagcacta	gtctgaactt	120
cacccatag	agaggcacca	tgggctacat	ggcgccggaa	tgggcgctca	actcgccgat	180
carcgcgaa	gttgatgtgt	acarctacgg	ggtcrtgstt	ctrgagatcg	tractgggat	240
carggcttcg	artggcatag	tgctagatga	gagRgcagat	agactttcgg	cagtttgtac	300
aggaggctaa	gcatatcctg	tctactggga	gtgtcagtga	tatcggtgat	gatagattgc	360
aaggccattt	tcacgcggac	caagcgggtt	cgatgggtcaa	aatagccttt	tcatgcctcg	420
aggaaagacg	caagaggcca	acgatggatg	agattgtcaa	ggtgctcatg	tcgtgtgggtg	480
atgacgatga	ctaccatcct	gcttattcat	attgacttgc	aacagatgtg	aaggtttccc	540
aaaagaaaac	agatgcaaag	atttgagagg	cagaggcaag	tgtacctttg	atcaatgata	600
gaagctgaac	tgaactgact	gatgaaatat	attcgaaagc	gtgccaaaatt	gtgatatttg	660
tgtagagtat	gttgggggtat	ctccatatct	ggtagattaa	aattgagtaa	tgttgttttg	720
ctctatttct	aaggggaggtg	tcttgcccta	taagtggaat	actataatat	tctctccggtt	780

cc

(2) INFORMATION FOR SEQ ID NO:3358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3358:

Met	Arg	Gly	Thr	Met	Gly	Tyr	Met	Ala	Pro	Glu	Trp	Ala	Leu	Asn	Ser
1				5					10					15	
Pro	Ile	Xaa	Ala	Lys	Val	Asp	Val	Tyr	Xaa	Tyr	Gly	Val	Xaa	Xaa	Xaa
				20				25					30		
Glu	Ile	Xaa	Thr	Gly	Ile	Xaa	Ala	Ser	Xaa	Gly	Ile	Val	Leu	Asp	Glu
				35				40					45		
Xaa	Ala	Asp	Arg	Leu	Ser	Ala	Val	Cys	Thr	Gly	Gly				
				50				55					60		

(2) INFORMATION FOR SEQ ID NO:3359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56

(D) OTHER INFORMATION: / Ceres Seq. ID 1576545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3359:

Met Gly Tyr Met Ala Pro Glu Trp Ala Leu Asn Ser Pro Ile Xaa Ala
1 5 10 15
Lys Val Asp Val Tyr Xaa Tyr Gly Val Xaa Xaa Xaa Glu Ile Xaa Thr
20 25 30
Gly Ile Xaa Ala Ser Xaa Gly Ile Val Leu Asp Glu Xaa Ala Asp Arg
35 40 45
Leu Ser Ala Val Cys Thr Gly Gly
50 55

(2) INFORMATION FOR SEQ ID NO:3360:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1576546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3360:

Met Arg Xaa Gln Ile Asp Phe Arg Gln Phe Val Gln Glu Ala Lys His
1 5 10 15
Ile Leu Ser Thr Gly Ser Val Ser Asp Ile Val Asp Asp Arg Leu Gln
20 25 30
Gly His Phe His Ala Asp Gln Ala Val Ala Met Val Lys Ile Ala Phe
35 40 45
Ser Cys Leu Glu Glu Arg Arg Lys Arg Pro Thr Met Asp Glu Ile Val
50 55 60
Lys Val Leu Met Ser Cys Gly Asp Asp Asp Tyr His Pro Ala Tyr
65 70 75 80
Ser Tyr

(2) INFORMATION FOR SEQ ID NO:3361:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 746 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..746

(D) OTHER INFORMATION: / Ceres Seq. ID 1576564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3361:

gccgtgtgca tagcagcaaa tagtggtcgg cctgttggtta ctctatatcg tcccttccag 60
tgtaccogtc ctccagccca ttatacatca tacttgctcc agataagacc aagagcatca 120
tggccaaacgc cttgectctc atcgtcgcgc tggtcgccgc cgccgggtgc gcggcgctgg 180
cttcggccac gtgtacacc gtcggcgact cgcagggtg gacgaccacc ggcgtcgact 240
acagcagctg ggccagccgc aacactttcg tcgtcggaga cacactagtg ttcaactacg 300
tgagcaaggc gcacacggtg acggaggtga gcaaggccgg ctacgacgcc tgctccggcg 360
ccaacgcgct cagcgacgac gacaccggct ccaccaccat cacgtccag accccgggca 420
cgcactatct catctgcaac gtccccggcc actgcgccaG cggcatgaag ctacgggtcg 480
cogtctccgc ctgcgccctcg ggcacggccc cttccaccgg agccctgcag gttccggcga 540
tggcatccgt cgtegcgcg cgcgggcgc tgccatcaag ctgcgcgtct tctgacggag 600
cacggccggg tcgtctcagg ggagagacag tgcattcaga ctacgttctt ggcggttgat 660
agtttcccgc tggcgattgt tcgccgcgca gttcatgtac gtatgtatgt gtgtatgcta 720
ctctgcggtg gcgaatgctt tttctg

(2) INFORMATION FOR SEQ ID NO:3362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..95
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576565
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3362:

Ala Val Cys Ile Ala Ala Asn Ser Gly Arg Pro Val Gly Thr Leu Tyr
1 5 10 15
Arg Pro Phe Gln Cys Thr Arg Pro Pro Ala His Tyr Thr Ser Tyr Leu
20 25 30
Leu Gln Ile Arg Pro Arg Ala Ser Trp Pro Thr Pro Cys Leu Ser Ser
35 40 45
Ser Arg Trp Ser Pro Pro Pro Gly Ala Arg Arg Trp Leu Arg Pro Arg
50 55 60
Arg Thr Pro Ser Ala Thr Arg Arg Ala Gly Arg Pro Pro Ala Ser Thr
65 70 75 80
Thr Ala Ala Gly Pro Ala Ala Thr Leu Ser Ser Ser Glu Thr His
85 90 95

(2) INFORMATION FOR SEQ ID NO:3363:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 179 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..179
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576566
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3363:

Met Ala Asn Ala Leu Pro Leu Ile Val Ala Leu Val Ala Ala Gly
1 5 10 15
Cys Ala Ala Leu Ala Ser Ala Thr Ser Tyr Thr Val Gly Asp Ser Gln
20 25 30
Gly Trp Thr Thr Thr Gly Val Asp Tyr Ser Ser Trp Ala Ser Arg Asn
35 40 45
Thr Phe Val Val Gly Asp Thr Leu Val Phe Asn Tyr Val Ser Lys Ala
50 55 60
His Thr Val Thr Glu Val Ser Lys Ala Gly Tyr Asp Ala Cys Ser Gly
65 70 75 80
Ala Asn Ala Leu Ser Asp Asp Asp Thr Gly Ser Thr Thr Ile Thr Leu
85 90 95
Gln Thr Pro Gly Thr His Tyr Phe Ile Cys Asn Val Pro Gly His Cys
100 105 110
Ala Ser Gly Met Lys Leu Ala Val Ala Val Ser Ala Ser Pro Ser Gly
115 120 125
Thr Ala Pro Ser Thr Gly Ala Leu Gln Val Pro Ala Met Ala Ser Val
130 135 140
Val Ala Arg Pro Arg Ala Leu Pro Ser Ser Ser Arg Ser Ser Asp Gly
145 150 155 160
Ala Arg Pro Gly Arg Leu Arg Gly Glu Thr Val His Ala Asp Tyr Val
165 170 175
Leu Gly Gly

(2) INFORMATION FOR SEQ ID NO:3364:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 782 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..782
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3364:

```
actcgccac caaccttccc gtccccgatg ggcgatcatgg cggccaccgc cactgccgtg      60
gcttccccct ccagctccac ctgcgccaggt cccctccaac ccagcccccg cttcctccct      120
cccgctccca cgcccgctcg ctgccatctc ctccccaagc cgcggcggtg gtgcgcgcgc      180
ctccacatcg agcgtcgggg ggccgctcggc agcgacgtgt cctcgtccca tgacgtggct      240
gcmgaggagg ccgctgctgc gtccaaggtc ggggaagcscg tgcgcgtcMa cggtgcccgt      300
ccgctgccac cacgttgcca aggcgcccgg cctggacctg cgcggcgatg agggcgctcg      360
caagcagtac atcggcggtt ggaaggggaa ggcgatcacg gccaatctcc cttcaagggt      420
ggagttcgag ctcaagctgg acggccatga caagccggtc cggttcatca cccacctccg      480
cgagcaagag ttcgagatcc tcggggagga atagagctct ggactagaga ataacgcgct      540
ctcatcggcg gctgtggcat ctgtatacta ttgtgtctgc gctaaagaag aacgtggtcg      600
agggtgcggg gagaatagga gattgcaact ttgctagtaa gttcctgttt gtttgcttat      660
ttgcggtgcg cttctccctt ctccaccctt taacattgaa attttcatat gtgaggattg      720
aggaattggt cgattgttga tacttatgat ccaaagtaat taaactgagg aatctgttca      780
gc
```

(2) INFORMATION FOR SEQ ID NO:3365:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..149
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3365:

```
Thr Arg Pro Pro Thr Phe Pro Ser Pro Met Ala Ile Met Ala Ala Thr
1          5          10          15
Ala Thr Ala Val Ala Ser Pro Ser Ser Thr Ser Pro Gly Pro Leu
20          25          30
Gln Pro Ser Pro Arg Phe Leu Pro Pro Val Ser Thr Pro Ala Arg Cys
35          40          45
His Leu Leu Pro Lys Pro Arg Arg Trp Cys Ala Arg Leu His Ile Glu
50          55          60
Arg Arg Val Ala Val Gly Ser Asp Val Ser Ser His Asp Val Ala
65          70          75          80
Xaa Glu Glu Ala Ala Ala Ser Lys Val Gly Lys Xaa Val Arg Val
85          90          95
Xaa Gly Ala Arg Pro Arg Pro Pro Arg Cys Gln Gly Ala Arg Pro Gly
100         105         110
Pro Ala Arg His Gly Gly Arg Arg Gln Ala Val His Arg Arg Leu Glu
115         120         125
Gly Glu Ala His His Gly Gln Ser Pro Leu Gln Gly Gly Val Arg Ala
130         135         140
Gln Ala Gly Arg Pro
145
```

(2) INFORMATION FOR SEQ ID NO:3366:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..170
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3366:

Leu Ala His Gln Pro Ser Arg Pro Arg Trp Arg Ser Trp Arg Pro Pro
1 5 10 15
Pro Leu Pro Trp Leu Pro Pro Pro Ala Pro Pro Arg Gln Val Pro Ser
20 25 30
Asn Pro Ala Pro Ala Ser Ser Leu Pro Ser Pro Arg Pro Leu Ala Ala
35 40 45
Ile Ser Ser Pro Ser Arg Gly Gly Gly Ala Arg Ala Ser Thr Ser Ser
50 55 60
Val Gly Trp Pro Ser Ala Ala Thr Cys Pro Arg Pro Met Thr Trp Leu
65 70 75 80
Xaa Arg Arg Pro Leu Leu Arg Pro Arg Ser Gly Ser Xaa Cys Ala Xaa
85 90 95
Thr Val Pro Val Arg Val His His Val Ala Lys Ala Pro Gly Leu Asp
100 105 110
Leu Arg Gly Met Glu Gly Val Val Lys Gln Tyr Ile Gly Val Trp Lys
115 120 125
Gly Lys Arg Ile Thr Ala Asn Leu Pro Phe Lys Val Glu Phe Glu Leu
130 135 140
Lys Leu Asp Gly His Asp Lys Pro Val Arg Phe Ile Thr His Leu Arg
145 150 155 160
Glu Gln Glu Phe Glu Ile Leu Gly Glu Glu
165 170

(2) INFORMATION FOR SEQ ID NO:3367:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 140 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3367:

Met Ala Ile Met Ala Ala Thr Ala Thr Ala Val Ala Ser Pro Ser Ser
1 5 10 15
Ser Thr Ser Pro Gly Pro Leu Gln Pro Ser Pro Arg Phe Leu Pro Pro
20 25 30
Val Ser Thr Pro Ala Arg Cys His Leu Leu Pro Lys Pro Arg Arg Trp
35 40 45
Cys Ala Arg Leu His Ile Glu Arg Arg Val Ala Val Gly Ser Asp Val
50 55 60
Ser Ser Ser His Asp Val Ala Xaa Glu Glu Ala Ala Ala Ser Lys
65 70 75 80
Val Gly Lys Xaa Val Arg Val Xaa Gly Ala Arg Pro Arg Pro Pro Arg
85 90 95
Cys Gln Gly Ala Arg Pro Gly Pro Ala Arg His Gly Gly Arg Arg Gln
100 105 110
Ala Val His Arg Arg Leu Glu Gly Glu Ala His His Gly Gln Ser Pro
115 120 125
Leu Gln Gly Gly Val Arg Ala Gln Ala Gly Arg Pro
130 135 140

(2) INFORMATION FOR SEQ ID NO:3368:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 810 base pairs

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3368:

(2) INFORMATION FOR SEQ ID NO:3369:

(A) LENGTH: 206 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 1576583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3369:

Thr 1	Gly	Lys	His	Leu 5	Ala	Thr	Cys	Ala	Leu 10	Thr	Arg	Leu	Arg	Ala 15	Arg
Gly	Gln	Gln	Gly 20	Thr	Ile	Thr	Val	Pro 25	Leu	Trp	Ser	Ile	Gly 30	Ala	His
Ser	Thr	Ala 35	Gln	Gly	Glu	Ala	Glu 40	Lys	Arg	Phe	Ser	Arg 45	Ser	Arg	Ser
Asp	Lys 50	Ser	Glu	Leu	Ala	Gly 55	Ala	His	Arg	His	Gly 60	Gly	His	Gly	Val
Leu 65	Arg	Gly	Ala	Pro	Arg 70	Arg	Arg	Ala	Pro	Pro 75	Arg	Arg	Ser	Ala	Leu 80
Arg	Pro	Pro	Pro	Ser 85	Ala	Xaa	Val	Cys	Gln 90	Leu	Arg	Phe	Gln 95	Asp	Ala
Pro	Arg	Leu 100	Ser	Leu	Leu	Arg	Ala	Lys 105	Ala	Ala	Ser	Glu	Asp 110	Thr	Ser
Ala	Ser	Gly 115	Asp	Glu	Leu	Ile	Glu 120	Asp	Leu	Lys	Ala	Lys 125	Trp	Asp	Ala
Val	Glu 130	Asp	Lys	Pro	Thr	Val 135	Leu	Leu	Tyr	Gly	Gly 140	Gly	Ala	Val	Val
Ala 145	Leu	Trp	Leu	Thr	Ser 150	Val	Val	Val	Gly	Ala 155	Ile	Asn	Ala	Val	Pro 160
Leu	Leu	Pro	Lys 165	Ile	Leu	Glu	Leu	Val 170	Gly	Leu	Gly	Tyr	Thr 175	Gly	Trp
Phe	Val	Tyr 180	Arg	Tyr	Leu	Leu	Phe	Lys 185	Glu	Ser	Arg	Lys	Glu 190	Leu	Ala
Ala	Asp	Ile 195	Glu	Thr	Leu	Lys	Lys 200	Lys	Ile	Ala	Gly	Thr 205	Glu		

(2) INFORMATION FOR SEQ ID NO:3370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..461
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3370:

aactcagatt	cagtacaagc	tcaagccagg	cacacagcaa	gacatcgacc	atggctgcct	60
accaacaagc	tcccgcctctc	ctgtgcgcct	gcctgatgct	cgtgctcatg	gcgggcgcgg	120
catccggcgg	ccgcgtagac	gtggaagaca	tgctgatgat	ggaccggttc	cgcgcggtggc	180
aagccacgta	caaccgctcg	tacctgaccg	ccgcggagyg	Tctgcgccgg	ttcgaggtgt	240
accgccagaa	catggagctc	atcgaggcca	cgaaccgccg	cgccgagctc	tcgtaccagc	300
tcggcgagac	cccgttcacc	gacctcacca	gcgaggagtt	cctcgccaca	cacaccatgt	360
ccacgcgcct	gcctgcgtcc	gaggccgctc	ggcggcaccg	ggagctcatc	acgacgcacg	420
caggccccgt	cagcgacgGc	ggtcgcCagt	ggaaccggcg	g		

(2) INFORMATION FOR SEQ ID NO:3371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3371:

Thr	Gln	Ile	Gln	Tyr	Lys	Leu	Lys	Pro	Gly	Thr	Gln	Gln	Asp	Ile	Asp	
1				5				10						15		
His	Gly	Cys	Leu	Pro	Thr	Ser	Ser	Arg	Ser	Pro	Val	Arg	Leu	Pro	Asp	
			20					25					30			
Ala	Arg	Ala	His	Gly	Gly	Arg	Gly	Ile	Arg	Arg	Pro	Arg	Arg	Arg	Gly	
		35					40					45				
Arg	His	Ala	Asp	Asp	Gly	Pro	Val	Pro	Arg	Val	Ala	Ser	His	Val	Gln	
		50				55					60					
Pro	Leu	Val	Pro	Asp	Arg	Arg	Gly	Xaa	Ser	Ala	Pro	Val	Arg	Gly	Val	
65				70					75					80		
Pro	Pro	Glu	His	Gly	Ala	His	Arg	Gly	His	Glu	Pro	Pro	Arg	Arg	Ala	
			85					90						95		
Leu	Val	Pro	Ala	Arg	Arg	Asp	Pro	Val	His	Arg	Pro	His	Gln	Arg	Gly	
		100					105						110			
Val	Pro	Arg	His	Thr	His	His	Val	His	Ala	Pro	Ala	Cys	Val	Arg	Gly	
		115					120					125				
Arg	Ser	Ala	Ala	Pro	Gly	Ala	His	His	Asp	Ala	Arg	Arg	Pro	Arg	Gln	
	130					135					140					
Arg	Arg	Arg	Ser	Pro	Val	Glu	Pro	Ala								
145						150										

(2) INFORMATION FOR SEQ ID NO:3372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1576594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3372:

Leu	Arg	Phe	Ser	Thr	Ser	Ser	Ser	Gln	Ala	His	Ser	Lys	Thr	Ser	Thr
1			5						10					15	
Met	Ala	Ala	Tyr	Gln	Gln	Ala	Pro	Ala	Leu	Leu	Cys	Ala	Cys	Leu	Met
			20					25					30		
Leu	Val	Leu	Met	Ala	Gly	Ala	Ala	Ser	Gly	Gly	Arg	Val	Asp	Val	Glu
			35				40					45			
Asp	Met	Leu	Met	Met	Asp	Arg	Phe	Arg	Ala	Trp	Gln	Ala	Thr	Tyr	Asn
50					55						60				
Arg	Ser	Tyr	Leu	Thr	Ala	Glu	Xaa	Leu	Arg	Arg	Phe	Glu	Val	Tyr	
65					70				75					80	
Arg	Gln	Asn	Met	Glu	Leu	Ile	Glu	Ala	Thr	Asn	Arg	Arg	Ala	Glu	Leu
			85					90						95	
Ser	Tyr	Gln	Leu	Gly	Glu	Thr	Pro	Phe	Thr	Asp	Leu	Thr	Ser	Glu	Glu
			100					105					110		
Phe	Leu	Ala	Thr	His	Thr	Met	Ser	Thr	Arg	Leu	His	Ala	Ser	Glu	Ala
		115					120					125			
Ala	Arg	Arg	His	Arg	Glu	Leu	Ile	Thr	Thr	His	Ala	Gly	Pro	Val	Ser
130					135						140				
Asp	Gly	Gly	Arg	Gln	Trp	Asn	Arg	Arg							
145					150										

(2) INFORMATION FOR SEQ ID NO:3373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1576595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3373:

Met	Ala	Ala	Tyr	Gln	Gln	Ala	Pro	Ala	Leu	Leu	Cys	Ala	Cys	Leu	Met
1			5						10					15	
Leu	Val	Leu	Met	Ala	Gly	Ala	Ala	Ser	Gly	Gly	Arg	Val	Asp	Val	Glu
			20					25					30		
Asp	Met	Leu	Met	Met	Asp	Arg	Phe	Arg	Ala	Trp	Gln	Ala	Thr	Tyr	Asn
			35				40					45			
Arg	Ser	Tyr	Leu	Thr	Ala	Ala	Glu	Xaa	Leu	Arg	Arg	Phe	Glu	Val	Tyr
50					55						60				
Arg	Gln	Asn	Met	Glu	Leu	Ile	Glu	Ala	Thr	Asn	Arg	Arg	Ala	Glu	Leu
65					70					75				80	
Ser	Tyr	Gln	Leu	Gly	Glu	Thr	Pro	Phe	Thr	Asp	Leu	Thr	Ser	Glu	Glu
			85					90						95	
Phe	Leu	Ala	Thr	His	Thr	Met	Ser	Thr	Arg	Leu	His	Ala	Ser	Glu	Ala
			100					105					110		
Ala	Arg	Arg	His	Arg	Glu	Leu	Ile	Thr	Thr	His	Ala	Gly	Pro	Val	Ser
			115				120					125			
Asp	Gly	Gly	Arg	Gln	Trp	Asn	Arg	Arg							
130					135										

(2) INFORMATION FOR SEQ ID NO:3374:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 677 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..677

(D) OTHER INFORMATION: / Ceres Seq. ID 1576618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3374:

aattgcgatt	gogagtcttc	caaaccatgg	cgctcgccct	ggcctctcca	atggcgtctc	60
tctccttcca	ctccgggagg	atctcggcgg	cgtctatcgg	aggcgtcggc	cgcactcgca	120
gggcgccccc	ggtggGcgta	tccgcctcgc	cgttcCtccg	gagctccttc	gtctcgtcct	180
cctccacgtc	gtccgcctcc	gcctccgcct	ccvccgcttc	gctcgcggcg	gctgtctcgg	240
cgtctctggc	atttacgtcc	tcctccgcgt	ttgcggggttc	atctttggga	atcgagttca	300
gctacagtat	aatgacaaca	cggagatccc	gtggtatgca	gattagggct	ggaaaaggctg	360
ccctctgcat	gaccaagagg	tcaaggtcta	ggaagtcact	tgcccgtaca	catggtttcc	420
gcagGcggat	gcggaactact	tctggaagga	aggtactgaa	gCgcaggcgc	gccaaaggca	480
ggaaggttct	ttgcacaagg	acaaactcaa	acagtgggaa	gaaaagaatg	ttctaattac	540
actgcaattt	gatgtgctcg	caactgtaag	tgtaatgtct	acttgcaatc	ttctaagccg	600
ccatctatgt	gtaacaatca	tgtagcatcc	tattcctgtt	taattgggta	aaaatatctg	660
gatcaccttc	tgcttcc					

(2) INFORMATION FOR SEQ ID NO:3375:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..177

(D) OTHER INFORMATION: / Ceres Seq. ID 1576619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3375:

Leu	Arg	Leu	Arg	Val	Leu	Gln	Thr	Met	Ala	Leu	Ala	Leu	Ala	Ser	Pro
1				5					10					15	
Met	Ala	Ser	Leu	Ser	Phe	His	Ser	Gly	Arg	Ile	Ser	Ala	Ala	Ser	Ile
				20				25					30		
Gly	Gly	Val	Gly	Arg	Thr	Arg	Arg	Ala	Ala	Pro	Val	Gly	Val	Ser	Ala
				35				40					45		
Ser	Pro	Phe	Leu	Arg	Ser	Ser	Phe	Val	Ser	Ser	Ser	Ser	Thr	Ser	Ser
				50			55				60				
Ala	Ser	Ala	Ser	Ala	Ser	Xaa	Ala	Ser	Leu	Ala	Ala	Ala	Val	Ser	Ala
65					70					75				80	
Ser	Leu	Ala	Phe	Thr	Ser	Ser	Ser	Ala	Phe	Ala	Gly	Ser	Ser	Leu	Gly
				85					90					95	
Ile	Glu	Phe	Ser	Tyr	Ser	Ile	Met	Thr	Thr	Arg	Arg	Ser	Arg	Gly	Met
				100					105				110		
Gln	Ile	Arg	Ala	Gly	Lys	Ala	Ala	Leu	Cys	Met	Thr	Lys	Arg	Ser	Arg
				115			120					125			
Ser	Arg	Lys	Ser	Leu	Ala	Arg	Thr	His	Gly	Phe	Arg	Arg	Arg	Met	Arg
				130			135				140				
Thr	Thr	Ser	Gly	Arg	Lys	Val	Leu	Lys	Arg	Arg	Ala	Lys	Gly	Arg	
145					150				155					160	
Lys	Val	Leu	Cys	Thr	Arg	Thr	Asn	Ser	Asn	Ser	Gly	Lys	Lys	Arg	Met
				165					170					175	
Phe															

(2) INFORMATION FOR SEQ ID NO:3376:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1576620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3376:

Met Ala Leu Ala Leu Ala Ser Pro Met Ala Ser Leu Ser Phe His Ser
1 5 10 15
Gly Arg Ile Ser Ala Ala Ser Ile Gly Gly Val Gly Arg Thr Arg Arg
20 25 30
Ala Ala Pro Val Gly Val Ser Ala Ser Pro Phe Leu Arg Ser Ser Phe
35 40 45
Val Ser Ser Ser Ser Thr Ser Ser Ala Ser Ala Ser Ala Ser Xaa Ala
50 55 60
Ser Leu Ala Ala Ala Val Ser Ala Ser Leu Ala Phe Thr Ser Ser Ser
65 70 75 80
Ala Phe Ala Gly Ser Ser Leu Gly Ile Glu Phe Ser Tyr Ser Ile Met
85 90 95
Thr Thr Arg Arg Ser Arg Gly Met Gln Ile Arg Ala Gly Lys Ala Ala
100 105 110
Leu Cys Met Thr Lys Arg Ser Arg Ser Arg Lys Ser Leu Ala Arg Thr
115 120 125
His Gly Phe Arg Arg Arg Met Arg Thr Thr Ser Gly Arg Lys Val Leu
130 135 140
Lys Arg Arg Arg Ala Lys Gly Arg Lys Val Leu Cys Thr Arg Thr Asn
145 150 155 160
Ser Asn Ser Gly Lys Lys Arg Met Phe
165

(2) INFORMATION FOR SEQ ID NO:3377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1576621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3377:

Met Ala Ser Leu Ser Phe His Ser Gly Arg Ile Ser Ala Ala Ser Ile
1 5 10 15
Gly Gly Val Gly Arg Thr Arg Arg Ala Ala Pro Val Gly Val Ser Ala
20 25 30
Ser Pro Phe Leu Arg Ser Ser Phe Val Ser Ser Ser Ser Thr Ser Ser
35 40 45
Ala Ser Ala Ser Ala Ser Xaa Ala Ser Leu Ala Ala Ala Val Ser Ala
50 55 60
Ser Leu Ala Phe Thr Ser Ser Ser Ala Phe Ala Gly Ser Ser Leu Gly
65 70 75 80
Ile Glu Phe Ser Tyr Ser Ile Met Thr Thr Arg Arg Ser Arg Gly Met
85 90 95
Gln Ile Arg Ala Gly Lys Ala Ala Leu Cys Met Thr Lys Arg Ser Arg
100 105 110
Ser Arg Lys Ser Leu Ala Arg Thr His Gly Phe Arg Arg Met Arg
115 120 125
Thr Thr Ser Gly Arg Lys Val Leu Lys Arg Arg Arg Ala Lys Gly Arg
130 135 140
Lys Val Leu Cys Thr Arg Thr Asn Ser Asn Ser Gly Lys Lys Arg Met
145 150 155 160
Phe

(2) INFORMATION FOR SEQ ID NO:3378:

(i) SEQUENCE CHARACTERISTICS:

(A1) SEQUENCE DESCRIPTION: SEQ ID NO: 1						
gttgcccggt	gtgctctctc	tctctattcg	tccccgcct	camcccgagc	cagccgtctc	60
gctagggttt	gcgcgcgcgc	gcgcgcgcgc	ccgcgcctat	gcctcgccgc	agctcaggcg	120
cggcaaattg	caggcggcag	ggttgacat	gctacctca	agggcccag	cgtggtgaag	180
gagatcttca	ttggaactgac	cctGgggtct	gatcgctgga	ggtatgtgga	agatgcacca	240
ctggaacgag	cagaggaaaa	ctagatcctt	ctacgacatg	cttgacaagg	gccagatcgt	300
cgtcgtcgag	gagtagtctc	cacgtgtcac	ctcagaagtt	tttttttttc	agttgttttt	360
gaaaactcac	tctggagagc	acgacaaagt	gaatgtctgt	gatatttggc	ttgaaaataa	420
gcataaccat	ttgaagaacac	cagcttctgt	tgaattgtct	tttcttgtca	tgactatttt	

[illegible]

Leu	Pro	Val	Val	Leu	Ser	Leu	Ser	Ile	Arg	Ser	Pro	Pro	Xaa	Pro	Glu
1				5					10					15	
Pro	Ala	Val	Ser	Leu	Gly	Phe	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Arg
			20					25					30		
Tyr	Ala	Ser	Pro	Gln	Leu	Arg	Arg	Gly	Lys	Trp	Gln	Ala	Ala	Gly	Leu
			35				40					45			
His	Met	Leu	Pro	Ser	Arg	Ala	Pro	Ala	Trp						

50 55
(2) INFORMATION FOR SEQ ID NO:3381:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..45
(D) OTHER INFORMATION: / Ceres Seq. ID 1576639
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3381:
Met Ala Gly Gly Arg Val Ala His Ala Thr Leu Lys Gly Pro Ser Val
1 5 10 15
Val Lys Glu Ile Phe Ile Gly Leu Thr Leu Gly Ser Asp Arg Trp Arg
20 25 30
Tyr Val Glu Asp Ala Pro Leu Glu Arg Ala Glu Glu Asn
35 40 45

(2) INFORMATION FOR SEQ ID NO:3382:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 719 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..719
(D) OTHER INFORMATION: / Ceres Seq. ID 1576648
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3382:
gttgatatatg cggatctcca ttaccaaatc gccttctctgt cgccctcccg ctggtgctcgg 60
cgaacgcgat ctgttcccca acctccgcag ccgctccacc gtctctccact ccggctgccc 120
aatcgaccog ccccgatcca gatcaggagc tgagggatgg acgcgaacag gcgccagagt 180
gggatccagc agttgctggc tgcggaScag gaggtcagc aaattgtgaa tgccCgctag 240
agctgccaag tcagcgaggc tcaggcaagc aaaagaggag gctgagcggg aaatagccga 300
ataccgtgcc cagatggagg ctgagtttca gaggaaggtt gcagagagca gcggcgactc 360
cggtgcaaac gtcaagcgtc tcgaggaaga aacggcggcg aagatcgagc aactcaccca 420
gcaggccgca agcatctccc cggatgtcat tcagatgctt ctgcggcattg tcaccaccgt 480
caagaactga ggagtgtgtt tcccgaacta tgctcgcaga cttgtaccgt cgatctattt 540
atttttgtca agagtgagag tggtagggaa taatatgccg gcttgtatcc ataattcctg 600
ttcgtaaacta cggaataagc cgccgcagct ttagcggcaa acgtgactag tactgtcaga 660
acctaccatt gttatttggt acaattggta aataatattg ttttaaactg gatttttcg

(2) INFORMATION FOR SEQ ID NO:3383:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..75
(D) OTHER INFORMATION: / Ceres Seq. ID 1576649
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3383:
Leu Tyr Met Arg Ile Ser Ile His Gln Ser Pro Ser Cys Arg Pro Pro
1 5 10 15
Ala Arg Leu Gly Glu Arg Asp Leu Phe Pro Asn Leu Arg Ser Arg Ser
20 25 30
Thr Val Leu His Ser Gly Cys Arg Ile Asp Pro Pro Arg Ser Arg Ser
35 40 45

Gly Ala Glu Gly Trp Thr Arg Thr Gly Ala Arg Val Gly Ser Ser Ser
50 55 60
Cys Trp Leu Arg Xaa Arg Arg Leu Ser Lys Leu
65 70 75

(2) INFORMATION FOR SEQ ID NO:3384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3384:

Cys Ile Cys Gly Ser Pro Phe Thr Asn Arg Leu Pro Val Ala Leu Pro
1 5 10 15
Leu Gly Ser Ala Asn Ala Ile Cys Ser Pro Thr Ser Ala Ala Pro
20 25 30
Pro Ser Ser Thr Pro Ala Ala Glu Ser Thr Arg Pro Asp Pro Asp Gln
35 40 45
Glu Leu Arg Asp Gly Arg Glu Gln Ala Pro Glu Trp Asp Pro Ala Val
50 55 60
Ala Gly Cys Gly Xaa Gly Gly Ser Ala Asn Cys Glu Cys Pro Leu Glu
65 70 75 80
Leu Pro Ser Gln Arg Gly Ser Gly Lys Gln Lys Arg Arg Leu Ser Gly
85 90 95
Lys

(2) INFORMATION FOR SEQ ID NO:3385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3385:

Met Pro Ala Arg Ala Ala Lys Ser Ala Arg Leu Arg Gln Ala Lys Glu
1 5 10 15
Glu Ala Glu Arg Glu Ile Ala Glu Tyr Arg Ala Gln Met Glu Ala Glu
20 25 30
Phe Gln Arg Lys Val Ala Glu Ser Ser Gly Asp Ser Gly Ala Asn Val
35 40 45
Lys Arg Leu Glu Glu Glu Thr Ala Ala Lys Ile Glu Gln Leu Thr Gln
50 55 60
Gln Ala Ala Ser Ile Ser Pro Asp Val Ile Gln Met Leu Leu Arg His
65 70 75 80
Val Thr Thr Val Lys Asn
85

(2) INFORMATION FOR SEQ ID NO:3386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..756
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3386:

atagggttct aagcctcggc cgttttcttcg tctccacagc tcccgcgcgc gcggaccagc	60
gcgtcactct accgggttcc ggcgtctccc cgtaccgcga gcgcggcatc catggcggas	120
agacggaaag ggctttcttg aagcagccca aggtgtttct ctgttccaag aaggccacca	180
aggtaaacaac acctggcaag ggaggaaaca gattctggaa gaacattggc cttggtttca	240
agacacccag ggaagccatt gaaggaacct acattgataa gaagtgtcca ttcaccggca	300
ctgtgtctat caggggtcgc atcatcgccg gaacatgcca cagtgtctaa atgaatagga	360
ccatcattgt tcgttagaat tatcttctac tcgtcaagaa gtaccagagg tatgagaaga	420
gacactccaa catccctgcg cacatttcac catgcttccg tgtcaaggaa ggagatcatg	480
tgatcattgg ccagtgcagg ccagtgtcga agactgNtaa ggttcaatgt ggtcaaagtt	540
attcctgcag gttcgaagag tggagcagtg aagaaagctt tctactgccg ttaagatcat	600
gacgagttca tcatccatgg cccggaaaag ctctgtgtta taacgttttg atgctgccta	660
ttagcctttt tccccgtaac tactatatgt gtacttgga ttggacttga attacatcca	720
gaacttgaaa tcctgaaaaa aaatcataac cctttg	

(2) INFORMATION FOR SEQ ID NO:3387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3387:

Met Asn Arg Thr Ile Ile Val Arg Arg Asn Tyr Leu His Phe Val Lys	
1 5 10 15	
Lys Tyr Gln Arg Tyr Glu Lys Arg His Ser Asn Ile Pro Ala His Ile	
20 25 30	
Ser Pro Cys Phe Arg Val Lys Glu Gly Asp His Val Ile Ile Gly Gln	
35 40 45	
Cys Arg Pro Val Ser Lys Thr Xaa Lys Val Gln Cys Gly Gln Ser Tyr	
50 55 60	
Ser Cys Arg Phe Glu Glu Trp Ser Ser Glu Glu Ser Phe His Cys Arg	
65 70 75 80	
Leu Arg Ser	

(2) INFORMATION FOR SEQ ID NO:3388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1034
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3388:

gtgtctctta tttctttgtg tgtttggttg ctggaaaggg agtggacttt tacaacttct	60
catgtcccta ttgttgggag gggttcggagt ccggtatcggg atttgccaca accagattgt	120
tcaacactcg gaaggctcac caaatcgtcc tacgcttctg ctctctctct caccaggtga	180
ggaaacccta gcgactgacc atggcggtgc tcccgcgcac cgcacgggtg gccttctct	240
ctaccccgcg gtcgtactcc gccgcccgcg ctgcgggcgc ctccccgacc tccccagcgc	300
catacggggg cgcgccccca ccggcgatgt cgaagaggnc cgagttcgtg gtctccaagg	360
ttgatgacct gatgaactgg gcgcgtaagg gctcgatttg gcccatgacc tttgggctcg	420

cctgctgcr c ggtcgagatg atgcacgccg gcgCgtcccg ctacgacttc gaccggGttc 480
ggcgtcatct tccgtccctc gccgcgcmag tccgattgca tgatcgtcgc cggcacgytc 540
accaacaaaa tggctccagc cctccgcaag gtttatgacc aaatgcctga gcctagatgg 600
gttatttcaa tgggcagctg tgccaacggt ggtggatact accattactc ctactctggt 660
gtacgtggat gtgacggtat agtccccgtg gacatctacg tccctgggtg cccaccaact 720
gctgaggcac tgctgtacgg tgttcttcag ctccaaaaga agatcaacag gcgtaaggat 780
ttccttcaact ggtggaccaa gtgaagcatg cttctgctgt tgctcgcttg ctacgtttct 840
ttgcactcga cctacctgtc ttatctgaaa taaggacgga ctttgctcgg attcacaaaat 900
ttgttggtgcc tggaaggatg tatgcccagg ttgtgacgaa catataactt gtgtacttgg 960
agtcagttcg cctgtaatgg acaccagacc tgctgtgaat ctgtttttaa gcttccattg 1020
taatacagca atac

(2) INFORMATION FOR SEQ ID NO:3389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3389:

Cys Leu Leu Phe Leu Cys Val Phe Gly Cys Trp Lys Gly Ser Gly Leu
1 5 10 15
Leu Gln Leu Leu Met Ser Leu Leu Leu Gly Gly Phe Gly Val Arg Ile
20 25 30
Gly Ile Cys His Asn Gln Ile Val Gln His Ser Glu Gly Ser Pro Asn
35 40 45
Arg Pro Thr Leu Leu Leu Pro Pro Arg Gly Glu Glu Thr Leu Ala
50 55 60
Thr Asp His Gly Val Ala Pro Ala His Arg Thr Val Gly Leu Pro Leu
65 70 75 80
Tyr Pro Ala Val Val Leu Arg Arg Arg Arg Cys Gly Arg Leu Pro Asp
85 90 95
Leu Pro Ser Ala Ile Arg Gly Arg Ala Pro Thr Gly Asp Val Glu Glu
100 105 110
Xaa Arg Val Arg Gly Leu Gln Gly
115 120

(2) INFORMATION FOR SEQ ID NO:3390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3390:

Met Ser Leu Leu Leu Gly Gly Phe Gly Val Arg Ile Gly Ile Cys His
1 5 10 15
Asn Gln Ile Val Gln His Ser Glu Gly Ser Pro Asn Arg Pro Thr Leu
20 25 30
Leu Leu Pro Pro Pro Arg Gly Glu Glu Thr Leu Ala Thr Asp His Gly
35 40 45
Val Ala Pro Ala His Arg Thr Val Gly Leu Pro Leu Tyr Pro Ala Val
50 55 60
Val Leu Arg Arg Arg Arg Cys Gly Arg Leu Pro Asp Leu Pro Ser Ala
65 70 75 80

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Ile Arg Gly Arg Ala Pro Thr Gly Asp Val Glu Glu Xaa Arg Val Arg
85 90 95
Gly Leu Gln Gly
100

(2) INFORMATION FOR SEQ ID NO:3391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3391:

Met Ala Leu Leu Pro Arg Thr Ala Arg Leu Ala Phe Leu Ser Thr Pro
1 5 10 15
Arg Ser Tyr Ser Ala Ala Ala Ala Gly Ala Ser Pro Thr Ser Pro
20 25 30
Ala Pro Tyr Gly Gly Ala Pro Pro Ala Met Ser Lys Arg Xaa Glu
35 40 45
Phe Val Val Ser Lys Val Asp Asp Leu Met Asn Trp Ala Arg Lys Gly
50 55 60
Ser Ile Trp Pro Met Thr Phe Gly Leu Ala Cys Cys Xaa Val Glu Met
65 70 75 80
Met His Ala Gly Ala Ser Arg Tyr Asp Phe Asp Arg Val Arg Arg His
85 90 95
Leu Pro Ser Leu Ala Ala Xaa Val Arg Leu His Asp Arg Arg Arg His
100 105 110
Xaa His Gln Gln Asn Gly Ser Ser Pro Pro Gln Gly Leu
115 120 125

(2) INFORMATION FOR SEQ ID NO:3392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 868 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..868
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3392:

adgcctctcc aaaattcgaa caccctcgcc tggaaccttc tacgagccag ctccgagcgg 60
ttgccgtccc ataattctgag agacggtgcc gtgggtttgc rgcgcctggg tcgccagtaa 120
agtgcgggcc gagatggagt cctcgctgctc rggcgggcggg ctggcgcggc ggcgagtag 180
cggcggtctgg ggcagcttca gcggcgacac ggaccggttc gacatccccg cgaagggcgc 240
acccctcgag cggttagga agtggcgga agcagccctt gtgctgaatg catcaaggcg 300
ctttaggtac acactcgatt ttggaagagc attggccttg gtttcaagac tcccagcgaa 360
Gcaattgaag ggacctacat tgacaagaaa tgtccattca ctggaaccgt ttctatcaga 420
ggcagaatta ttgctggaac atgccacagt gctaagatga acagaaccat cattgttcgc 480
aggaactatc tccactttgt taagaaatac cagaggtatg aaaagaggca ctccaacatt 540
ccagctcaca tctccccatg cttcogtgtg aagggaaggc accatgtcat cattggccag 600
tgcaggcccc tatcaaaaac tgtgagggttc aatgtcgtca aagtcattcc agctggatct 660
gctgctgccg gcaagaaggc tttcacccga gcctgagttt aagactatgt tccatgagta 720
gtttatatag tgatgtcttt ttttgttaaa aaaactgcct tctaggcttg tgcctttcga 780
ctatggtttg gagattgttc ccatcttaat gaagtccaat catctgaaca tgttactgtt 840
tattgtacct tgtcgtgcaa agttttcc

(2) INFORMATION FOR SEQ ID NO:3393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..108
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576683
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3393:

Met Glu Ser Ser Ser Xaa Gly Gly Gly Leu Ala Arg Arg Arg Ser Ser
1 5 10 15
Gly Gly Trp Gly Ser Phe Ser Gly Asp Thr Asp Pro Phe Asp Ile Pro
20 25 30
Ala Lys Gly Ala Pro Leu Glu Arg Leu Arg Lys Trp Arg Gln Ala Ala
35 40 45
Leu Val Leu Asn Ala Ser Arg Arg Phe Arg Tyr Thr Leu Asp Phe Gly
50 55 60
Arg Ala Leu Ala Leu Val Ser Arg Leu Pro Ala Lys Gln Leu Lys Gly
65 70 75 80
Pro Thr Leu Thr Arg Asn Val His Ser Leu Glu Pro Phe Leu Ser Glu
85 90 95
Ala Glu Leu Leu Leu Glu His Ala Thr Val Leu Arg
100 105

(2) INFORMATION FOR SEQ ID NO:3394:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..79
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576684
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3394:

Met Asn Arg Thr Ile Ile Val Arg Arg Asn Tyr Leu His Phe Val Lys
1 5 10 15
Lys Tyr Gln Arg Tyr Glu Lys Arg His Ser Asn Ile Pro Ala His Ile
20 25 30
Ser Pro Cys Phe Arg Val Lys Glu Gly Asp His Val Ile Ile Gly Gln
35 40 45
Cys Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Val Lys Val Ile
50 55 60
Pro Ala Gly Ser Ala Ala Gly Lys Lys Ala Phe Thr Ala Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:3395:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..63
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576685
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3395:

Met Leu Pro Cys Glu Gly Arg Arg Pro Cys His His Trp Pro Val Gln
1 5 10 15
Ala Pro Ile Lys Asn Cys Glu Val Gln Cys Arg Gln Ser His Ser Ser

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20 25 30
Trp Ile Cys Cys Arg Gln Glu Gly Phe His Arg Ser Leu Ser Leu
35 40 45
Arg Leu Cys Ser Met Ser Ser Leu Tyr Ser Asp Val Phe Phe Cys
50 55 60

(2) INFORMATION FOR SEQ ID NO:3396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..921
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3396:

atcctctagc tctctctctc tctcttctct cacacacaca cacagtcaca gacaccccta 60
tcaattagac tgtgctagta ggtagcggcc gcgtaatgga gcaggagctc agccttgagc 120
tcacctctct ccacctctcg gcctcgccgc cggagccacc gggctacttc gtctgcatgt 180
actgcgaccg caagttcttc agctcgagg ctctcggtgg ccaccagaac gcgcacaagt 240
acgagcgcas ctggccaagc gccgcaggga gatagccgcc gccctgcgcy gcgcacggggc 300
ggcgcgccacc gmaccgggcg cyccggagga cgacgmcygc gccgcgatgg gctctcgca 360
tgtccccgcc aggccacaag gcacgggtac cggagtcgtc gtcgttgaag atgagagtgc 420
aaccaggatg atggGacaag cagaaggctc ctgctgctga tgacgasstc ccgcgaccgc 480
gtcgtcgagc aacatgaaga ggtcgtcgga gtacggctac ggcgtcgagg agctggatct 540
ctccctcagg ctttgattgg ttctctcttc tcctccacyn nnanatataa ttgcggccgt 600
tngetnagat aattcgatct ttgtggtcag tgcaatcatc tgtttcgcgt gcgtggatc 660
tcagtgtctg atccgtcact ttcttctca tgtagttgtt gtgcagttat attcttccat 720
ccgatgatgg aacctatcgg caagaactat tgcggccca tcctgctatc caaagggcgt 780
ggatatttgg gtgctctttt cggttttctg ccttgagtct tctttgtgcg atctaaattc 840
gcagcttggt ttttccaaaa cggcggaac agttttgccg caatttcgtt tggacctttt 900
tcaagtgact ctaaattggg c

(2) INFORMATION FOR SEQ ID NO:3397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..59
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3397:

Met Glu Gln Glu Ser Leu Glu Leu Thr Leu Leu His Pro Ser Ala
1 5 10 15
Ser Pro Pro Glu Pro Pro Gly Tyr Phe Val Cys Met Tyr Cys Asp Arg
20 25 30
Lys Phe Phe Ser Ser Gln Ala Leu Gly Gly His Gln Asn Ala His Lys
35 40 45
Tyr Glu Arg Xaa Trp Pro Ser Ala Ala Gly Arg
50 55

(2) INFORMATION FOR SEQ ID NO:3398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..37
(D) OTHER INFORMATION: / Ceres Seq. ID 1576715
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3398:
Met Gly Ser Arg Asp Val Pro Ala Arg Pro Gln Gly Thr Gly Thr Gly
1 5 10 15
Val Val Val Val Glu Asp Glu Ser Ala Thr Arg Met Met Gly Gln Ala
20 25 30
Glu Gly Ser Cys Cys
35

(2) INFORMATION FOR SEQ ID NO:3399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1576716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3399:

Met Thr Xaa Ser Arg Asp Arg Val Val Glu Gln His Glu Glu Val Val
1 5 10 15
Gly Val Arg Leu Arg Arg Arg Gly Ala Gly Ser Leu Pro Gln Ala Leu
20 25 30
Ile Gly Ser Ser Ser Ser Ser Xaa Xaa Xaa Tyr Asn Ser Pro Arg Xaa
35 40 45
Xaa Arg
50

(2) INFORMATION FOR SEQ ID NO:3400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..831

(D) OTHER INFORMATION: / Ceres Seq. ID 1576730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3400:

tcaagcacct	atatagtagt	acctcataat	ggcaggcaaa	aacctaatac	cattggggct	60
cattatcctc	atgaccatgg	gattagccaa	tgctgttagg	gtggtttagat	actctagtgc	120
cgatggtact	ggcacaggac	agggagaagg	tggtggatat	gtgaatggcg	ggggatcagg	180
gtctgggtct	ggcaccggat	caggtgatag	tggtccttat	ggtgcacatg	caagtrctag	240
tmgaggtggt	ggaggggggtg	gaactagcca	gtacggtggtg	tctggatatg	gttctgggtc	300
agggtcaggg	tcaggatcta	gtacatatag	tcaaggagggtg	tattctgggtt	atggagaatc	360
ttctagtgtc	ggtRggcatc	ggtgggggtg	gaggtggagg	acaagctgca	ggcgcatgga	420
attccaatgc	tcaaggatcc	ggtagtggaa	ctggttcttg	ctctagctat	gctaacaggt	480
attggtacgg	atcaagtga	gcagggtgcaa	gtgctaattg	caatgggtgt	ggcacaggaa	540
atagtcaaaa	cggtggaagt	ggtggtggct	caggtgctgg	atctgggttt	ggcaatgcct	600
acccctaatt	tctatatcta	agtcaacct	tagttggagc	ccaacagtat	ttgtcatttc	660
aagttgtggt	attagttagt	ttgtttgtac	ctctattaca	cttttgctag	aactaaataa	720
ataaagggcc	caactattct	agtaattggca	gcagtttagt	gtgaggttca	gcttgtaaga	780
atttgttgta	aacatgtcag	tctatgaatg	aaataataac	ttcccttttag	c	

(2) INFORMATION FOR SEQ ID NO:3401:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..138
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576731
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3401:

Met Ala Gly Lys Asn Leu Ile Pro Leu Gly Leu Ile Ile Leu Met Thr
1 5 10 15
Met Gly Leu Ala Asn Ala Val Arg Val Val Arg Tyr Ser Ser Ala Asp
 20 25 30
Gly Thr Gly Thr Gly Gln Gly Glu Gly Gly Gly Tyr Val Asn Gly Gly
 35 40 45
Gly Ser Gly Ser Gly Ser Gly Thr Gly Ser Gly Asp Ser Gly Pro Tyr
 50 55 60
Gly Ala His Ala Ser Xaa Ser Xaa Gly Gly Gly Gly Gly Gly Thr Ser
65 70 75 80
Gln Tyr Gly Gly Ser Gly Tyr Gly Ser Gly Ser Gly Ser Gly Ser Gly
 85 90 95
Ser Ser Thr Tyr Ser Gln Gly Gly Tyr Ser Gly Tyr Gly Glu Ser Ser
 100 105 110
Ser Ala Gly Xaa His Arg Trp Gly Trp Arg Trp Arg Thr Ser Cys Arg
 115 120 125
Arg Met Glu Phe Gln Cys Ser Arg Ile Arg
130 135

(2) INFORMATION FOR SEQ ID NO:3402:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 147 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..147

 (D) OTHER INFORMATION: / Ceres Seq. ID 1576732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3402:

Met Ala Gly Asp Gln Gly Leu Gly Leu Ala Pro Asp Gln Val Ile Val
1 5 10 15
Val Leu Met Val His Met Gln Xaa Leu Xaa Glu Val Val Glu Gly Val
 20 25 30
Glu Leu Ala Ser Thr Val Gly Leu Asp Met Val Leu Gly Gln Gly Gln
 35 40 45
Gly Gln Asp Leu Val His Ile Val Lys Glu Gly Ile Leu Val Met Glu
50 55 60
Asn Leu Leu Val Leu Xaa Gly Ile Gly Gly Gly Gly Gly Gly Gln
65 70 75 80
Ala Ala Gly Ala Trp Asn Ser Asn Ala Gln Gly Ser Gly Ser Gly Thr
 85 90 95
Gly Ser Gly Ser Ser Tyr Ala Asn Arg Tyr Trp Tyr Gly Ser Ser Glu
 100 105 110
Ala Gly Ala Ser Ala Asn Gly Asn Gly Gly Gly Thr Gly Asn Ser Gln
 115 120 125
Asn Gly Gly Ser Gly Gly Gly Ser Gly Ala Gly Ser Gly Phe Gly Asn
130 135 140
Ala Tyr Pro
145

(2) INFORMATION FOR SEQ ID NO:3403:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 amino acids
 (B) TYPE: amino acid

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- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..129
(D) OTHER INFORMATION: / Ceres Seq. ID 1576733
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3403:

Met Val His Met Gln Xaa Leu Xaa Glu Val Val Glu Gly Val Glu Leu
1 5 10 15
Ala Ser Thr Val Gly Leu Asp Met Val Leu Gly Gln Gly Gln Gly Gln
20 25 30
Asp Leu Val His Ile Val Lys Glu Gly Ile Leu Val Met Glu Asn Leu
35 40 45
Leu Val Leu Xaa Gly Ile Gly Gly Gly Gly Gly Gly Gly Gln Ala Ala
50 55 60
Gly Ala Trp Asn Ser Asn Ala Gln Gly Ser Gly Ser Gly Thr Gly Ser
65 70 75 80
Gly Ser Ser Tyr Ala Asn Arg Tyr Trp Tyr Gly Ser Ser Glu Ala Gly
85 90 95
Ala Ser Ala Asn Gly Asn Gly Gly Gly Thr Gly Asn Ser Gln Asn Gly
100 105 110
Gly Ser Gly Gly Gly Ser Gly Ala Gly Ser Gly Phe Gly Asn Ala Tyr
115 120 125
Pro

- (2) INFORMATION FOR SEQ ID NO:3404:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 744 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..744
(D) OTHER INFORMATION: / Ceres Seq. ID 1576754

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3404:

ctcacgtca cggccgcgc ctccaccgt cgccgcttcc tcccgttaga ctaggttagg 60
ctaggctagg gtgtcgacca gctcgcggt atggtggcct tcaggttcca tcagtaccag 120
gwggtggggc gcgcgctgcc gacgcccgc gacgagcacc ccaagatcta ccgcatgaag 180
ctctgggcca ccaacgaagt ccgcgccaa agcaagttct ggtacttctt gaggaagttg 240
aagaaggtta agaagagcaa cggtcaggtc ctggccatca acgagatctt cgagcgtaac 300
ccgacgacga tcaagaacta tggcatctgg Ctgcgctacc agagcagaac cggctaccac 360
aacatgtaca aggagtaccg cgacacaacc ctgaacggcg ctgtagagca gatgtacaat 420
gagatggctt ctgcgccacc cgtgagggtc cctgcattcc agatcatcaa gaccgccaca 480
gtacacttca agctgtgcaa gagggacaac accaagcagt ttcacaacag tgagatcaag 540
ttcccaactcg tgtaccgcaa ggtcaggccg ccgaccagga agctgaagac cacgttcaag 600
gcttcgaggc ccaacctgtt catgtgattt agctgtggtc agtgtatgtg atcgtaagaa 660
tctgtgtttt aagttttgac gctaagactt gggtggtttg aagattcaac tcgttttgaa 720
acgtgcatgg tgaaccattt gccg

- (2) INFORMATION FOR SEQ ID NO:3405:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..178

000001-166666

(D) OTHER INFORMATION: / Ceres Seq. ID 1576755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3405:

Met Val Ala Phe 5 Phe His Gln Tyr 10 Gln Xaa Val Gly Arg Ala Leu 15
Pro Thr Pro Gly Asp Glu His Pro Lys Ile Tyr Arg Met Lys Leu Trp 30
20 25 30
Ala Thr Asn Glu Val Arg Ala Lys Ser Lys Phe Trp Tyr Phe Leu Arg 45
35 40 45
Lys Leu Lys Lys Val Lys Lys Ser Asn Gly Gln Val Leu Ala Ile Asn 60
50 55 60
Glu Ile Phe Glu Arg Asn Pro Thr Thr Ile Lys Asn Tyr Gly Ile Trp 80
65 70 75 80
Leu Arg Tyr Gln Ser Arg Thr Gly Tyr His Asn Met Tyr Lys Glu Tyr 95
85 90 95
Arg Asp Thr Thr Leu Asn Gly Ala Val Glu Gln Met Tyr Asn Glu Met 110
100 105 110
Ala Ser Arg His Arg Val Arg Ser Pro Cys Ile Gln Ile Ile Lys Thr 125
115 120 125
Ala Thr Val His Phe Lys Leu Cys Lys Arg Asp Asn Thr Lys Gln Phe 140
130 135 140
His Asn Ser Glu Ile Lys Phe Pro Leu Val Tyr Arg Lys Val Arg Pro 160
145 150 155 160
Pro Thr Arg Lys Leu Lys Thr Thr Phe Lys Ala Ser Arg Pro Asn Leu 175
165 170 175
Phe Met

(2) INFORMATION FOR SEQ ID NO:3406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1576756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3406:

Met Lys Leu Trp Ala Thr Asn Glu Val Arg Ala Lys Ser Lys Phe Trp 15
1 5 10 15
Tyr Phe Leu Arg Lys Leu Lys Lys Val Lys Lys Ser Asn Gly Gln Val 30
20 25 30
Leu Ala Ile Asn Glu Ile Phe Glu Arg Asn Pro Thr Thr Ile Lys Asn 45
35 40 45
Tyr Gly Ile Trp Leu Arg Tyr Gln Ser Arg Thr Gly Tyr His Asn Met 60
50 55 60
Tyr Lys Glu Tyr Arg Asp Thr Thr Leu Asn Gly Ala Val Glu Gln Met 80
65 70 75 80
Tyr Asn Glu Met Ala Ser Arg His Arg Val Arg Ser Pro Cys Ile Gln 95
85 90 95
Ile Ile Lys Thr Ala Thr Val His Phe Lys Leu Cys Lys Arg Asp Asn 110
100 105 110
Thr Lys Gln Phe His Asn Ser Glu Ile Lys Phe Pro Leu Val Tyr Arg 125
115 120 125
Lys Val Arg Pro Pro Thr Arg Lys Leu Lys Thr Thr Phe Lys Ala Ser 140
130 135 140
Arg Pro Asn Leu Phe Met 150
145 150

(2) INFORMATION FOR SEQ ID NO:3407:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 654 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..654
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3407:

ggacottttct atcgcgcgca ttttctttcc gaccagccga vcgcccgcgc cctccggcag	60
gtcttctttcc cgccacgac caccacgccc aggtctttccc ggccccgaac gcgagcacc	120
agccctcctc caggtctttcc ccggcgacga gcgcgtagaa gaggggatcc ttagcacaat	180
ggaagaagga gcaccagggc cgtcgcaagc catcccggat tctggagaca cgtaccgcaa	240
cagctccacc gcgcccgtgg gcagcagctc accgtctgtc gcgaagCtcc ggaagctgct	300
gttccggcgg atgctcatcg gcgtcaacga cggccgctac ttccacggcc tgttccaactg	360
catcgacaag cagggaacaa tcctctcca ggacgccgta gactaccgca gcgcccggca	420
ctgctcgctt ccgacggagc agcgggtgctt ggggctcatc ctgatcccgg ccgctgccc	480
gtcgtcgtgc caggtcgatt gctccgttga agagaagatg tcgctcctgt gttttgagtg	540
aatcgtgctt caaagggaat acactacgca tgtactaagt tactggggct catctctgct	600
atctgaaact gagaggcatg attggtgttt cctatttttg aaggattgtt tatt	

(2) INFORMATION FOR SEQ ID NO:3408:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 179 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..179
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3408:

Asp	Leu	Ser	Ile	Ala	Arg	Ile	Phe	Phe	Pro	Thr	Ser	Arg	Xaa	Pro	Pro
1				5					10					15	
Pro	Ser	Gly	Arg	Ser	Ser	Ser	Arg	Pro	Arg	Pro	Pro	Thr	Pro	Gly	Leu
				20				25					30		
Pro	Gly	Pro	Glu	Arg	Glu	His	Pro	Ala	Leu	Leu	Gln	Val	Phe	Pro	Gly
				35			40					45			
Asp	Glu	Arg	Val	Glu	Glu	Gly	Ile	Leu	Ser	Thr	Met	Glu	Glu	Gly	Ala
				50		55					60				
Pro	Gly	Pro	Ser	Gln	Ala	Ile	Pro	Asp	Ser	Gly	Asp	Thr	Tyr	Arg	Asn
				65		70				75				80	
Ser	Ser	Thr	Ala	Pro	Val	Gly	Ser	Ser	Ser	Pro	Ser	Val	Ala	Lys	Leu
				85				90						95	
Arg	Lys	Leu	Leu	Phe	Arg	Arg	Met	Leu	Ile	Gly	Val	Asn	Asp	Gly	Arg
				100				105					110		
Tyr	Phe	His	Gly	Leu	Phe	His	Cys	Ile	Asp	Lys	Gln	Gly	Asn	Ile	Ile
				115			120					125			
Leu	Gln	Asp	Ala	Val	Glu	Tyr	Arg	Ser	Ala	Arg	His	Cys	Ser	Pro	Pro
				130			135				140				
Thr	Glu	Gln	Arg	Cys	Leu	Gly	Leu	Ile	Leu	Ile	Pro	Ala	Ala	Cys	Arg
				145			150				155			160	
Ser	Ser	Cys	Gln	Val	Asp	Cys	Ser	Val	Glu	Lys	Met	Ser	Leu	Leu	
				165				170					175		
Cys	Phe	Glu													

(2) INFORMATION FOR SEQ ID NO:3409:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..120
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576759
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3409:

Met Glu Glu Gly Ala Pro Gly Pro Ser Gln Ala Ile Pro Asp Ser Gly
1 5 10 15
Asp Thr Tyr Arg Asn Ser Ser Thr Ala Pro Val Gly Ser Ser Ser Pro
 20 25 30
Ser Val Ala Lys Leu Arg Lys Leu Phe Arg Arg Met Leu Ile Gly
 35 40 45
Val Asn Asp Gly Arg Tyr Phe His Gly Leu Phe His Cys Ile Asp Lys
 50 55 60
Gln Gly Asn Ile Ile Leu Gln Asp Ala Val Glu Tyr Arg Ser Ala Arg
65 70 75 80
His Cys Ser Pro Pro Thr Glu Gln Arg Cys Leu Gly Leu Ile Leu Ile
 85 90 95
Pro Ala Ala Cys Arg Ser Ser Cys Gln Val Asp Cys Ser Val Glu Glu
 100 105 110
Lys Met Ser Leu Leu Cys Phe Glu
 115 120

(2) INFORMATION FOR SEQ ID NO:3410:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 555 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..555
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576763
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3410:

gactccacgc cgccagtcac gaccacgccg cgcctccgcc tggaaccctt tagccgagcg 60
gasaagggaa gaaatgggga aggggtacggg cagcttcggc aagcgccgga acaagacgca 120
cacgtctctgc atccgctgcg gcggccggcg tggagcgggc gcgtcaagaa cccgcatcta 180
aatcgggcgc ccagccccga gagctccgac gccgagtgc atgagaagcg agcgagcagc 240
agcagcagca gccaccgcaa aggtcaacg acgacgacgt ccgttgttgc gacggcgccc 300
agcgcagCat gccgctgtcg tcttcgttcg tatccacgta cgtacgacgg cccagctgac 360
ccgtttgcct acccgtccgt tctgtgcgac tggatggctg gtcggcgggc gtcgcggcga 420
gggctttcgg tacgtcgtgg ataagcacga ggggagggcg ggcaggcggg aacggaggcg 480
gaggcgggcg cccaagtgg cggctcttcc aaatgtcaaa aaggacagct gtaacagtga 540
taagaaaaac aagtc

(2) INFORMATION FOR SEQ ID NO:3411:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..72
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576764
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3411:

Asp Ser Thr Pro Pro Val Thr Thr Thr Pro Arg Leu Arg Leu Glu Pro
1 5 10 15
Phe Ser Arg Ala Xaa Lys Gly Arg Asn Gly Glu Gly Tyr Gly Gln Leu
 20 25 30

(A) NAME/KEY: -

(D) OTHER INFORMATION: / Ceres Seq. ID 1576795

gccagttcac	ctccgcctcc	gtccctcccc	tccccctccc	gtcctgccat	ggccaccgca	60
gcacgcgccc	tcgtagccgc	acgcccggca	cggccgtgc	tgccgtctcg	ggcctcccg	120
tctctctct	ccatccgtcc	cgcgcggcaa	cgtgctggcg	tgggtgcgt	ccgctgcattg	180
gctcggcggc	cggattccac	ctattccccg	ctgcgttcgg	gccagggcgg	tgaccgtgca	240
ccgactgaaa	tggcgcctct	gttccctggc	tgcgactacg	agcactggct	catcgctcatg	300
gacaagcccc	ggggcgaggg	cgcaccaaag	cagcaaatga	tagattgtta	cattccagacc	360
cttgcccagg	tggtagggag	tgaagaggag	gcgaagaaga	ggatatataa	tgtgtcctgc	420
gagcgtctatt	ttggattcgg	atgcgaattt	gacgaggaga	cctCccaaca	aactcgaagg	480
ccttccaggg	gttctttttg	tgtttcctga	ctcttacggt	gatgctgaga	acaaggatta	540
tgggtgctgag	ttattttgtga	acggtgaaat	cgttcagcga	tctccagaaa	ggcagagaag	600
ggtggagcca	gtgcctcaga	gagctcagga	tgcaccacgg	tacagtgacc	ggaccgcgta	660
tgtgaagcgg	agggagaacc	aatcttacca	gagatgatgt	ttccgtctct	gaagatgtaa	720
aatgtcacgg	tttccacaag	tgtccaaatg	cggtagctga	gatgcagcag	caactcccca	780
ctactcatat	gagaattgca	tccgttctgt	ttgccgcgca	ttttaagctg	tatatgctta	840
ttatgcattt	gggcttgtac	ctcagtcgat	atgaacgatg	tatcctttga	actaacgcatt	900
tataattttt	gaaaccgttt	taqcc				

(i) SEQUENCE CHARACTERISTICS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..169
(D) OTHER INFORMATION: / Ceres Seq. ID 1576796

Ala 1	Ser	Ser	Pro 5	Pro	Pro	Pro	Leu	Leu 10	Pro	Ser	Pro	Ser	Arg 15	Pro	Ala
Met	Ala	Thr	Ala 20	Ala	Arg	Ala	Leu	Val 25	Ala	Ala	Arg	Pro	Ala 30	Arg	Pro
Leu	Leu	Pro 35	Ser	Arg	Arg	Leu	Pro 40	Ser	Ser	Ser	Ser	Ile 45	Arg	Pro	Ala
Arg	Gln	Arg	Ala 50	Gly	Val	Gly 55	Cys	Val	Arg	Cys	Met	Ala 60	Arg	Arg	Pro
Asp 65	Ser	Thr	Tyr	Ser	Pro 70	Leu	Arg	Ser	Gly	Gln	Gly	Gly 75	Asp	Arg	Ala 80
Pro	Thr	Glu	Met	Ala 85	Pro	Leu	Phe	Pro	Gly 90	Cys	Asp	Tyr	Glu	His 95	Trp
Leu	Ile	Val	Met 100	Asp	Lys	Pro	Gly	Gly 105	Glu	Gly	Ala	Thr	Lys 110	Gln	Gln
Met	Ile	Asp 115	Cys	Tyr	Ile	Gln	Thr	Leu 120	Ala	Gln	Val	Val 125	Gly	Ser	Glu
Glu	Glu	Ala 130	Lys	Lys	Arg	Ile	Tyr	Asn 135	Val	Ser	Cys	Glu 140	Arg	Tyr	Phe
Gly 145	Phe	Gly	Cys	Glu	Ile 150	Asp	Glu	Glu	Thr	Ser 155	Gln	Gln	Thr	Arg	Arg 160
Pro	Ser	Arg	Gly 165	Ser	Phe	Cys	Ala	Ser							

(i) SEQUENCE CHARACTERISTICS:

(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3416:

Pro	Val	His	Leu	Arg	Leu	Arg	Ser	Ser	Pro	Pro	Pro	Pro	Val	Leu	Pro
1			5						10				15		
Trp	Pro	Pro	Gln	His	Ala	Pro	Ser	Ser	Pro	His	Ala	Arg	His	Gly	Arg
			20					25					30		
Cys	Cys	Arg	Leu	Gly	Ala	Ser	Arg	Pro	Pro	Leu	Pro	Ser	Val	Pro	Arg
		35					40					45			
Gly	Asn	Val	Leu	Ala	Ser	Gly	Ala	Ser	Ala	Ala	Trp	Leu	Gly	Gly	Arg
	50					55					60				
Ile	Pro	Pro	Ile	Pro	Arg	Cys	Val	Arg	Ala	Arg	Ala	Val	Thr	Val	His
65					70				75						80
Arg	Leu	Lys	Trp	Arg	Leu	Cys	Ser	Leu	Ala	Ala	Thr	Thr	Ser	Thr	Gly
			85						90					95	
Ser	Ser	Ser	Trp	Thr	Ser	Pro	Gly	Ala	Arg	Ala	Pro	Pro	Ser	Ser	Lys
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:3417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3417:

Met	Ala	Thr	Ala	Ala	Arg	Ala	Leu	Val	Ala	Ala	Arg	Pro	Ala	Arg	Pro
1				5					10				15		
Leu	Leu	Pro	Ser	Arg	Arg	Leu	Pro	Ser	Ser	Ser	Ser	Ile	Arg	Pro	Ala
			20					25					30		
Arg	Gln	Arg	Ala	Gly	Val	Gly	Cys	Val	Arg	Cys	Met	Ala	Arg	Arg	Pro
		35					40					45			
Asp	Ser	Thr	Tyr	Ser	Pro	Leu	Arg	Ser	Gly	Gln	Gly	Gly	Asp	Arg	Ala
	50					55					60				
Pro	Thr	Glu	Met	Ala	Pro	Leu	Phe	Pro	Gly	Cys	Asp	Tyr	Glu	His	Trp
65				70					75						80
Leu	Ile	Val	Met	Asp	Lys	Pro	Gly	Gly	Glu	Gly	Ala	Thr	Lys	Gln	Gln
			85						90					95	
Met	Ile	Asp	Cys	Tyr	Ile	Gln	Thr	Leu	Ala	Gln	Val	Val	Gly	Ser	Glu
		100						105					110		
Glu	Glu	Ala	Lys	Lys	Arg	Ile	Tyr	Asn	Val	Ser	Cys	Glu	Arg	Tyr	Phe
		115					120					125			
Gly	Phe	Gly	Cys	Glu	Ile	Asp	Glu	Glu	Thr	Ser	Gln	Gln	Thr	Arg	Arg
	130					135					140				
Pro	Ser	Arg	Gly	Ser	Phe	Cys	Ala	Ser							
145						150									

(2) INFORMATION FOR SEQ ID NO:3418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..545

(D) OTHER INFORMATION: / Ceres Seq. ID 1576799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3418:

aatcttccag	cccaaagtgc	catccattg	ctcgtctgt	ccctccgttc	acaacctcct	60
ccacgaccga	acgagcagag	cagacccttc	cccctcacca	gctccgggtt	ccagcggcgg	120
cggcggcgaa	gatgatcata	ccggtgcgt	gcttcaCctg	cggcaaggtg	attgggaaca	180
agtgggacct	ctacctcgac	ctcctccagg	ccgactactc	ggaaggggat	gctctggatg	240
ctttggaatt	gttccgctac	tgctgcaggc	gaatgctcat	gacccatgtt	gacctcattg	300
agaagtgtgt	caactacaac	acactggaga	agactgagac	aagttaagtg	agcaagcata	360
tcatgctctg	aaagcactac	tgtttcgcag	tatcatatat	attgtaggcg	gtatgttgtt	420
tcttctctat	caggagagga	ttgttgtGga	gtgtgaactt	gcttttgctc	tcgagcattc	480
aaggactgac	aagggcattg	tgcatctatg	ttacgatgtt	ggagatttta	atcgatataa	540
cggt						

(2) INFORMATION FOR SEQ ID NO:3419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1576800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3419:

Ile	Phe	Gln	Pro	Lys	Val	Pro	Ser	His	Cys	Ser	Leu	Cys	Pro	Ser	Val	
1				5					10						15	
His	Asn	Leu	Leu	His	Asp	Arg	Thr	Ser	Arg	Ala	Asp	Pro	Ser	Pro	Ser	
			20					25					30			
Pro	Ala	Pro	Gly	Ser	Ser	Gly	Gly	Gly	Gly	Glu	Asp	Asp	His	Thr	Gly	
			35				40					45				
Ala	Leu	Leu	His	Leu	Arg	Gln	Gly	Asp	Trp	Glu	Gln	Val	Gly	Pro	Leu	
			50			55					60					
Pro	Arg	Pro	Pro	Pro	Gly	Arg	Leu	Leu	Gly	Arg	Gly	Cys	Ser	Gly	Cys	
65					70					75					80	
Phe	Gly	Ile	Val	Pro	Leu	Leu	Leu	Gln	Ala	Asn	Ala	His	Asp	Pro	Cys	
				85					90					95		

(2) INFORMATION FOR SEQ ID NO:3420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1576801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3420:

Ser	Ser	Ser	Pro	Lys	Phe	His	Pro	Ile	Ala	Arg	Ser	Val	Pro	Pro	Phe	
1				5					10						15	
Thr	Thr	Ser	Ser	Thr	Thr	Glu	Arg	Ala	Glu	Gln	Thr	Leu	Pro	Pro	His	
			20					25				30				
Gln	Leu	Arg	Val	Pro	Ala	Ala	Ala	Ala	Ala	Lys	Met	Ile	Ile	Pro	Val	
			35				40					45				
Arg	Cys	Phe	Thr	Cys	Gly	Lys	Val	Ile	Gly	Asn	Lys	Trp	Asp	Leu	Tyr	
			50			55				60						
Leu	Asp	Leu	Leu	Gln	Ala	Asp	Tyr	Ser	Glu	Gly	Asp	Ala	Leu	Asp	Ala	
65				70					75					80		

Leu Glu Leu Phe Arg Tyr Cys Cys Arg Arg Met Leu Met Thr His Val
85 90 95
Asp Leu Ile Glu Lys Leu Leu Asn Tyr Asn Thr Leu Glu Lys Thr Glu
100 105 110
Thr Ser

(2) INFORMATION FOR SEQ ID NO:3421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3421:

Met Ile Ile Pro Val Arg Cys Phe Thr Cys Gly Lys Val Ile Gly Asn
1 5 10 15
Lys Trp Asp Leu Tyr Leu Asp Leu Leu Gln Ala Asp Tyr Ser Glu Gly
20 25 30
Asp Ala Leu Asp Ala Leu Glu Leu Phe Arg Tyr Cys Cys Arg Arg Met
35 40 45
Leu Met Thr His Val Asp Leu Ile Glu Lys Leu Leu Asn Tyr Asn Thr
50 55 60
Leu Glu Lys Thr Glu Thr Ser
65 70

(2) INFORMATION FOR SEQ ID NO:3422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..748
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3422:

aacttaacca ctactccgca tctactgacg ccgccgccgc cgccgccgcg ctctctccgt	60
cggactagtc agagcatccg tcatggcgaa gaacccaag gtgttcttcg acatcctcat	120
cggcaagtcc aaggccgggc gggtcgtgat ggagctcttc gccgacaagg tgcccaagac	180
ggccgagaac ttccgctgcc tgtgcacggg cgagaagggc ctgggstccg cggggaagcc	240
gctgcactac aagggtcgg ccttccaccg cgtcatcccg ggcttcatgt gccagggcgg	300
cgacttcacc cggggcaacg gcacgggcgg cgagtccatc tacggcgcca gggtcgccga	360
cgagaacttc aagCtgcgcc acacgggacc cggcgtgctc tccatggcca acgcggggcc	420
cgacaccaac ggctcccagt tcttcatctg caccgcgcag acgccctggc ttgacggcaa	480
gcacgtcgtc ttccggcaag tcgtcgawgk ctacgccgtc gtggacaaga tggaggctgt	540
cggttctcag tcaggtgcca cggccgagag cgtacgcata gaggactgcg gccagcttgc	600
cgacgactga gggcctcgt gtgtccgatt gtaaccaa atgaatgatcaa taaatttctt	660
tctttcattc ttttgtttct gtggagatgg ataccggcct gtagttaatt aaccaatata	720
aactatggat ggatggggcg gtgatttg	

(2) INFORMATION FOR SEQ ID NO:3423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..157
(D) OTHER INFORMATION: / Ceres Seq. ID 1576804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3423:

Asn Leu Thr Thr Thr Pro His Leu Leu Thr Pro Pro Pro Pro Pro Pro
1 5 10 15
Arg Ser Leu Arg Arg Thr Ser Gln Ser Ile Arg His Gly Glu Glu Pro
20 25 30
Gln Gly Val Leu Arg His Pro His Arg Gln Val Gln Gly Arg Ala Gly
35 40 45
Arg Asp Gly Ala Leu Arg Arg Gln Gly Ala Gln Asp Gly Arg Glu Leu
50 55 60
Pro Leu Pro Val His Gly Arg Glu Gly Pro Gly Xaa Arg Gly Glu Ala
65 70 75 80
Ala Ala Leu Gln Gly Leu Gly Leu Pro Pro Arg His Pro Gly Leu His
85 90 95
Val Pro Gly Arg Arg Leu His Pro Gly Gln Arg His Gly Arg Arg Val
100 105 110
His Leu Arg Arg Gln Val Arg Arg Glu Leu Gln Ala Ala Pro His
115 120 125
Gly Thr Arg Arg Ala Leu His Gly Gln Arg Gly Ala Arg His Gln Arg
130 135 140
Leu Pro Val Leu His Leu His Arg Ala Asp Ala Leu Ala
145 150 155

(2) INFORMATION FOR SEQ ID NO:3424:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..175
(D) OTHER INFORMATION: / Ceres Seq. ID 1576805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3424:

Met Ala Lys Asn Pro Lys Val Phe Phe Asp Ile Leu Ile Gly Lys Ser
1 5 10 15
Lys Ala Gly Arg Val Val Met Glu Leu Phe Ala Asp Lys Val Pro Lys
20 25 30
Thr Ala Glu Asn Phe Arg Cys Leu Cys Thr Gly Glu Lys Gly Leu Xaa
35 40 45
Ser Ala Gly Lys Pro Leu His Tyr Lys Gly Ser Ala Phe His Arg Val
50 55 60
Ile Pro Gly Phe Met Cys Gln Gly Gly Asp Phe Thr Arg Gly Asn Gly
65 70 75 80
Thr Gly Gly Glu Ser Ile Tyr Gly Ala Arg Phe Ala Asp Glu Asn Phe
85 90 95
Lys Leu Arg His Thr Gly Pro Gly Val Leu Ser Met Ala Asn Ala Gly
100 105 110
Pro Asp Thr Asn Gly Ser Gln Phe Phe Ile Cys Thr Ala Gln Thr Pro
115 120 125
Trp Leu Asp Gly Lys His Val Val Phe Gly Lys Val Val Xaa Xaa Tyr
130 135 140
Ala Val Val Asp Lys Met Glu Ala Val Gly Ser Gln Ser Gly Ala Thr
145 150 155 160
Ala Glu Ser Val Arg Ile Glu Asp Cys Gly Gln Leu Ala Asp Asp
165 170 175

(2) INFORMATION FOR SEQ ID NO:3425:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

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- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..153
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576806
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3425:

Met Glu Leu Phe Ala Asp Lys Val Pro Lys Thr Ala Glu Asn Phe Arg
1 5 10 15
Cys Leu Cys Thr Gly Glu Lys Gly Leu Xaa Ser Ala Gly Lys Pro Leu
20 25 30
His Tyr Lys Gly Ser Ala Phe His Arg Val Ile Pro Gly Phe Met Cys
35 40 45
Gln Gly Gly Asp Phe Thr Arg Gly Asn Gly Thr Gly Gly Glu Ser Ile
50 55 60
Tyr Gly Ala Arg Phe Ala Asp Glu Asn Phe Lys Leu Arg His Thr Gly
65 70 75 80
Pro Gly Val Leu Ser Met Ala Asn Ala Gly Pro Asp Thr Asn Gly Ser
85 90 95
Gln Phe Phe Ile Cys Thr Ala Gln Thr Pro Trp Leu Asp Gly Lys His
100 105 110
Val Val Phe Gly Lys Val Val Xaa Xaa Tyr Ala Val Val Asp Lys Met
115 120 125
Glu Ala Val Gly Ser Gln Ser Gly Ala Thr Ala Glu Ser Val Arg Ile
130 135 140
Glu Asp Cys Gly Gln Leu Ala Asp Asp
145 150

- (2) INFORMATION FOR SEQ ID NO:3426:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 642 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..642
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576807
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3426:

caattcatcc agacaagtca tatctagcta tagctctccc ttgagaagca tttgarggag 60
gagccatgtc tgaggagaag caccaccacc acctgtttca ccaccgcaag ccagaggagg 120
agggcgcctc cggcgagggtc gactacgaga agaaggagaa gcaccacaag cacatggaga 180
agctcggcga gctcggcgcc atcgccgccg gcgcgtacgc cctgcacgag aagcacaagg 240
ccaagaagga ccagagaaac gagcacgggc accgggtcaa ggaggagggtg gccgcgctcg 300
cgcgcgtggg ctccgcgggc ttgcgtttcc acgagcacca cgagaagaag gacgccaaaga 360
agcacgcccc caactgatcc gtcgcggttg ctgttccatc tgtttttcca gcctcgtctt 420
cgtctactgt gtgccggcca ggccttgatt tgggctaccg atatttgcat ggacgtagga 480
actgtgttgg tcggctctcg gcgttcTttg tatcaagatc aaatcaggcc ttgaataagt 540
gtgtgtgcat atatcttttt ttttaatttt tatctctttt ttttttgtat cgagagatgt 600
cctgaataat gtgaatttac gtgtgtttat ataaacgaat tt

- (2) INFORMATION FOR SEQ ID NO:3427:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1576808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3427:

Met Ser Glu Glu Lys His His His His Leu Phe His His Arg Lys Pro
1 5 10 15
Glu Glu Glu Gly Ala Ser Gly Glu Val Asp Tyr Glu Lys Lys Glu Lys
20 25 30
His His Lys His Met Glu Lys Leu Gly Glu Leu Gly Ala Ile Ala Ala
35 40 45
Gly Ala Tyr Ala Leu His Glu Lys His Lys Ala Lys Lys Asp Pro Glu
50 55 60
Asn Glu His Gly His Arg Val Lys Glu Glu Val Ala Ala Val Ala Ala
65 70 75 80
Val Gly Ser Ala Gly Phe Ala Phe His Glu His His Glu Lys Lys Asp
85 90 95
Ala Lys Lys His Ala His Asn
100

(2) INFORMATION FOR SEQ ID NO:3428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1576809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3428:

Met Glu Lys Leu Gly Glu Leu Gly Ala Ile Ala Ala Gly Ala Tyr Ala
1 5 10 15
Leu His Glu Lys His Lys Ala Lys Lys Asp Pro Glu Asn Glu His Gly
20 25 30
His Arg Val Lys Glu Glu Val Ala Ala Val Ala Ala Val Gly Ser Ala
35 40 45
Gly Phe Ala Phe His Glu His His Glu Lys Lys Asp Ala Lys Lys His
50 55 60
Ala His Asn
65

(2) INFORMATION FOR SEQ ID NO:3429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 722 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..722

(D) OTHER INFORMATION: / Ceres Seq. ID 1576816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3429:

acacaagtca tccgagaagc aagcacaagc accgcaccga acgagcagcg agcgtgttga 60
ggcaggcagt cagtggcagt gggagtagga gacaaggcta ccgagatgaa gggcctcttg 120
ttgctcgtcc tcgccctggt cgcgtccgct gcatgcctcg tggccgtNcg cggcgcGggc 180
gagtgcGggg cgacgccgcc ggacaggatg gcgctgaagc tggcgcgctg Cscgtccgcg 240
gcgcagaacc ccagctcggc gccgtccaac ggctgctgca cggcggtgca caccatcggg 300
aagcagagcc ccagtgccct ctgcgccgtc atgctgtcca agaccgcca gaagtccggg 360
atcaagccc aggtggccat caccatcccc aagcgtgca acctcgtcga ccgccccgtc 420
ggctacaagt gcggagatta cactctgcca tgastgcgcg agagctgctt gagcacatgt 480
gcatgatccg tgtcggagtt agcacgacgt ccgcaggaag tgacggtgac gtgtcagtgt 540
atgtgtgcgt tggttaataaa cgtcgcggca ctccgcactt gttgtgatta ccatacatgt 600

ggaagtccag tatgatatga gtgtctcaca gtcttcaaaa gaaatatggg tcgtatcgta 660
tgtaagtgtc agggttccag agatgctgtc ctgcatcctc gaaataaaac ttgtcttctt 720
gg

(2) INFORMATION FOR SEQ ID NO:3430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..194
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3430:

Thr Ser His Pro Arg Ser Lys His Lys His Arg Thr Glu Arg Ala Ala
1 5 10 15
Ser Val Leu Arg Gln Ala Val Ser Gly Ser Gly Ser Arg Arg Gln Gly
20 25 30
Tyr Arg Asp Glu Gly Pro Leu Val Ala Arg Pro Arg Pro Gly Arg Val
35 40 45
Arg Cys Met Pro Arg Gly Arg Xaa Arg Arg Gly Arg Val Arg Gly Asp
50 55 60
Ala Ala Gly Gln Asp Gly Ala Glu Ala Gly Ala Val Xaa Val Arg Gly
65 70 75 80
Ala Glu Pro Gln Leu Gly Ala Val Gln Arg Leu Leu His Gly Gly Ala
85 90 95
His His Arg Glu Ala Glu Pro Pro Val Pro Leu Arg Arg His Ala Val
100 105 110
Gln Asp Arg Gln Glu Val Arg Asp Gln Ala Arg Gly Gly His His His
115 120 125
Pro Gln Ala Leu Gln Pro Arg Arg Pro Pro Arg Arg Leu Gln Val Arg
130 135 140
Arg Leu His Ser Ala Met Xaa Ala Arg Glu Leu Leu Glu His Met Cys
145 150 155 160
Met Ile Arg Val Gly Val Ser Thr Thr Ser Ala Gly Ser Asp Gly Asp
165 170 175
Val Ser Val Tyr Val Cys Val Gly Asn Lys Arg Arg Gly Thr Pro His
180 185 190
Leu Leu

(2) INFORMATION FOR SEQ ID NO:3431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3431:

Met Lys Gly Leu Leu Leu Val Leu Ala Leu Val Ala Ser Ala Ala
1 5 10 15
Cys Leu Val Ala Xaa Arg Gly Ala Gly Glu Cys Gly Ala Thr Pro Pro
20 25 30
Asp Arg Met Ala Leu Lys Leu Ala Pro Cys Xaa Ser Ala Ala Gln Asn
35 40 45
Pro Ser Ser Ala Pro Ser Asn Gly Cys Cys Thr Ala Val His Thr Ile
50 55 60

Gly Lys Gln Ser Pro Gln Cys Leu Cys Ala Val Met Leu Ser Lys Thr
65 70 75 80
Ala Lys Lys Ser Gly Ile Lys Pro Glu Val Ala Ile Thr Ile Pro Lys
85 90 95
Arg Cys Asn Leu Val Asp Arg Pro Val Gly Tyr Lys Cys Gly Asp Tyr
100 105 110
Thr Leu Pro
115

(2) INFORMATION FOR SEQ ID NO:3432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1576819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3432:

Met Pro Arg Gly Arg Xaa Arg Arg Gly Arg Val Arg Gly Asp Ala Ala
1 5 10 15
Gly Gln Asp Gly Ala Glu Ala Gly Ala Val Xaa Val Arg Gly Ala Glu
20 25 30
Pro Gln Leu Gly Ala Val Gln Arg Leu Leu His Gly Gly Ala His His
35 40 45
Arg Glu Ala Glu Pro Pro Val Pro Leu Arg Arg His Ala Val Gln Asp
50 55 60
Arg Gln Glu Val Arg Asp Gln Ala Arg Gly Gly His His His Pro Gln
65 70 75 80
Ala Leu Gln Pro Arg Arg Pro Pro Arg Arg Leu Gln Val Arg Arg Leu
85 90 95
His Ser Ala Met Xaa Ala Arg Glu Leu Leu Glu His Met Cys Met Ile
100 105 110
Arg Val Gly Val Ser Thr Thr Ser Ala Gly Ser Asp Gly Asp Val Ser
115 120 125
Val Tyr Val Cys Val Gly Asn Lys Arg Arg Gly Thr Pro His Leu Leu
130 135 140

(2) INFORMATION FOR SEQ ID NO:3433:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 702 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..702

(D) OTHER INFORMATION: / Ceres Seq. ID 1576842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3433:

ttcagttggc agttgcgact tgcgagtggc tccaacaagg caacacaatc caccggcacc 60
aaccacagcg ggcgccaccg gcgaccgcta ccccttccc cggagagcga tggcgacgga 120
gctgacggcg gcgcactgcg cgcgtacgac ggcaccgacc cgtccaagcc catctacgtc 180
tccgtccggg gcaaggtcta cgacgtcaacc tccggccgCc ggctttctaag gccNccggcg 240
gcgcctacgc cgtcttcgcg ggccgcgagg Ccagccgcgc cctcggcaag atgtccaagg 300
acgaggccga cgtctccggg gacctctccg ggctcaccga caaggagctc ggcgtcctcg 360
ccgactggga gaccaagttc caGggccaag taccocgctg tcgcccgaact cgccgccgac 420
gcctgaactc ggcagtctcg gtgtaaattt actctgtcct gcctcttgcg gtgttcagtg 480
ttgtgcttgc ttgcttgttg ctagtgtgctt tgctaSccca ataactctgaa tGggaaggac 540

gtatgtgatg tgcctgctga atagctcgag ctccctagctc ttgcatacac tgctgtgcta 600
ccacatgaca tgatgtactc gtgtgtgctt tgggtgttgt gtaattccat gaccatgatc 660
agtaatctga ataaaaaata ttggagatgt gcttgcttcc tg

(2) INFORMATION FOR SEQ ID NO:3434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3434:

Phe	Ser	Trp	Gln	Leu	Arg	Leu	Ala	Ser	Gly	Ser	Asn	Lys	Ala	Thr	Gln	
1			5						10					15		
Ser	Thr	Gly	Thr	Asn	Pro	Ala	Arg	Arg	His	Arg	Arg	Pro	Val	Pro	Pro	
		20						25					30			
Ser	Pro	Glu	Ser	Asp	Gly	Asp	Gly	Ala	Asp	Gly	Gly	Ala	Leu	Arg	Ala	
		35				40						45				
Tyr	Asp	Gly	Thr	Asp	Pro	Ser	Lys	Pro	Ile	Tyr	Val	Ser	Val	Arg	Gly	
	50					55					60					
Lys	Val	Tyr	Asp	Val	Thr	Ser	Gly	Arg	Arg	Leu	Leu	Arg	Xaa	Pro	Ala	
65					70					75				80		
Ala	Pro	Thr	Pro	Ser	Ser	Arg	Ala	Ala	Arg	Pro	Ala	Ala	Pro	Ser	Ala	
				85					90					95		
Arg	Cys	Pro	Arg	Thr	Arg	Pro	Thr	Ser	Pro	Gly	Thr	Ser	Pro	Gly	Ser	
		100						105					110			
Pro	Thr	Arg	Ser	Ser	Ala	Ser	Ser	Pro	Thr	Gly	Arg	Pro	Ser	Ser	Arg	
		115					120					125				
Ala	Lys	Tyr	Pro	Val	Val	Ala	Arg	Leu	Ala	Ala	Asp	Ala				
	130					135					140					

(2) INFORMATION FOR SEQ ID NO:3435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3435:

Ser	Val	Gly	Ser	Cys	Asp	Leu	Arg	Val	Ala	Pro	Thr	Arg	Gln	His	Asn	
1				5					10					15		
Pro	Pro	Ala	Pro	Thr	Gln	Arg	Gly	Ala	Thr	Gly	Asp	Pro	Tyr	Pro	Leu	
		20						25					30			
Pro	Arg	Arg	Ala	Met	Ala	Thr	Glu	Leu	Thr	Ala	Ala	His	Cys	Ala	Arg	
		35					40					45				
Thr	Thr	Ala	Pro	Thr	Arg	Pro	Ser	Pro	Ser	Thr	Ser	Pro	Ser	Gly	Ala	
	50					55					60					
Arg	Ser	Thr	Thr	Ser	Pro	Ala	Ala	Gly	Phe	Tyr	Gly	Xaa	Arg	Arg		
65					70				75					80		
Arg	Leu	Arg	Arg	Leu	Arg	Gly	Pro	Arg	Gly	Gln	Pro	Arg	Pro	Arg	Gln	
				85					90					95		
Asp	Val	Gln	Gly	Arg	Gly	Arg	Arg	Leu	Arg	Gly	Pro	Leu	Arg	Ala	His	
		100						105				110				
Arg	Gln	Gly	Ala	Arg	Arg	Pro	Arg	Arg	Leu	Gly	Asp	Gln	Val	Pro	Gly	
		115					120					125				

Pro Ser Thr Pro Ser Ser Pro Asp Ser Pro Pro Thr Pro Glu Leu Gly
130 135 140
Ser Leu Gly Val Asn Leu Leu Cys Pro Ala Ser Cys Gly Val Gln Cys
145 150 155 160
Cys Ala Cys Leu Leu Val Ala Ser Cys Phe Ala Xaa Pro Ile Ile
165 170 175

(2) INFORMATION FOR SEQ ID NO:3436:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1576845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3436:

Met Ala Thr Glu Leu Thr Ala Ala His Cys Ala Arg Thr Thr Ala Pro
1 5 10 15
Thr Arg Pro Ser Pro Ser Thr Ser Pro Ser Gly Ala Arg Ser Thr Thr
20 25 30
Ser Pro Pro Ala Ala Gly Phe Tyr Gly Xaa Arg Arg Arg Leu Arg Arg
35 40 45
Leu Arg Gly Pro Arg Gly Gln Pro Arg Pro Arg Gln Asp Val Gln Gly
50 55 60
Arg Gly Arg Arg Leu Arg Gly Pro Leu Arg Ala His Arg Gln Gly Ala
65 70 75 80
Arg Arg Pro Arg Arg Leu Gly Asp Gln Val Pro Gly Pro Ser Thr Pro
85 90 95
Ser Ser Pro Asp Ser Pro Pro Thr Pro Glu Leu Gly Ser Leu Gly Val
100 105 110
Asn Leu Leu Cys Pro Ala Ser Cys Gly Val Gln Cys Cys Ala Cys Leu
115 120 125
Leu Val Ala Ser Cys Phe Ala Xaa Pro Ile Ile
130 135

(2) INFORMATION FOR SEQ ID NO:3437:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 828 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..828

(D) OTHER INFORMATION: / Ceres Seq. ID 1576855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3437:

acggttggtc cacctcctcc tgctcctctg gcctctgagg tgctcctcc cgggtcccag 60
tcccggccat gtcgtcgccg ctggaggatg tcagcgtggg catggaggag gaggatcagc 120
ggcccctgaa ccgggccctg ctccaccgga ggcgccaccac caacgcctcc cagggtggcca 180
tggtcggtc caatccctgc cctatcgaga gcctcgacta cgagatgata gagaacgagc 240
tggtcgacca gaactggagg acgaggcgca aggcggacca ggtgcggtac gtggtgctca 300
agtggacctt ctgCttcgcc atcggcatcc tcaccgggat cgtcggttc ttcacacacc 360
tcgccgtcga gaacgtcgcg ggcttcaagc accaggccgt ttccgCccct catggactcc 420
gccagctact ggacggcggt ctgggtgttc gccggctgca acctggcgct cctgctgctg 480
gcgtcgacca tcacggcggt cttgtcgccg gcggccggcg ggtcgggat cccggaggtc 540
aaggcctacc tcaacggcgt cgacgcgcc aacatcttct cgctcgggac cctcgctgtc 600
aagggtcgcc gtgtgtgttc cgttcccatt ctctgccct cgccgnygt ttcgcttgc 660
gcagtgcaca tgctcccctc accatttcct ggtgccastg cgcaaatgga ttaccatcca 720
cactaatata atgtaacaag ggcattcatt cctccatcca actgcatgat ctacgagaaa 780

ggaaagcaac cagcaagtaa ataaacaatc ataattagac ttttctkg

(2) INFORMATION FOR SEQ ID NO:3438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..244

(D) OTHER INFORMATION: / Ceres Seq. ID 1576856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3438:

Arg Leu Val His Leu Leu Leu Leu Leu Trp Pro Leu Arg Cys Leu Leu
1 5 10 15
Pro Val Pro Ser Pro Gly His Val Val Ala Ala Gly Gly Cys Gln Arg
20 25 30
Gly His Gly Gly Gly Gly Ser Ala Ala Pro Glu Pro Gly Pro Ala Pro
35 40 45
Pro Glu Arg His His Gln Arg Leu Pro Gly Gly His Gly Arg Leu Gln
50 55 60
Ser Leu Pro Tyr Arg Glu Pro Arg Leu Arg Asp Asp Arg Glu Arg Ala
65 70 75 80
Val Arg Pro Glu Leu Glu Asp Glu Ala Gln Gly Gly Pro Gly Ala Val
85 90 95
Arg Gly Ala Gln Val Asp Leu Leu Leu Arg His Arg His Pro His Arg
100 105 110
Asp Arg Arg Leu Leu His Gln Pro Arg Arg Arg Glu Arg Arg Gly Leu
115 120 125
Gln Ala Pro Gly Arg Phe Arg Pro Ser Trp Thr Pro Pro Ala Thr Gly
130 135 140
Arg Arg Ser Gly Cys Ser Pro Ala Ala Thr Trp Arg Ser Cys Cys Trp
145 150 155 160
Arg Arg Pro Ser Arg Arg Ser Cys Arg Arg Arg Pro Ala Gly Arg Glu
165 170 175
Ser Arg Arg Ser Arg Pro Thr Ser Thr Ala Ser Thr Arg Pro Thr Ser
180 185 190
Ser Arg Cys Gly Pro Ser Leu Ser Arg Cys Ala Val Cys Val Pro Phe
195 200 205
Pro Ser Ser Cys Pro Arg Xaa Xaa Phe Arg Leu Leu Gln Cys Thr Cys
210 215 220
Ser Pro His His Phe Leu Val Pro Xaa Arg Lys Trp Ile Thr Ile His
225 230 235 240
Thr Asn Ile Met

(2) INFORMATION FOR SEQ ID NO:3439:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..242

(D) OTHER INFORMATION: / Ceres Seq. ID 1576857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3439:

Gly Trp Ser Thr Ser Ser Cys Ser Ser Gly Leu Cys Gly Ala Ser Ser
1 5 10 15
Arg Ser Arg Val Pro Ala Met Ser Ser Pro Leu Glu Asp Val Ser Val
20 25 30

Gly Met Glu Glu Glu Asp Gln Arg Pro Leu Asn Arg Ala Leu Leu His
35 40 45
Arg Ser Ala Thr Thr Asn Ala Ser Gln Val Ala Met Val Gly Ser Asn
50 55 60
Pro Cys Pro Ile Glu Ser Leu Asp Tyr Glu Met Ile Glu Asn Glu Leu
65 70 75 80
Phe Asp Gln Asn Trp Arg Thr Arg Arg Lys Ala Asp Gln Val Arg Tyr
85 90 95
Val Val Leu Lys Trp Thr Phe Cys Phe Ala Ile Gly Ile Leu Thr Gly
100 105 110
Ile Val Gly Phe Phe Ile Asn Leu Ala Val Glu Asn Val Ala Gly Phe
115 120 125
Lys His Gln Ala Val Ser Ala Pro His Gly Leu Arg Gln Leu Leu Asp
130 135 140
Gly Val Leu Gly Val Arg Arg Leu Gln Pro Gly Ala Pro Ala Ala Gly
145 150 155 160
Val Val His His Gly Val Leu Val Ala Gly Gly Arg Arg Val Gly Asn
165 170 175
Pro Gly Gly Gln Gly Leu Pro Gln Arg Arg Arg Arg Ala Gln His Leu
180 185 190
Leu Ala Ala Asp Pro Arg Cys Gln Gly Ala Pro Cys Val Phe Arg Ser
195 200 205
His Pro Pro Ala Leu Ala Xaa Ala Phe Ala Cys Cys Ser Ala His Ala
210 215 220
Pro Leu Thr Ile Ser Trp Cys Xaa Cys Ala Asn Gly Leu Pro Ser Thr
225 230 235 240
Leu Ile

(2) INFORMATION FOR SEQ ID NO:3440:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..220

(D) OTHER INFORMATION: / Ceres Seq. ID 1576858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3440:

Met Ser Ser Pro Leu Glu Asp Val Ser Val Gly Met Glu Glu Glu Asp
1 5 10 15
Gln Arg Pro Leu Asn Arg Ala Leu Leu His Arg Ser Ala Thr Thr Asn
20 25 30
Ala Ser Gln Val Ala Met Val Gly Ser Asn Pro Cys Pro Ile Glu Ser
35 40 45
Leu Asp Tyr Glu Met Ile Glu Asn Glu Leu Phe Asp Gln Asn Trp Arg
50 55 60
Thr Arg Arg Lys Ala Asp Gln Val Arg Tyr Val Val Leu Lys Trp Thr
65 70 75 80
Phe Cys Phe Ala Ile Gly Ile Leu Thr Gly Ile Val Gly Phe Phe Ile
85 90 95
Asn Leu Ala Val Glu Asn Val Ala Gly Phe Lys His Gln Ala Val Ser
100 105 110
Ala Pro His Gly Leu Arg Gln Leu Leu Asp Gly Val Leu Gly Val Arg
115 120 125
Arg Leu Gln Pro Gly Ala Pro Ala Ala Gly Val Val His His Gly Val
130 135 140
Leu Val Ala Gly Gly Arg Arg Val Gly Asn Pro Gly Gly Gln Gly Leu
145 150 155 160
Pro Gln Arg Arg Arg Arg Ala Gln His Leu Leu Ala Ala Asp Pro Arg

165 170 175
Cys Gln Gly Ala Pro Cys Val Phe Arg Ser His Pro Pro Ala Leu Ala
180 185 190
Xaa Ala Phe Ala Cys Cys Ser Ala His Ala Pro Leu Thr Ile Ser Trp
195 200 205
Cys Xaa Cys Ala Asn Gly Leu Pro Ser Thr Leu Ile
210 215 220

(2) INFORMATION FOR SEQ ID NO:3441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 955 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..955
(D) OTHER INFORMATION: / Ceres Seq. ID 1576876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3441:

aagcgtcagg gcctctcgat cgctcatcag tcgccagagg agtagttgat cgaggtgagt 60
gaggttgaaa agcaggcggc gaacaaaggc accatcgta tggacggcgg atactacggc 120
ggccgcgata agcgctacac cngcgggtac tacggcggcg gtggcatcgc gacgccgggg 180
tacgctccgg cggtcccgtc cgggatgtcg caggtgaaca tcgadggcha cgggtgcngg 240
cdggcrtgc cgccgcagcc gaccgtgaag gtgtactgcc gcgccaaccc caactacgcc 300
atgarcgtcc gckacgggaa ggtrgtgctg gcgcccgcga accccaagga cgagtaccag 360
cactggatca aggacatgcn gtggagcacg agcatcaagg acgakaagg ttaccggcg 420
ttcgcrctgg tgaacaargc gaccggggag gccatcaagR cactcgctGg gggcagtcgc 480
acccgggtgcg cctgggtgcc tacaaccggg acttttttga cgagtcgggt ctgtggacgg 540
agagccgcga cgtcggcaac ggcttccgct gcgtccgcat ggtcaacaac atctacctca 600
acttcgacgc cctccacggc gacaagtggc acggcggcgt ccgtgacggc accgacgtcg 660
tgctctggaa gtggtgcgag ggcgacaacc agcgtggaa gatccagccc tactactgaa 720
ccaacggatg atatgacat cgcgccatc gatcgtgcac atgcatgcat acgtactagc 780
agaataacag gggctcttat tcccgaggcg tcttttgcac gcatgccagc agttgcatag 840
ataaagcagg agcgagacaa aggggtgtta tgtatatgtc agctgtatca ctgtatgtat 900
gtgccattgt gccttgtaat aatacatata ataataaagt tgctcggagt gtatt

(2) INFORMATION FOR SEQ ID NO:3442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..246
(D) OTHER INFORMATION: / Ceres Seq. ID 1576877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3442:

Met Asp Gly Gly Tyr Gly Gly Arg Asp Gln Arg Tyr Xaa Xaa Gly
1 5 10 15
Tyr Tyr Gly Gly Gly Gly Ile Ala Thr Pro Gly Tyr Ala Pro Ala Val
20 25 30
Pro Tyr Gly Met Ser Gln Val Asn Ile Xaa Gly Xaa Gly Cys Xaa Xaa
35 40 45
Xaa Leu Pro Pro Gln Pro Thr Val Lys Val Tyr Cys Arg Ala Asn Pro
50 55 60
Asn Tyr Ala Met Xaa Val Arg Xaa Gly Lys Xaa Val Leu Ala Pro Ala
65 70 75 80
Asn Pro Lys Asp Glu Tyr Gln His Trp Ile Lys Asp Met Xaa Trp Ser
85 90 95
Thr Ser Ile Lys Asp Xaa Glu Gly Tyr Pro Ala Phe Xaa Leu Val Asn
100 105 110

Xaa Ala Thr Gly Glu Ala Ile Lys Xaa Leu Ala Gly Gly Ser Pro Thr
115 120 125
Arg Cys Ala Trp Cys Pro Thr Arg Thr Phe Trp Thr Ser Arg Cys
130 135 140
Cys Gly Arg Arg Ala Ala Thr Ser Ala Thr Ala Ser Ala Ala Ser Ala
145 150 155 160
Trp Ser Thr Thr Ser Thr Ser Thr Ser Thr Pro Ser Thr Ala Thr Ser
165 170 175
Gly Thr Ala Ala Ser Val Thr Ala Pro Thr Ser Cys Ser Gly Ser Gly
180 185 190
Ala Arg Ala Thr Thr Ser Ala Gly Arg Ser Ser Pro Thr Thr Glu Pro
195 200 205
Thr Asp Asp Met Thr Ile Ala Pro Ile Asp Arg Ala His Ala Cys Ile
210 215 220
Arg Thr Ser Arg Ile Thr Gly Val Leu Ser Pro Glu Ala Ser Phe Ala
225 230 235 240
Cys Met Pro Ala Val Ala
245

(2) INFORMATION FOR SEQ ID NO:3443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..211

(D) OTHER INFORMATION: / Ceres Seq. ID 1576878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3443:

Met Ser Gln Val Asn Ile Xaa Gly Xaa Gly Cys Xaa Xaa Xaa Leu Pro
1 5 10 15
Pro Gln Pro Thr Val Lys Val Tyr Cys Arg Ala Asn Pro Asn Tyr Ala
20 25 30
Met Xaa Val Arg Xaa Gly Lys Xaa Val Leu Ala Pro Ala Asn Pro Lys
35 40 45
Asp Glu Tyr Gln His Trp Ile Lys Asp Met Xaa Trp Ser Thr Ser Ile
50 55 60
Lys Asp Xaa Glu Gly Tyr Pro Ala Phe Xaa Leu Val Asn Xaa Ala Thr
65 70 75 80
Gly Glu Ala Ile Lys Xaa Leu Ala Gly Gly Ser Pro Thr Arg Cys Ala
85 90 95
Trp Cys Pro Thr Thr Arg Thr Phe Trp Thr Ser Arg Cys Cys Gly Arg
100 105 110
Arg Ala Ala Thr Ser Ala Thr Ala Ser Ala Ala Ser Ala Trp Ser Thr
115 120 125
Thr Ser Thr Ser Thr Ser Thr Pro Ser Thr Ala Thr Ser Gly Thr Ala
130 135 140
Ala Ser Val Thr Ala Pro Thr Ser Cys Ser Gly Ser Gly Ala Arg Ala
145 150 155 160
Thr Thr Ser Ala Gly Arg Ser Ser Pro Thr Thr Glu Pro Thr Asp Asp
165 170 175
Met Thr Ile Ala Pro Ile Asp Arg Ala His Ala Cys Ile Arg Thr Ser
180 185 190
Arg Ile Thr Gly Val Leu Ser Pro Glu Ala Ser Phe Ala Cys Met Pro
195 200 205
Ala Val Ala
210

(2) INFORMATION FOR SEQ ID NO:3444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..179
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576879
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3444:

Met Xaa Val Arg Xaa Gly Lys Xaa Val Leu Ala Pro Ala Asn Pro Lys
1 5 10 15
Asp Glu Tyr Gln His Trp Ile Lys Asp Met Xaa Trp Ser Thr Ser Ile
20 25 30
Lys Asp Xaa Glu Gly Tyr Pro Ala Phe Xaa Leu Val Asn Xaa Ala Thr
35 40 45
Gly Glu Ala Ile Lys Xaa Leu Ala Gly Gly Ser Pro Thr Arg Cys Ala
50 55 60
Trp Cys Pro Thr Thr Arg Thr Phe Trp Thr Ser Arg Cys Cys Gly Arg
65 70 75 80
Arg Ala Ala Thr Ser Ala Thr Ala Ser Ala Ser Ala Trp Ser Thr
85 90 95
Thr Ser Thr Ser Thr Ser Thr Pro Ser Thr Ala Thr Ser Gly Thr Ala
100 105 110
Ala Ser Val Thr Ala Pro Thr Ser Cys Ser Gly Ser Gly Ala Arg Ala
115 120 125
Thr Thr Ser Ala Gly Arg Ser Ser Pro Thr Thr Glu Pro Thr Asp Asp
130 135 140
Met Thr Ile Ala Pro Ile Asp Arg Ala His Ala Cys Ile Arg Thr Ser
145 150 155 160
Arg Ile Thr Gly Val Leu Ser Pro Glu Ala Ser Phe Ala Cys Met Pro
165 170 175
Ala Val Ala

(2) INFORMATION FOR SEQ ID NO:3445:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 727 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..727
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576888
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3445:

cttgctcgct gcgcgcgcgc ctccgacatc gtcccttctgt cccacgagc aaccgataat 60
ccgcggcggt tgagatgttg gtttatcagg atctctatc tggcgacgag ctctgtcggt 120
attCcatcA acctacaagg agctcgagaa cGggcgctct gtgggaggtc gagggaaagt 180
gggtcaccca aggtctgtt gatgtggaca ttggtgccaa tccatccgcc gaggggtggtg 240
aggacgaaag cgttgatgac acagctgtga aggtggttga tattgttgac acattccgtc 300
tacaggagca acctccttt gacaagaaat catttgtgtc ttacatcaaa aaatacatca 360
agaatctcac tgctgtgttg gagccagaga aagcggatga gttcaaaaag ggtgtcgagg 420
gtgcaaccaa gtttctcctt agcaagctga aggacctcca attttttGgt tgggtgagtc 480
atgaaggatg atgcgtctgt ggtattcgcc tattacaagg atggtgccac taatccgaca 540
ttcctctatt tctctcatgg tcttaaggag atcaagtgtc aggcgtgcgg cgaaattagt 600
taccatggt gggtactatc tatgtactat tattatatcc aaaactatag ttgtcctggc 660
tgaattgaac tcaaaagggt ttgtttgaga aaaaattgtc ccaagattgg attgcttgtt 720
aaagccc

(2) INFORMATION FOR SEQ ID NO:3446:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..89
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3446:

Leu Ala Arg Cys Ala Ala Ala Ser Asp Ile Val Pro Ser Ser Pro Arg
1 5 10 15
Ala Thr Asp Asn Pro Pro Ala Leu Arg Cys Trp Phe Ile Arg Ile Ser
20 25 30
Tyr Leu Ala Thr Ser Ser Cys Arg Ile Pro Phe Asn Leu Gln Gly Ala
35 40 45
Arg Glu Arg Ala Ser Cys Gly Arg Ser Arg Glu Ser Gly Ser Pro Lys
50 55 60
Val Leu Leu Met Trp Thr Leu Val Pro Ile His Pro Pro Arg Val Val
65 70 75 80
Arg Thr Lys Ala Leu Met Thr Gln Leu
85

(2) INFORMATION FOR SEQ ID NO:3447:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..133
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3447:

Met Leu Val Tyr Gln Asp Leu Leu Ser Gly Asp Glu Leu Leu Ser Asp
1 5 10 15
Ser Ile Gln Pro Thr Arg Ser Ser Arg Thr Gly Val Leu Trp Glu Val
20 25 30
Glu Gly Lys Trp Val Thr Gln Gly Pro Val Asp Val Asp Ile Gly Ala
35 40 45
Asn Pro Ser Ala Glu Gly Gly Glu Asp Glu Ser Val Asp Asp Thr Ala
50 55 60
Val Lys Val Val Asp Ile Val Asp Thr Phe Arg Leu Gln Glu Gln Pro
65 70 75 80
Pro Phe Asp Lys Lys Ser Phe Val Ser Tyr Ile Lys Lys Tyr Ile Lys
85 90 95
Asn Leu Thr Ala Val Leu Glu Pro Glu Lys Ala Asp Glu Phe Lys Lys
100 105 110
Gly Val Glu Gly Ala Thr Lys Phe Leu Leu Ser Lys Leu Lys Asp Leu
115 120 125
Gln Phe Phe Gly Trp
130

(2) INFORMATION FOR SEQ ID NO:3448:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1576891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3448:

Met Met Arg Leu Trp Tyr Ser Pro Ile Thr Arg Met Val Pro Leu Ile
1 5 10 15
Arg His Ser Ser Ile Ser Leu Met Val Leu Arg Arg Ser Ser Ala Arg
20 25 30
Arg Ala Ala Lys Leu Val Thr His Val Gly Tyr Tyr Leu Cys Thr Ile
35 40 45
Ile Ile Ser Lys Thr Ile Val Val Leu Ala Glu Leu Asn Ser Lys Gly
50 55 60
Phe Val
65

(2) INFORMATION FOR SEQ ID NO:3449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..663

(D) OTHER INFORMATION: / Ceres Seq. ID 1576896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3449:

aaacaccgcc gaagaancca gccaacctt cagcacccgc atttcccaag ggaaccatac 60
cagagcggca gaggcttccc ctccgctccc cagtcccacc cgcaccctag ccctcagcaa 120
accctaaccg ctcgctcgcca tgaaggacac ctcgttcaag gccaccggCg ccaagcgcaa 180
gaaggtcggc ggcGccaagc gcgggctcac ccccttcttc gcgttttttg ctgagtttag 240
gccgcagtac ctggagaagc accctgagct caagggcgta aaggaggtga gcaaggcggc 300
tggggagaag tggcgctcta tgtcggtatga ggagaaggcg aagtatggca gtagcaagaa 360
gcaggatggc aaagcaagca agaaggagaa cactagctcc aagaaggcca aagctgatat 420
tcgggagggg gatgaagcag aaggttctaa caagtcaaaa tctgaggttg aggatgatga 480
gcaggatggt aatgaggatg aggatgagta aatagtagca tggggaacag cagctttgca 540
tttgagtgtt tgctgcttta cttatttttc tatatgctgt tccttttgat gttatatgct 600
gtaaggaaaa tctgtacatg atggtacctt aggggtatggc atgctggagt tcccctttaa 660
ccc

(2) INFORMATION FOR SEQ ID NO:3450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1576897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3450:

Lys His Arg Arg Arg Xaa Gln Pro Asn Leu His Ala Pro His Phe Pro
1 5 10 15
Arg Glu Pro Tyr Gln Ser Gly Arg Ala Phe Pro Ser Ala Pro Gln Ser
20 25 30
His Pro His Pro Ser Pro Gln Gln Thr Leu Thr Ala Arg His Glu
35 40 45
Gly His Leu Val Gln Gly His Arg Arg Gln Ala Gln Glu Gly Arg Arg
50 55 60
Arg Gln Ala Arg Ala His Pro Leu Leu Arg Val Phe Gly
65 70 75

(2) INFORMATION FOR SEQ ID NO:3451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..123
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576898
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3451:

Met Lys Asp Thr Ser Phe Lys Ala Thr Gly Ala Lys Arg Lys Lys Val
1 5 10 15
Gly Gly Ala Lys Arg Gly Leu Thr Pro Phe Phe Ala Phe Leu Ala Glu
20 25 30
Phe Arg Pro Gln Tyr Leu Glu Lys His Pro Glu Leu Lys Gly Val Lys
35 40 45
Glu Val Ser Lys Ala Ala Gly Glu Lys Trp Arg Ser Met Ser Asp Glu
50 55 60
Glu Lys Ala Lys Tyr Gly Ser Ser Lys Lys Gln Asp Gly Lys Ala Ser
65 70 75 80
Lys Lys Glu Asn Thr Ser Ser Lys Lys Ala Lys Ala Asp Ile Arg Glu
85 90 95
Gly Asp Glu Ala Glu Gly Ser Asn Lys Ser Lys Ser Glu Val Glu Asp
100 105 110
Asp Glu Gln Asp Gly Asn Glu Asp Glu Asp Glu
115 120

(2) INFORMATION FOR SEQ ID NO:3452:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..63
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576899
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3452:

Met Ser Asp Glu Lys Lys Ala Lys Tyr Gly Ser Ser Lys Lys Gln Asp
1 5 10 15
Gly Lys Ala Ser Lys Lys Glu Asn Thr Ser Ser Lys Lys Ala Lys Ala
20 25 30
Asp Ile Arg Glu Gly Asp Glu Ala Glu Gly Ser Asn Lys Ser Lys Ser
35 40 45
Glu Val Glu Asp Asp Glu Gln Asp Gly Asn Glu Asp Glu Asp Glu
50 55 60

(2) INFORMATION FOR SEQ ID NO:3453:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 829 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..829
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576923
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3453:

aaactctttt cttcaccaga cgtccagacc tgctcacggc ctcccaaact cgcgcgccgc 60
cctgcttcca gtctcccctg gcaatctcog ccttgcaaac cctagccgct gccatggcat 120
atctagctcc cgcgaccgcc gcctcttccc tccgcacccc catctacgta gccgcctctt 180
cccggcgccg ttcttttctc cctgcccgcc tcaaagccat cgccagttct gcacatccca 240

```
tctctctctc cctccgcatg gccgcctccg ccgcccgttct cttcgcgcgc acctccccgg 300
cactcgcgtg caccctctcc gttcctccgc ccccgcctcac tctcttgaca gtcacgggtgt 360
cccacgacga cgccatccta gacgcctccc gactcttcga gaagctgata atcgagactg 420
cctgchtcgA scgcgtcggc cgcgcggacg aagcgcgctc gcgcctgtcc acagccggat 480
gtggagagaG ctacgcccgc ctcttagccg ctcaggttct gttcgtggac gggaagttgg 540
acgaggcgat cgcagcattc gaggagcttg cgcgggagga ccccgccgac tatcgccctc 600
tgttctgcca gggcgtgctg tacctcgccc ttggaaggga ggcggaatca gagtccatgc 660
tcgagcgatg ccgcgaggtc ggcgcgacg cgctaactgt agatccgtca ctgatgataa 720
cgccgaccgt ggagacggaa ttcgatggg agaagccgga gccggcgaag gtttgacctg 780
taactctgca gcgatgatc tcagaataag gtaacactgg cattttggt
```

(2) INFORMATION FOR SEQ ID NO:3454:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..270

(D) OTHER INFORMATION: / Ceres Seq. ID 1576924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3454:

```
Asn Ser Phe Leu His Gln Thr Ser Arg Pro Ala His Gly Leu Pro Asn
1      5      10      15
Ser Ala Ala Ala Leu Leu Pro Val Ser Pro Gly Asn Leu Arg Leu Ala
20      25      30
Asn Pro Ser Arg Cys His Gly Ile Ser Ser Ser Arg Asp Arg Arg Leu
35      40      45
Phe Pro Pro His Pro His Leu Arg Ser Arg Leu Phe Pro Ala Pro Phe
50      55      60
Leu Ser Pro Cys Arg Arg Gln Ser His Arg Gln Phe Cys Thr Ser His
65      70      75      80
Pro Leu Leu Pro Pro His Gly Arg Leu Arg Arg Arg Ser Leu Arg Arg
85      90      95
His Leu Pro Gly Thr Arg Val His Pro Leu Arg Ser Ser Ala Pro Ala
100     105     110
His Ser Ser Asp Ser His Gly Val Pro Arg Arg Arg His Pro Arg Arg
115     120     125
Leu Pro Thr Leu Arg Glu Ala Asp Asn Arg Asp Cys Leu Xaa Arg Xaa
130     135     140
Arg Arg Pro Arg Gly Arg Ser Ala Leu Ala Pro Val His Ser Arg Met
145     150     155     160
Trp Arg Glu Leu Arg Pro Pro Pro Ser Arg Ser Gly Ser Val Arg Gly
165     170     175
Arg Glu Val Gly Arg Gly Asp Arg Ser Ile Arg Gly Ala Cys Ala Gly
180     185     190
Gly Pro Arg Arg Leu Ser Pro Ser Val Leu Pro Gly Arg Ala Val Pro
195     200     205
Arg Pro Trp Lys Gly Gly Gly Ile Arg Val His Ala Arg Ala Met Pro
210     215     220
Arg Gly Arg Arg Arg Arg Ala Asn Arg Arg Ser Val Thr Asp Asp Asn
225     230     235     240
Ala Asp Arg Gly Asp Gly Ile Arg Trp Gly Glu Ala Gly Ala Gly Glu
245     250     255
Gly Leu Thr Cys Asn Ser Ala Ala Asp Asp Leu Arg Ile Arg
260     265     270
```

(2) INFORMATION FOR SEQ ID NO:3455:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

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- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..257
(D) OTHER INFORMATION: / Ceres Seq. ID 1576925
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3455:

Thr Leu Phe Phe Thr Arg Arg Pro Asp Leu Leu Thr Ala Ser Gln Thr
1 5 10 15
Pro Pro Pro Pro Cys Phe Gln Ser Pro Leu Ala Ile Ser Ala Leu Gln
 20 25 30
Thr Leu Ala Ala Ala Met Ala Tyr Leu Ala Pro Ala Thr Ala Ala Ser
 35 40 45
Ser Leu Arg Thr Pro Ile Tyr Val Ala Ala Ser Ser Arg Arg Arg Ser
50 55 60
Phe Leu Pro Ala Ala Val Lys Ala Ile Ala Ser Ser Ala His Pro Ile
65 70 75 80
Leu Ser Ser Leu Arg Met Ala Ala Ser Ala Ala Val Leu Phe Ala Ala
 85 90 95
Thr Ser Pro Ala Leu Ala Cys Thr Pro Ser Val Pro Pro Pro Leu
 100 105 110
Thr Pro Leu Thr Val Thr Val Ser His Asp Asp Ala Ile Leu Asp Ala
115 120 125
Ser Arg Leu Phe Glu Lys Leu Ile Ile Glu Thr Ala Cys Xaa Xaa Arg
130 135 140
Val Gly Arg Ala Asp Glu Ala Arg Ser Arg Leu Ser Thr Ala Gly Cys
145 150 155 160
Gly Glu Ser Tyr Ala Arg Leu Leu Ala Ala Gln Val Leu Phe Val Asp
 165 170 175
Gly Lys Leu Asp Glu Ala Ile Ala Ala Phe Glu Glu Leu Ala Arg Glu
 180 185 190
Asp Pro Ala Asp Tyr Arg Pro Leu Phe Cys Gln Gly Val Leu Tyr Leu
195 200 205
Ala Leu Gly Arg Glu Ala Glu Ser Glu Ser Met Leu Glu Arg Cys Arg
210 215 220
Glu Val Gly Gly Asp Ala Leu Ile Val Asp Pro Ser Leu Met Ile Thr
225 230 235 240
Pro Thr Val Glu Thr Glu Phe Asp Gly Glu Lys Pro Glu Pro Ala Lys
 245 250 255
Val

- (2) INFORMATION FOR SEQ ID NO:3456:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 220 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..220
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576926
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3456:

Met Ala Tyr Leu Ala Pro Ala Thr Ala Ser Ser Leu Arg Thr Pro
1 5 10 15
Ile Tyr Val Ala Ala Ser Ser Arg Arg Arg Ser Phe Leu Pro Ala Ala
 20 25 30
Val Lys Ala Ile Ala Ser Ser Ala His Pro Ile Leu Ser Ser Leu Arg
35 40 45
Met Ala Ala Ser Ala Ala Val Leu Phe Ala Ala Thr Ser Pro Ala Leu
50 55 60

Ala Cys Thr Pro Ser Val Pro Pro Pro Pro Leu Thr Pro Leu Thr Val
65 70 75 80
Thr Val Ser His Asp Asp Ala Ile Leu Asp Ala Ser Arg Leu Phe Glu
85 90 95
Lys Leu Ile Ile Glu Thr Ala Cys Xaa Xaa Arg Val Gly Arg Ala Asp
100 105 110
Glu Ala Arg Ser Arg Leu Ser Thr Ala Gly Cys Gly Glu Ser Tyr Ala
115 120 125
Arg Leu Leu Ala Ala Gln Val Leu Phe Val Asp Gly Lys Leu Asp Glu
130 135 140
Ala Ile Ala Ala Phe Glu Leu Ala Arg Glu Asp Pro Ala Asp Tyr
145 150 155 160
Arg Pro Leu Phe Cys Gln Gly Val Leu Tyr Leu Ala Leu Gly Arg Glu
165 170 175
Ala Glu Ser Glu Ser Met Leu Glu Arg Cys Arg Glu Val Gly Gly Asp
180 185 190
Ala Leu Ile Val Asp Pro Ser Leu Met Ile Thr Pro Thr Val Glu Thr
195 200 205
Glu Phe Asp Gly Glu Lys Pro Glu Pro Ala Lys Val
210 215 220

(2) INFORMATION FOR SEQ ID NO:3457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..600
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3457:

gagtgctctcg gtagcttctt cccattcac attcggccat tctccaccgt ccaaccaacc	60
accggcgcg gcacaaggga agcgaagagg aatcaacgcg atgtctgcga ccacggcggc	120
ggtgcccttc tggcgggcgg ccgggatgac ctacatcggc tactccaaca tctGcgctgc	180
gctggtacgg aactgcctca aggagccctt caagtccaag gccgcgtccc gcgagaaggt	240
ccatttctcc atctccaagt ggacggatgg caaacaggag aagcccactg tccgcacaga	300
atccgatgaa taaagctctg gtgccatagt ggcatagtcc ttgctacaga tgatttgaag	360
tggtgttgca agtttccgga acatgctatt tagctggctt gattttatag tcaatgctga	420
ataataaata ctttttacga caattgtctt tttcgttgct aattgcactc gccctacctg	480
aatcagtcac gtgaacatca tggaatgctt cagttttgta caaactaaat ttgttgtgct	540
gtccgacaga ttctatgtct ggtccttaaa aataaaggaa taatgaatgt agtgttttcg	600

(2) INFORMATION FOR SEQ ID NO:3458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3458:

Glu Cys Leu Gly Ser Phe Phe Pro Ile His Ile Arg Pro Phe Ser Thr	
1 5 10 15	
Val Gln Pro Thr Thr Gly Gly Gly Thr Arg Glu Ala Lys Arg Asn Gln	
20 25 30	
Arg Asp Val Cys Asp His Gly Gly Gly Ala Leu Leu Ala Gly Gly Arg	
35 40 45	

Asp Asp Leu His Arg Leu Leu Gln His Leu Arg Cys Ala Gly Thr Glu
50 55 60
Leu Pro Gln Gly Ala Leu Gln Val Gln Gly Arg Val Pro Arg Glu Gly
65 70 75 80
Pro Phe Leu His Leu Gln Val Asp Gly Trp Gln Thr Gly Glu Ala His
85 90 95
Cys Pro His Arg Ile Arg
100

(2) INFORMATION FOR SEQ ID NO:3459:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1576937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3459:

Ser Val Ser Val Ala Ser Ser Pro Phe Thr Phe Gly His Ser Pro Pro
1 5 10 15
Ser Asn Gln Pro Pro Ala Ala Ala Gln Gly Lys Arg Arg Gly Ile Asn
20 25 30
Ala Met Ser Ala Thr Thr Ala Ala Val Pro Phe Trp Arg Ala Ala Gly
35 40 45
Met Thr Tyr Ile Gly Tyr Ser Asn Ile Cys Ala Ala Leu Val Arg Asn
50 55 60
Cys Leu Lys Glu Pro Phe Lys Ser Lys Ala Ala Ser Arg Glu Lys Val
65 70 75 80
His Phe Ser Ile Ser Lys Trp Thr Asp Gly Lys Gln Glu Lys Pro Thr
85 90 95
Val Arg Thr Glu Ser Asp Glu
100

(2) INFORMATION FOR SEQ ID NO:3460:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1576938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3460:

Met Ser Ala Thr Thr Ala Ala Val Pro Phe Trp Arg Ala Ala Gly Met
1 5 10 15
Thr Tyr Ile Gly Tyr Ser Asn Ile Cys Ala Ala Leu Val Arg Asn Cys
20 25 30
Leu Lys Glu Pro Phe Lys Ser Lys Ala Ala Ser Arg Glu Lys Val His
35 40 45
Phe Ser Ile Ser Lys Trp Thr Asp Gly Lys Gln Glu Lys Pro Thr Val
50 55 60
Arg Thr Glu Ser Asp Glu
65 70

(2) INFORMATION FOR SEQ ID NO:3461:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 815 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..815
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3461:

```
agctctcccc ctctagcctc acctgcccta tacacagcca ctactgtcga tcgattgaat      60
ttgaacccac caggatcagg attaggatta cagcatgtcg gcgtccccgg agttgtacag      120
gcccgcggaa gscgcgcctt ctgcgcgtcc tgcgccacgc agccgctcgt gttcgcgggc      180
gacgactact gctgcaggac gccgacgggc agcgggatct gctacctgag ggagcccacc      240
acgtgccccg ccgcgccccg gaagccgcgc ccgcgcgcgc cccatgtgca ggaagcgcc      300
cttccaagcg gcggatcagc agcttgctga ggcgggcccc gtccctgtta tcagcatccg      360
cctcgacgag ctggagcgcc tcttccgccc ctgtccgcgc ccgaccacca ccaccaccga      420
caagcggcgc cgctccggct ccggccccag cccagatcc gccacgaaac atggtgctca      480
gctgcagCtg cgcaGcatNg aattgaattg ggtagcgta acgtagcttg cacgcaccaa      540
ccaaccactC cccttttttag tttttgctgc tgcattctgtc tgcttcttgt tgctgcaaca      600
agcaaagcgc aagcgggtggc gcttcttttt atttatttat ttatttatta cggagtactt      660
gcttccgttc tcaaataatt gtcatttgat agttcatttc aaaaatttga caaataaaaa      720
agaacgacga agcaagcagt acccacctgt gtaaatcaaa tcaaataatgc aaagttaccg      780
ccatagcaat aaaatcaccc gtgtaaatca gatcg
```

(2) INFORMATION FOR SEQ ID NO:3462:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..109
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3462:

```
Ser Ser Pro Pro Leu Ala Ser Pro Ala Leu Tyr Thr Ala Thr Thr Val
1          5          10          15
Asp Arg Leu Asn Leu Asn Pro Pro Gly Ser Gly Leu Gly Leu Gln His
          20          25          30
Val Gly Val Pro Gly Val Val Gln Ala Arg Gly Xaa Pro Ala Phe Ser
          35          40          45
Pro Ser Cys Ala Thr Gln Pro Leu Val Phe Ala Gly Asp Asp Tyr Cys
          50          55          60
Cys Arg Thr Pro Thr Gly Ser Gly Ile Cys Tyr Leu Arg Glu Pro Thr
65          70          75          80
Thr Cys Pro Pro Ala Pro Arg Lys Pro Pro Pro Pro Pro His Val
          85          90          95
Gln Glu Ala Pro Leu Pro Ser Gly Gly Ser Ala Ala Cys
          100         105
```

(2) INFORMATION FOR SEQ ID NO:3463:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 167 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..167
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3463:

```
Leu Ser Pro Ser Ser Leu Thr Cys Pro Ile His Ser His Tyr Cys Arg
1          5          10          15
```

Ser Ile Glu Phe Glu Pro Thr Arg Ile Arg Ile Arg Ile Thr Ala Cys
20 25 30
Arg Arg Pro Arg Ser Cys Thr Gly Pro Arg Lys Xaa Gly Leu Leu Ala
35 40 45
Val Leu Arg His Ala Ala Ala Arg Val Arg Arg Arg Arg Leu Leu Leu
50 55 60
Gln Asp Ala Asp Gly Gln Arg Asp Leu Leu Pro Glu Gly Ala His His
65 70 75 80
Val Pro Ala Arg Ala Pro Glu Ala Ala Ala Ala Ala Pro Cys Ala
85 90 95
Gly Ser Ala Ser Ser Lys Arg Arg Ile Ser Ser Leu Leu Arg Arg Ala
100 105 110
Pro Ser Leu Leu Ser Ala Ser Ala Ser Thr Ser Trp Ser Ala Ser Ser
115 120 125
Ala Pro Val Arg Arg Arg Pro Pro Pro Pro Pro Thr Ser Gly Ala Ala
130 135 140
Pro Ala Pro Ala Pro Ala Pro Asp Pro Pro Arg Asn Met Val Leu Ser
145 150 155 160
Cys Ser Cys Ala Ala Xaa Asn
165

(2) INFORMATION FOR SEQ ID NO:3464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 958 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..958
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3464:

angtctcagc	acccgatccg	agtaaccgct	gccgatctct	cctcgtcatt	tcgtcgtcgt	60
ctccatctcg	cttttgatcg	actcagaaaa	ttccccacca	aaatctcctc	cccctgaagt	120
cccgaagctc	gcggaagscc	gagatgtacc	atccccacgag	aggcggcgctc	cgcggcggca	180
gagatcaatt	caaatgggac	gatgtgaagg	ttgacaagca	tcgggagaat	taccttggtc	240
atagtgttaa	ggctccggtt	ggtagatggc	agaaaggaaa	ggatctttac	tggtatactc	300
gggataagaa	atccgacacg	gaagatgctc	ttaagggaaga	aatcaggaga	gtgaaggaag	360
aggaggaaca	ggctatgcgt	gaggctcttg	gcttagctcc	taagcgcaGc	aatcgaactc	420
agggtaatcg	cttgataag	catgaatatg	ctgagctgat	taagagagga	tcaactgcgg	480
aggacttggg	agcagggcac	gctgaagcag	cacaagtgca	gggtctagga	ttgtacaagg	540
cccctcgcg	tgagggtgga	tcaagttctt	tgagccttga	ccctcaaattg	gagcctgagc	600
aggctgaacc	cctactagca	cccaagcagg	aggatgattt	ggaagataat	aggaagggga	660
aaaggccacg	tgaacgtgac	gagaagagag	gggagaagga	gcggaaacga	gacaggcatg	720
gtgatggaaa	ggagaggagg	cgggacaagc	acgagaggag	gcacgacttg	gaggacagat	780
caaagcggca	ccgcaaagac	aagcagaaga	ggaggcacga	ttccgattct	gattgataac	840
ggcctgcgc	ctgctcctgt	atgactactg	tatactgcga	aatttcaaac	ccatggagcc	900
gcttttggtt	gatgtatgcc	tacgctttta	attatgtttg	ccctaattgat	gtttaagg	

(2) INFORMATION FOR SEQ ID NO:3465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..230
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3465:

Met Tyr His Pro Thr Arg Gly Gly Val Arg Gly Gly Arg Asp Gln Phe

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1 5 10 15
Lys Trp Asp Asp Val Lys Val Asp Lys His Arg Glu Asn Tyr Leu Gly
20 25 30
His Ser Val Lys Ala Pro Val Gly Arg Trp Gln Lys Gly Lys Asp Leu
35 40 45
Tyr Trp Tyr Thr Arg Asp Lys Lys Ser Asp Thr Glu Asp Ala Leu Lys
50 55 60
Glu Glu Ile Arg Arg Val Lys Glu Glu Glu Glu Gln Ala Met Arg Glu
65 70 75 80
Ala Leu Gly Leu Ala Pro Lys Arg Ser Asn Arg Thr Gln Gly Asn Arg
85 90 95
Leu Asp Lys His Glu Tyr Ala Glu Leu Ile Lys Arg Gly Ser Thr Ala
100 105 110
Glu Asp Leu Gly Ala Gly His Ala Glu Ala Ala Gln Val Gln Gly Leu
115 120 125
Gly Leu Tyr Lys Ala Pro Arg Asp Glu Gly Gly Ser Ser Ser Leu Ser
130 135 140
Leu Asp Pro Gln Met Glu Pro Glu Gln Ala Glu Pro Leu Leu Ala Pro
145 150 155 160
Lys Gln Glu Asp Asp Leu Glu Asp Asn Arg Lys Gly Lys Arg Pro Arg
165 170 175
Glu Arg Asp Glu Lys Arg Gly Glu Lys Glu Arg Lys Arg Asp Arg His
180 185 190
Gly Asp Gly Lys Glu Arg Arg Arg Asp Lys His Glu Arg Arg His Asp
195 200 205
Leu Glu Asp Arg Ser Lys Arg His Arg Lys Asp Lys Gln Lys Arg Arg
210 215 220
His Asp Ser Asp Ser Asp
225 230

(2) INFORMATION FOR SEQ ID NO:3466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3466:

Met Arg Glu Ala Leu Gly Leu Ala Pro Lys Arg Ser Asn Arg Thr Gln
1 5 10 15
Gly Asn Arg Leu Asp Lys His Glu Tyr Ala Glu Leu Ile Lys Arg Gly
20 25 30
Ser Thr Ala Glu Asp Leu Gly Ala Gly His Ala Glu Ala Ala Gln Val
35 40 45
Gln Gly Leu Gly Leu Tyr Lys Ala Pro Arg Asp Glu Gly Gly Ser Ser
50 55 60
Ser Leu Ser Leu Asp Pro Gln Met Glu Pro Glu Gln Ala Glu Pro Leu
65 70 75 80
Leu Ala Pro Lys Gln Glu Asp Asp Leu Glu Asp Asn Arg Lys Gly Lys
85 90 95
Arg Pro Arg Glu Arg Asp Glu Lys Arg Gly Glu Lys Glu Arg Lys Arg
100 105 110
Asp Arg His Gly Asp Gly Lys Glu Arg Arg Arg Asp Lys His Glu Arg
115 120 125
Arg His Asp Leu Glu Asp Arg Ser Lys Arg His Arg Lys Asp Lys Gln
130 135 140
Lys Arg Arg His Asp Ser Asp Ser Asp
145 150

(2) INFORMATION FOR SEQ ID NO:3467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..618
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3467:

gccgcaaaac gcaggtgcat gcgtcgtcgc caagcccaaa ggccagtctg agtgtgcggt	60
cgattcgctt gtgctgcagc tagggtttag aggtttttctg ggcgcnagagC Gggadgcggc	120
ggcggctatg gctgcggcgg aggaggagat cgcggtgaag gagccgctgg atctgatacg	180
cctcagcctc gacgagcgca tctacgtcaa gctccgatcc gaccgcgagC tgcgcggcaa	240
gctccatgcg tatgatcaac atttaaacad gatacttgga gatgttgaag aggtcgtgac	300
aactgttgag atagatgatg aaacatatga agaaattgtg cgcaccacga aacgcactat	360
cccctttctt tttgtccgag gtgatggtgt catattggtt tctccacccc ttcgtacggc	420
atgaagtttg aagttagatc atgctggttg ttaattatga taactggtgt atttgccac	480
ttgatggcgt tgcattggagt gGtatgttat gggcctagcc gctacttttt ctgatgggat	540
gtaggtttta catgtgatac aatcgtgtaa acaactgctt gtgcttgga tctctgtcgg	600
atctcagggg tttctccc	

(2) INFORMATION FOR SEQ ID NO:3468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3468:

Pro	Gln	Asn	Ala	Gly	Ala	Cys	Val	Val	Ala	Lys	Pro	Gln	Gly	Gln	Ser
1				5						10				15	
Glu	Cys	Ala	Phe	Asp	Ser	Leu	Val	Leu	Gln	Leu	Gly	Phe	Arg	Gly	Phe
			20					25				30			
Leu	Gly	Xaa	Glu	Arg	Xaa	Ala	Ala	Ala	Ala	Met	Ala	Ala	Ala	Glu	Glu
		35				40				45					
Glu	Ile	Ala	Val	Lys	Glu	Pro	Leu	Asp	Leu	Ile	Arg	Leu	Ser	Leu	Asp
		50				55				60					
Glu	Arg	Ile	Tyr	Val	Lys	Leu	Arg	Ser	Asp	Arg	Glu	Leu	Arg	Gly	Lys
65					70				75					80	
Leu	His	Ala	Tyr	Asp	Gln	His	Leu	Asn	Met	Ile	Leu	Gly	Asp	Val	Glu
			85					90					95		
Glu	Val	Val	Thr	Thr	Val	Glu	Ile	Asp	Asp	Glu	Thr	Tyr	Glu	Glu	Ile
			100					105					110		
Val	Arg	Thr	Thr	Lys	Arg	Thr	Ile	Pro	Phe	Leu	Phe	Val	Arg	Gly	Asp
		115				120						125			
Gly	Val	Ile	Leu	Val	Ser	Pro	Pro	Leu	Arg	Thr	Ala				
		130				135					140				

(2) INFORMATION FOR SEQ ID NO:3469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..98
(D) OTHER INFORMATION: / Ceres Seq. ID 1576961

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3469:

Met Ala Ala Ala Glu Glu Glu Ile Ala Val Lys Glu Pro Leu Asp Leu
1 5 10 15
Ile Arg Leu Ser Leu Asp Glu Arg Ile Tyr Val Lys Leu Arg Ser Asp
20 25 30
Arg Glu Leu Arg Gly Lys Leu His Ala Tyr Asp Gln His Leu Asn Met
35 40 45
Ile Leu Gly Asp Val Glu Glu Val Val Thr Thr Val Glu Ile Asp Asp
50 55 60
Glu Thr Tyr Glu Glu Ile Val Arg Thr Thr Lys Arg Thr Ile Pro Phe
65 70 75 80
Leu Phe Val Arg Gly Asp Gly Val Ile Leu Val Ser Pro Pro Leu Arg
85 90 95
Thr Ala

(2) INFORMATION FOR SEQ ID NO:3470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 960 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..960
(D) OTHER INFORMATION: / Ceres Seq. ID 1576970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3470:

accaccacca ccaagccagc aggtgctgcg atacattgca cacaacaaca accccagctc 60
tgccccagcc cgccacaggg agttcccgcga tctccctctg gtctgggtcac aggagttccg 120
agacctctcc aatggcggtt aagatctacg ttgtgtacta ttccatgtat gggcatgttg 180
gcaaaactagc tgaagagatc aagaaaggtg ccttatctgt tgaaggtgtt gaggctaaaa 240
tatggcaggt ccctgaaatt ctctctgaag aagtgccttg aaagatgggc gcgcccccta 300
agcccgcagt gccagtcata acaccgcaga acttgacagag gctgacggta tcctctttgg 360
gttcccagaca aggttcggaa tgatggcagc tcagatgaag gcgttcttcg atgccaccgg 420
tgggctcttg agggagcaga gcctcgctgg caaGcctgcc ggcattgtct tcagcactgg 480
aaccagggtt ggtggccaag agactacacc gctgacggcg attaccagtg tgacgcacca 540
cggcatggtg tttgtgcccg tgggctacac ttcggcgccg agctgttcgg catggaccag 600
gtccagggtg gcagccccta cggcgccggc acgttcgncg ccgacggctc gaggtggccg 660
agcgagggtg agctggagca cgccttcac caggggaaat acttcgcggg catcgccaag 720
aagytcaagg gctctgcttg atctgcacat acccctctgt cagatatcat aaaacattta 780
cagattcgtc ataccogtca ccgtcaatag attggtctgt gttctctcgt ggtgcctcga 840
tgctatgtag ttcatgggta ctgctgccgt atgaatttcg atgattgctc tggtgacttg 900
gtttgtaatt tggagttgga ctatcgttgt ttctgccgca taaatttcga tgatttggtc 960

(2) INFORMATION FOR SEQ ID NO:3471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..126
(D) OTHER INFORMATION: / Ceres Seq. ID 1576971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3471:

His His His Gln Ala Ser Arg Cys Cys Asp Thr Leu His Thr Thr Thr
1 5 10 15

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Thr Pro Ala Leu Pro Gln Pro Ala His Arg Ser Ser Arg Ile Ser Leu
20 25 30
Trp Ser Gly His Arg Ser Ser Glu Thr Ser Pro Met Ala Val Lys Ile
35 40 45
Tyr Val Val Tyr Tyr Ser Met Tyr Gly His Val Gly Lys Leu Ala Glu
50 55 60
Glu Ile Lys Lys Gly Ala Leu Ser Val Glu Gly Val Glu Ala Lys Ile
65 70 75 80
Trp Gln Val Pro Glu Ile Leu Ser Glu Glu Val Leu Gly Lys Met Gly
85 90 95
Ala Pro Pro Lys Pro Asp Val Pro Val Ile Thr Pro Gln Asn Leu Gln
100 105 110
Arg Leu Thr Val Ser Ser Leu Gly Ser Arg Gln Gly Ser Glu
115 120 125

(2) INFORMATION FOR SEQ ID NO:3472:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1576972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3472:

Met Met Ala Ala Gln Met Lys Ala Phe Phe Asp Ala Thr Gly Gly Leu
1 5 10 15
Trp Arg Glu Gln Ser Leu Ala Gly Lys Pro Ala Gly Met Phe Phe Ser
20 25 30
Thr Gly Thr Gln Gly Gly Gly Gln Glu Thr Thr Pro Leu Thr Ala Ile
35 40 45
Thr Gln Leu Thr His His Gly Met Val Phe Val Pro Val Gly Tyr Thr
50 55 60
Ser Ala Pro Ser Cys Ser Ala Trp Thr Arg Ser Arg Val Ala Ala Pro
65 70 75 80
Thr Ala Pro Ala Arg Ser Xaa Pro Thr Ala Arg Gly Gly Arg Ala Arg
85 90 95
Trp Ser Trp Ser Thr Pro Ser Thr Arg Gly Asn Thr Ser Arg Ala Ser
100 105 110
Pro Arg Xaa Ser Arg Ala Leu Leu Asp Leu His Ile Pro Leu Cys Gln
115 120 125
Ile Ser
130

(2) INFORMATION FOR SEQ ID NO:3473:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1576973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3473:

Met Ala Ala Gln Met Lys Ala Phe Phe Asp Ala Thr Gly Gly Leu Trp
1 5 10 15
Arg Glu Gln Ser Leu Ala Gly Lys Pro Ala Gly Met Phe Phe Ser Thr
20 25 30
Gly Thr Gln Gly Gly Gly Gln Glu Thr Thr Pro Leu Thr Ala Ile Thr

35 40 45
Gln Leu Thr His His Gly Met Val Phe Val Pro Val Gly Tyr Thr Ser
50 55 60
Ala Pro Ser Cys Ser Ala Trp Thr Arg Ser Arg Val Ala Ala Pro Thr
65 70 75 80
Ala Pro Ala Arg Ser Xaa Pro Thr Ala Arg Gly Gly Arg Ala Arg Trp
85 90 95
Ser Trp Ser Thr Pro Ser Thr Arg Gly Asn Thr Ser Arg Ala Ser Pro
100 105 110
Arg Xaa Ser Arg Ala Leu Leu Asp Leu His Ile Pro Leu Cys Gln Ile
115 120 125
Ser

(2) INFORMATION FOR SEQ ID NO:3474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 877 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..877
(D) OTHER INFORMATION: / Ceres Seq. ID 1576996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3474:

gtcatcaciaa actcactaca cgatcggtta tagcgagcta acagaagctc tatcaagtag 60
tgtgtaggcc atggccggag ccctcgctctt cgtcgctgtt ctccctcgccg caagcgctcg 120
cgctacgacg gctaccacgc tgaccatcca caacctctgc cccaccccggt tgtggccgct 180
ggtagccccg agctcgggct tccctccat ctccaccaac accgcgcggc tgggccccaa 240
cgcgctgctc tccctctcct tcccgcccac cttctgggac ggccgcgtcg ccgcgcgcac 300
gggctgcgac gccgcgcgct ccggtgctgt gacgggggacc acgcgcgccg ccaccgtcgt 360
gcaggtcacc gtccacgacg gcgggaacct ggaccaggcc acctacagcg tgtctctcgt 420
cgacggcttc aacgtgcccc tgggtgtcag cccgcaGgcc gtccggcgcg ggcagtGcc 480
ggcgctcggg tgccccatca acctcaactg cgactgcct cccagaacc gcaccgccga 540
ngngnctcy gtgccgcggc ccgcccggagt acttcaagaa ccggtgcccg ytcaccagga 600
ccacgcccac cgacgtcgag ccggtgaccg cagagctgcc gcgccccggg ggagctcaag 660
gtcatcttct gccaggcgac catcgtcaca tgcggcgcg aagcagagcg caccgtcctc 720
gccgacagct agacagatcg agccgtccag ctccattcgc ctccaggtcc gctgaatcct 780
tacagtaatt gtcatgcttt cttttgctcc atgtgtttgt tagctttggc ttcgacgcgc 840
gtgtactccg gtggttttat tttagaaatc agcagtg

(2) INFORMATION FOR SEQ ID NO:3475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..234
(D) OTHER INFORMATION: / Ceres Seq. ID 1576997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3475:

Met Ala Gly Ala Leu Val Phe Val Ala Val Leu Leu Ala Ala Ser Val
1 5 10 15
Gly Ala Thr Thr Ala Thr Thr Leu Thr Ile His Asn Leu Cys Pro His
20 25 30
Pro Val Trp Pro Leu Val Thr Pro Ser Ser Gly Phe Pro Ser Ile Ser
35 40 45
Thr Asn Thr Ala Arg Leu Gly Pro Asn Ala Leu Leu Ser Leu Ser Phe
50 55 60
Pro Pro Thr Phe Trp Ala Gly Arg Val Ala Ala Arg Thr Gly Cys Asp

(2) INFORMATION FOR SEO ID NO:3476:

(A) LENGTH: 893 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..893

(D) OTHER INFORMATION: / Ceres Seq. ID 1576998

(xi) SEQUENCE DESCRIPTION: SEO ID NO:3476:

aaaaacccaa	gcacagcagc	aggtagaccg	ctgcagcaaa	accgncccc	accgctwccc	60
cgtwmcccac	cccgaccgac	tgtctcccct	ccccgcacc	agcctcaagg	catcgccggc	120
gccgcaacat	cgctgaggaa	gcccgcaccc	ctgcccgat	cgatggcca	acagcaacct	180
cccgcgcg	atcatcaagg	agactcagcg	gctgctcagc	gagccagcac	cggggatcag	240
cgcgtcgccc	tcggaGgaga	acatgcgcta	cttcaacgtt	atgatccttG	gggcccggcg	300
agtcgccta	tgaaggtgga	gtttttaagc	ttgaactctt	tttacctatg	gaatatccaa	360
tggctgcccc	aaaggttagg	tctctgacaa	agatctatca	tcccaactat	gacaagcttg	420
gtaggatatg	cctcgacatt	ctcaaggaca	aatggagccc	agcacttcag	attcgaaacg	480
ttcttttgag	tatacaggct	ctactgagtg	cgccaaatcc	agacgaccct	ctttcggata	540
acattgcaaa	gcactggaaa	gccaatgagg	tagaagctgt	tgaacagct	aaggagtgga	600
ctcgctgta	tgcgagcgg	gcatgagaac	gcagtgatgt	tcttgatgta	ataaccatc	660
atacttcagt	cctcatctat	tgccatttgt	ttgataaaaa	ataggctgga	gatatttgcc	720
atggaatgaa	gtctctacat	gactatcact	ctgaattggt	tggttgtaca	cctgtggctg	780
gttcccttta	ccttggggca	cccttgacaa	atcagtatct	gtggtagaac	tgtctgatac	840
tgtaatatat	ttgttacttc	atgtagaaga	gcttctcaac	ttgtccattt	gtc	

(2) INFORMATION FOR SEQ ID NO:3477:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1576999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3477:

Lys Asn Pro Ser Thr Ala Ala Gly Arg Pro Leu Gln Gln Asn Arg Xaa

(2) INFORMATION FOR SEO ID NO:3478:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1577000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3478:

[illegible]

(2) INFORMATION FOR SEQ ID NO:3479:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 636 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..636

(D) OTHER INFORMATION: / Ceres Seq. ID 1577001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3479:

accaccaggc	accagcatag	atctcgttct	cgcactatt	attctgcaca	gcaacgcata	60
aagccttcta	gaaccatctc	gccgcgcgca	caccacaacc	cgtcgaagcg	aaGcaagcaa	120
tggccggagt	cggatcgaag	gccctcgccg	ttgccgcctt	tctggcggcc	gtctccctct	180
cggtgggcgc	cgcggcgag	gcgcgggcgc	ccagccccgt	cNtcgCgc	cgtcgcggck	240
tcgtcgccct	tgcgcgggc	cctcgctgcc	tccgcgcgcg	ccttcctctt	cgcgcgcgtc	300
cgcactgag	cogatggggc	ctcgtgcctg	caggctacct	agcagtaatt	ccgccgcctgc	360
tggccgcgcc	gcctagatct	atttattgga	gtgctatcca	gtgtaactag	tagtgtgag	420
atttcttcgg	tgtgtgctg	tgtgtgtgc	attttggtcg	gatctggttt	ccttqgtqca	480

gggaggggttt ctataccatg tgcgcggtg Gggttggtgtg atctcatccc cccttgtaga 540
tagtactctg ctatctcgtc gtgatcgtga gtggtgattc tgtctggttg atatttgcta 600
ctgatattgg tccatttga gatatgcgtt gctgct

(2) INFORMATION FOR SEQ ID NO:3480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3480:

Thr Thr Arg His Gln His Arg Ser Arg Ser Arg His Tyr Tyr Ser Ala
1 5 10 15
Gln Gln Arg Ile Lys Pro Ser Arg Thr Ile Ser Pro Pro Pro His His
20 25 30
Asn Pro Ser Lys Arg Ser Lys Gln Trp Pro Glu Ser Asp Arg Arg Pro
35 40 45
Ser Pro Leu Pro Pro Phe Trp Arg Pro Ser Pro Ser Arg Trp Pro Pro
50 55 60
Arg Pro Arg Arg Arg Arg Pro Ala Pro Xaa Ser Ala Ala Val Ala Xaa
65 70 75 80
Ser Ser Pro Phe Ala Ala Ala Leu Val Ala Ser Ala Ala Ala Phe Leu
85 90 95
Phe Ala Ala Val Arg His
100

(2) INFORMATION FOR SEQ ID NO:3481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3481:

Pro Pro Gly Thr Ser Ile Asp Leu Val Leu Ala Thr Ile Ile Leu His
1 5 10 15
Ser Asn Ala Ser Ser Leu Leu Glu Pro Ser Arg Arg Arg His Thr Thr
20 25 30
Thr Arg Arg Ser Glu Ala Ser Asn Gly Arg Ser Arg Ile Glu Gly Pro
35 40 45
Arg Arg Cys Arg Arg Ser Gly Gly Arg Leu Pro Leu Gly Gly Arg Arg
50 55 60
Gly Arg Gly Ala Gly Ala Gln Pro Arg Xaa Pro Pro Pro Ser Arg Xaa
65 70 75 80
Arg Arg Pro Ser Pro Arg Pro Ser Ser Pro Pro Pro Pro Ser Ser
85 90 95
Ser Pro Pro Ser Ala Thr Glu Pro Met Gly Pro Arg Ala Cys Arg Leu
100 105 110
Pro Ser Ser Thr Ser Ala Ala Ala Ala Ala Ala
115 120

(2) INFORMATION FOR SEQ ID NO:3482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..94
(D) OTHER INFORMATION: / Ceres Seq. ID 1577004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3482:

Met Ala Gly Val Gly Ser Lys Ala Leu Ala Val Ala Ala Val Leu Ala
1 5 10 15
Ala Val Ser Leu Ser Val Ala Ala Ala Glu Ala Pro Ala Pro Ser
20 25 30
Pro Val Xaa Arg Arg Arg Arg Gly Xaa Val Ala Leu Arg Arg Gly Pro
35 40 45
Arg Arg Leu Arg Arg Arg Leu Pro Leu Arg Arg Arg Pro Pro Leu Ser
50 55 60
Arg Trp Gly Leu Val Pro Ala Gly Tyr Leu Ala Val Leu Pro Pro Leu
65 70 75 80
Leu Pro Pro Pro Pro Arg Ser Ile Tyr Trp Ser Ala Ile Gln
85 90

(2) INFORMATION FOR SEQ ID NO:3483:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 722 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..722
(D) OTHER INFORMATION: / Ceres Seq. ID 1577048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3483:

ccggaaactg gtaccatccg ccgmcgcagc catccgcttg ttctcttcgg ttcagttctc 60
gagtttccag gatgaaggta atagctgcct atctgcttgc tgttctgggt ggaaacactt 120
ccccgactgc tgatgatgtt aagagcatto tggaatcagt tgggtgctgaa gctgatgaag 180
aaaaactaga gttcctgctc acagaactca aagacaagga cataacagaa gtgattgcag 240
ctggaaggga aaggttatcc tctgtgcctt caggtggttg tgcaattgac atgggagctc 300
cagcagctgt agctggcgtt ggcgcagcac ctgctGgaag aggcaaagaa ggaagaaaag 360
gttgaagaga aggaagagtc tgatgragat atgggtttca gcttgttcga ttaaaacagc 420
actaccagtt tacagtttct tcgcgaatgg tctcataata ttggccggtt tccacaaaat 480
aagattgtcA atagctacta cgtacttatg ctattctgca tgtgatgtac gagtgtgcat 540
cttcaagaat ctttaagttg aatggtcggt ggtcccataa taatattggt aacaatgtaa 600
attgtatgtc ctgtacgtac tttgggtatcg cgacatctca gtgtgcatct tcaaggatca 660
taagttgaat gttatcatta aggtcagttt gggttcagata aatataattg ctagttatag 720
cc

(2) INFORMATION FOR SEQ ID NO:3484:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..120
(D) OTHER INFORMATION: / Ceres Seq. ID 1577049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3484:

Gly Asn Trp Tyr His Pro Pro Xaa Gln Pro Ser Ala Cys Ser Leu Arg
1 5 10 15
Phe Ser Ser Arg Val Ser Arg Met Lys Val Ile Ala Ala Tyr Leu Leu
20 25 30

Ala Val Leu Gly Gly Asn Thr Ser Pro Thr Ala Asp Asp Val Lys Ser
35 40 45
Ile Leu Glu Ser Val Gly Ala Glu Ala Asp Glu Glu Lys Leu Glu Phe
50 55 60
Leu Leu Thr Glu Leu Lys Asp Lys Asp Ile Thr Glu Val Ile Ala Ala
65 70 75 80
Gly Arg Glu Arg Leu Ser Ser Val Pro Ser Gly Gly Gly Ala Ile Asp
85 90 95
Met Gly Ala Pro Ala Ala Val Ala Gly Gly Gly Ala Ala Pro Ala Gly
100 105 110
Arg Gly Lys Glu Gly Arg Lys Gly
115 120

(2) INFORMATION FOR SEQ ID NO:3485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3485:

Met Lys Val Ile Ala Ala Tyr Leu Leu Ala Val Leu Gly Gly Asn Thr
1 5 10 15
Ser Pro Thr Ala Asp Asp Val Lys Ser Ile Leu Glu Ser Val Gly Ala
20 25 30
Glu Ala Asp Glu Glu Lys Leu Glu Phe Leu Leu Thr Glu Leu Lys Asp
35 40 45
Lys Asp Ile Thr Glu Val Ile Ala Ala Gly Arg Glu Arg Leu Ser Ser
50 55 60
Val Pro Ser Gly Gly Gly Ala Ile Asp Met Gly Ala Pro Ala Ala Val
65 70 75 80
Ala Gly Gly Gly Ala Ala Pro Ala Gly Arg Gly Lys Glu Gly Arg Lys
85 90 95
Gly

(2) INFORMATION FOR SEQ ID NO:3486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..831
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3486:

acccctcatc	ttcctctcct	tccctcccaa	cctcggtcac	cagtccatcg	atcctcgaat	60
cgctcgcttg	cactgcactg	caaggtacat	acgccatgaa	gctgagcatg	cctttcttcg	120
gctcgcttcc	ctcctcctcc	ggcaagaaga	ggaaggggtc	aaagaccggc	ggctcctctt	180
ccttcgtctc	caccgcgtcg	tgctcctcgt	cgacagagtg	cgcatcgccg	tcagccgtca	240
cgacgacgcc	acgcaccgtc	ctccaatccc	agcgtccgc	ccccaacccg	aaGcctccgg	300
cggNtagtag	cgcgcgcgtg	gacgcgggag	gacctggagg	tggcGctgcg	ccgggtggtc	360
cgcagcgagg	acgagctggc	cgcggtgctg	gccgaggcgg	aggccNgccG	Ggctcgcgcc	420
cgagcaggcc	gcgtccgcGg	aggcggaggga	cgaggccgag	ctCcgcgacg	cgttcgcggt	480
gttcgacgcg	gacggcgacg	gcaggatctc	cgcgaggagg	tccgcgccgt	gctcgccgcg	540
ctcggcgacg	ccgcctgctc	cgtcgaggac	tgccgcgcga	tgatcgggcg	cgtcgacggc	600
gatggcgacg	gcttcgtctg	cttccacgac	ttctcgcgca	tgatgatgca	gggggcgtga	660

ttctggcgctc gtcgtgcctg gctgggttgt gtcggtctcc gcgtgtttct tctgttgcaa 720
aatctctcta cctgtatgtg gacctgtttt ttcggtgtca tctactcgta tcatctccgt 780
cgtgcgagat gaatgaaccc aaaagagatc tatatatattt catcttttcc g

(2) INFORMATION FOR SEQ ID NO:3487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..276
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3487:

Pro Ser Ser Ser Ser Pro Ser Leu Pro Thr Ser Val Thr Ser Pro Ser
1 5 10 15
Ile Leu Glu Ser Leu Ala Cys Thr Ala Leu Gln Gly Thr Tyr Ala Met
20 25 30
Lys Leu Ser Met Pro Phe Phe Gly Ser Ser Ser Ser Ser Gly Lys
35 40 45
Lys Arg Lys Gly Ser Lys Thr Gly Gly Ser Ser Ser Phe Val Ser Thr
50 55 60
Ala Ser Ser Ser Ser Ser Asp Glu Cys Ala Ser Pro Ser Ala Val Thr
65 70 75 80
Thr Thr Pro Arg Thr Val Leu Gln Ser Gln Pro Ser Ala Pro Asn Pro
85 90 95
Lys Pro Pro Ala Xaa Ser Ser Arg Arg Arg Asp Ala Gly Gly Pro Gly
100 105 110
Gly Gly Ala Ala Pro Gly Gly Pro Gln Arg Gly Arg Ala Gly Arg Gly
115 120 125
Ala Gly Arg Gly Gly Gly Xaa Pro Gly Ser Arg Pro Ser Arg Pro Arg
130 135 140
Pro Arg Arg Arg Arg Thr Arg Pro Ser Ser Ala Thr Arg Ser Arg Cys
145 150 155 160
Ser Thr Arg Thr Ala Thr Ala Gly Ser Pro Arg Arg Xaa Pro Arg Arg
165 170 175
Ala Arg Arg Ala Arg Arg Arg Arg Leu Leu Arg Arg Gly Leu Pro Pro
180 185 190
His Asp Arg Pro Arg Arg Arg Arg Trp Arg Arg Leu Arg Leu Leu Pro
195 200 205
Arg Leu Leu Ala His Asp Asp Ala Gly Gly Val Ile Leu Ala Ser Ser
210 215 220
Cys Leu Ala Gly Leu Cys Arg Ser Pro Arg Val Ser Ser Val Ala Lys
225 230 235 240
Ser Leu Tyr Leu Tyr Val Asp Leu Phe Phe Arg Cys His Leu Leu Val
245 250 255
Ser Ser Pro Ser Cys Glu Met Asn Glu Pro Lys Arg Asp Leu Tyr Ile
260 265 270
Phe Ile Phe Ser
275

(2) INFORMATION FOR SEQ ID NO:3488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..245

(D) OTHER INFORMATION: / Ceres Seq. ID 1577060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3488:

Met Lys Leu Ser Met Pro Phe Phe Gly Ser Ser Ser Ser Ser Gly
1 5 10 15
Lys Lys Arg Lys Gly Ser Lys Thr Gly Gly Ser Ser Ser Phe Val Ser
20 25 30
Thr Ala Ser Ser Ser Ser Ser Asp Glu Cys Ala Ser Pro Ser Ala Val
35 40 45
Thr Thr Thr Pro Arg Thr Val Leu Gln Ser Gln Pro Ser Ala Pro Asn
50 55 60
Pro Lys Pro Pro Ala Xaa Ser Ser Arg Arg Arg Asp Ala Gly Gly Pro
65 70 75 80
Gly Gly Gly Ala Ala Pro Gly Gly Pro Gln Arg Gly Arg Ala Gly Arg
85 90 95
Gly Ala Gly Arg Gly Gly Gly Xaa Pro Gly Ser Arg Pro Ser Arg Pro
100 105 110
Arg Pro Arg Arg Arg Arg Thr Arg Pro Ser Ser Ala Thr Arg Ser Arg
115 120 125
Cys Ser Thr Arg Thr Ala Thr Ala Gly Ser Pro Arg Arg Xaa Pro Arg
130 135 140
Arg Ala Arg Arg Ala Arg Arg Arg Arg Leu Leu Arg Arg Gly Leu Pro
145 150 155 160
Pro His Asp Arg Pro Arg Arg Arg Arg Trp Arg Arg Leu Arg Leu Leu
165 170 175
Pro Arg Leu Leu Ala His Asp Asp Ala Gly Gly Val Ile Leu Ala Ser
180 185 190
Ser Cys Leu Ala Gly Leu Cys Arg Ser Pro Arg Val Ser Ser Val Ala
195 200 205
Lys Ser Leu Tyr Leu Tyr Val Asp Leu Phe Phe Arg Cys His Leu Leu
210 215 220
Val Ser Ser Pro Ser Cys Glu Met Asn Glu Pro Lys Arg Asp Leu Tyr
225 230 235 240
Ile Phe Ile Phe Ser
245

(2) INFORMATION FOR SEQ ID NO:3489:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..241

(D) OTHER INFORMATION: / Ceres Seq. ID 1577061

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3489:

Met Pro Phe Phe Gly Ser Ser Ser Ser Ser Ser Gly Lys Lys Arg Lys
1 5 10 15
Gly Ser Lys Thr Gly Gly Ser Ser Ser Phe Val Ser Thr Ala Ser Ser
20 25 30
Ser Ser Ser Asp Glu Cys Ala Ser Pro Ser Ala Val Thr Thr Thr Pro
35 40 45
Arg Thr Val Leu Gln Ser Gln Pro Ser Ala Pro Asn Pro Lys Pro Pro
50 55 60
Ala Xaa Ser Ser Arg Arg Arg Asp Ala Gly Gly Pro Gly Gly Gly Ala
65 70 75 80
Ala Pro Gly Gly Pro Gln Arg Gly Arg Ala Gly Arg Gly Ala Gly Arg
85 90 95
Gly Gly Gly Xaa Pro Gly Ser Arg Pro Ser Arg Pro Arg Pro Arg Arg
100 105 110
Arg Arg Thr Arg Pro Ser Ser Ala Thr Arg Ser Arg Cys Ser Thr Arg

115	120	125
Thr Ala Thr Ala Gly Ser Pro Arg Arg Xaa Pro Arg Arg Ala Arg Arg		
130	135	140
Ala Arg Arg Arg Arg Leu Leu Arg Arg Gly Leu Pro Pro His Asp Arg		
145	150	155
Pro Arg Arg Arg Arg Trp Arg Arg Leu Arg Leu Leu Pro Arg Leu Leu		160
	165	170
Ala His Asp Asp Ala Gly Gly Val Ile Leu Ala Ser Ser Cys Leu Ala		175
	180	185
Gly Leu Cys Arg Ser Pro Arg Val Ser Ser Val Ala Lys Ser Leu Tyr		190
	195	200
Leu Tyr Val Asp Leu Phe Phe Arg Cys His Leu Leu Val Ser Ser Pro		205
	210	215
Ser Cys Glu Met Asn Glu Pro Lys Arg Asp Leu Tyr Ile Phe Ile Phe		220
225	230	235
Ser		240

(2) INFORMATION FOR SEQ ID NO:3490:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 876 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..876

(D) OTHER INFORMATION: / Ceres Seq. ID 1577062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3490:

tccaactctg	cgccgcaatc	cactcaagaa	ggttagccct	cgtgggtctcg	gatttggata	60
atcctccgcc	gaggtatgaa	acaggangcg	gccaccagca	tagtggtgac	ccaggaggac	120
gtcctgcacc	actacaagga	gcctccaccc	cgmcgcgagg	acgatycgcc	agcactggct	180
gcgtcgctgt	cgttgccgtc	gtcactgtcg	gaggacaatg	gcgacgccat	gccgcagcca	240
tcttcatacg	cggtcttgcc	gcgcggggat	ggcgagctgg	tgtctgcgga	ggagctgctg	300
ctgAgtgccg	ccgtcaaat	tgcCccatgg	tggaccacgg	cgtgtaccgc	tccggNattc	360
ccggacgcct	ccaacttgcc	gtttcttgag	acgctccgac	tccgctccgt	cctgtgcctg	420
tgcccggagc	catacccgga	ggctaactctg	gagttcctcc	gtgcccacgg	gatcaagctc	480
ttccagttcg	gaatcgacgg	ctccaaggaa	ccatttgtga	acataccaga	agatagaatc	540
cgtgaagctc	tagaagtcac	cctagatgca	agcaaccatc	cggttcttat	tcactgcaag	600
cgaggaaagc	atcgaaccgg	ctgtgtgggt	ggatgcttta	ggaaattgca	acgctgggtg	660
ctaacttcaa	tatttgacga	ataccagcgt	tttgctgctg	ccaaaacaag	agtttctgac	720
tacggttcat	ggagctatct	gatgtatcga	gcataaagca	tttagcattt	gagtcgtctg	780
tatgatagta	acattgggtgc	atgataacaa	ctcaataactg	gttccattac	ggtgtcatct	840
ttttcattta	agaaaaaaaa	tcattttctaa	aaatgc			

(2) INFORMATION FOR SEQ ID NO:3491:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1577063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3491:

Gln Leu Cys Ala Ala Ile His Ser Arg Arg Leu Ala Leu Val Val Ser		
1	5	10
Asp Leu Asp Asn Pro Pro Pro Arg Tyr Glu Thr Gly Xaa Gly His Gln		15
	20	25
His Ser Gly Asp Pro Gly Gly Arg Pro Ala Pro Leu Gln Gly Ala Ser		30

(2) INFORMATION FOR SEQ ID NO:3492:

(A) LENGTH: 226 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..226

(D) OTHER INFORMATION: / Ceres Seq. ID 1577064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3492:

(2) INFORMATION FOR SEQ ID NO:3493:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1577065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3493:

Met Pro Gln Pro Ser Ser Tyr Ala Val Leu Pro Arg Arg Asp Gly Glu
1 5 10 15
Leu Val Ser Ala Glu Glu Leu Leu Leu Ser Ala Ala Ala Gln Leu Arg
20 25 30
Pro Trp Trp Thr Thr Ala Cys Thr Ala Pro Xaa Phe Pro Asp Ala Ser
35 40 45
Asn Leu Pro Phe Leu Glu Thr Leu Arg Leu Arg Ser Val Leu Cys Leu
50 55 60
Cys Pro Glu Pro Tyr Pro Glu Ala Asn Leu Glu Phe Leu Arg Ala His
65 70 75 80
Gly Ile Lys Leu Phe Gln Phe Gly Ile Asp Gly Ser Lys Glu Pro Phe
85 90 95
Val Asn Ile Pro Glu Asp Arg Ile Arg Glu Ala Leu Glu Val Ile Leu
100 105 110
Asp Ala Ser Asn His Pro Val Leu Ile His Cys Lys Arg Gly Lys His
115 120 125
Arg Thr Gly Cys Val Val Gly Cys Phe Arg Lys Leu Gln Arg Trp Cys
130 135 140
Leu Thr Ser Ile Phe Asp Glu Tyr Gln Arg Phe Ala Ala Ala Lys Thr
145 150 155 160
Arg Val Ser Asp Tyr Gly Ser Trp Ser Tyr Leu Met Tyr Arg Ala
165 170 175

(2) INFORMATION FOR SEQ ID NO:3494:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 630 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..630

(D) OTHER INFORMATION: / Ceres Seq. ID 1577073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3494:

aaaattaaag gaaaacggtg gactagaaac ttccaaatcg aacggcacac aaaaatcaca 60
acccggaaag ggaccagcag cgcaaagggtg agcgagcttt ccttcggaac tctctcgtgc 120
tcacctcAat ccgtccgaca gatccacacg aatcctctga ttcagagcag ggtggtggca 180
ttgatcagac gcctgccatg gctgatcagt tcgaggattc ggccaacaat gtgatcattg 240
aggaggtgaa caagggcctg aacccaggaa tgggtggttct gcttgtggtt gcaagcttcc 300
tgctgatctt ctttgtgggg aactatgcgc tgtatgtgta tgcgcagaag acgctcccgc 360
caaagaagaa gaagccggtg tcgaagaaga agctgaagaa ggaaaagctg aagcaggggg 420
tctctgcgcc gggagagtaa acggccatgc tgccgatcct cccgtccaga gctcctattc 480
acatgattat tagagaaaaa aattatatat atataccaga tggagccgta gtgtDtgagg 540
tAactttgtt ctgtagatgc tctgtcttta atggtacatc tgtattggag actttgagac 600
cttgtttcag caactgatga atcttagccc

(2) INFORMATION FOR SEQ ID NO:3495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1577074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3495:

Lys Ile Lys Gly Lys Arg Trp Thr Arg Asn Phe Gln Ile Glu Arg His
1 5 10 15
Thr Lys Ile Thr Thr Arg Lys Gly Thr Ser Ser Ala Lys Val Ser Glu
20 25 30
Leu Ser Phe Gly Thr Leu Ser Cys Ser Pro Gln Ser Val Arg Gln Ile
35 40 45
His Thr Asn Pro Leu Ile Gln Ser Arg Val Leu Ala Leu Ile Arg Arg
50 55 60
Leu Pro Trp Leu Ile Ser Ser Arg Ile Arg Arg Thr Met
65 70 75

(2) INFORMATION FOR SEQ ID NO:3496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1577075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3496:

Met Ala Asp Gln Phe Glu Asp Ser Ala Asn Asn Val Ile Ile Glu Glu
1 5 10 15
Val Asn Lys Gly Leu Asn Pro Gly Met Val Val Leu Leu Val Val Ala
20 25 30
Ser Phe Leu Leu Ile Phe Phe Val Gly Asn Tyr Ala Leu Tyr Val Tyr
35 40 45
Ala Gln Lys Thr Leu Pro Pro Lys Lys Lys Lys Pro Val Ser Lys Lys
50 55 60
Lys Leu Lys Lys Glu Lys Leu Lys Gln Gly Val Ser Ala Pro Gly Glu
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:3497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56

(D) OTHER INFORMATION: / Ceres Seq. ID 1577076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3497:

Met Leu Pro Ile Leu Pro Ser Arg Ala Pro Ile His Met Ile Ile Arg
1 5 10 15
Glu Lys Asn Tyr Ile Tyr Ile Pro Asp Gly Ala Val Val Xaa Gly Val
20 25 30
Thr Leu Phe Cys Arg Cys Ser Val Phe Asn Gly Thr Ser Val Leu Glu
35 40 45
Thr Leu Arg Pro Cys Phe Ser Asn
50 55

(2) INFORMATION FOR SEQ ID NO:3498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..885
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3498:

atccgagtcc	acccaactaa	tcacgcccaa	tcagaacaga	ctcggtcgct	tcaccactcc	60
actcgccgca	ggcgccgggc	gccgcccagg	ggatcgaggc	aagatgttct	tccacatcgt	120
gctggagcgg	aacatgcagc	tgcacccacg	acacttcggg	ccgcacctcc	gcgacaagct	180
cgtttccaag	ctcatcaagg	acgtcgaggg	cacctgcagc	gggcggcacg	ggttcgttgt	240
ggcgatcacg	ggtgtggagg	acatcggcaa	ggggctcatc	cgggaaggca	cgggatacgt	300
caccttcccc	gycaagtacc	agtgcgttgt	ctttagaccc	ttcaagggcg	agatcctcga	360
agctgtcgtc	accatggtga	acaagatggg	cttctttgcg	gaggctgggc	cgggtgcagat	420
cttcgtgtcc	aaccatttga	ttccagacga	tatggagttc	caatcaRgga	gatgtgccga	480
actacacaac	ttctgatgga	tcggtgaaaa	ttcaaaaaga	gagtgagggtg	cggctgaaga	540
ttattGggta	ctcgtgtcga	tgctacagaa	attttttgca	ttggcacAat	Aaaaggatga	600
ttttctgggt	gktatcacg	atcctggtgc	gscagtgtaa	atggtctaag	aagcgagatt	660
gtactccatt	gttctgactt	ctgagtacta	tcgcagacgt	gtgtaatcgc	tggtcgcgta	720
aaactgcaat	ggctgtactg	actgcggaac	ttgttgagaa	tgatgtgact	aggaccttgt	780
ttagggcctg	tttggttctt	tagtatggcc	ctgattggca	caactgctgt	ttattgaaaa	840
aacagcttat	ctgataagct	ggtgaaaaat	agcttctgct	tgttg		

(2) INFORMATION FOR SEQ ID NO:3499:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..164
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3499:

Ser	Glu	Ser	Thr	Gln	Leu	Ile	Thr	Pro	Asn	Gln	Asn	Arg	Leu	Gly	Arg
1				5					10					15	
Phe	Thr	Thr	Pro	Leu	Ala	Ala	Gly	Ala	Gly	Arg	Arg	Arg	Gly	Asp	Arg
			20					25					30		
Ser	Lys	Met	Phe	Phe	His	Ile	Val	Leu	Glu	Arg	Asn	Met	Gln	Leu	His
		35					40					45			
Pro	Arg	His	Phe	Gly	Pro	His	Leu	Arg	Asp	Lys	Leu	Val	Ser	Lys	Leu
		50				55					60				
Ile	Lys	Asp	Val	Glu	Gly	Thr	Cys	Ser	Gly	Arg	His	Gly	Phe	Val	Val
65				70					75					80	
Ala	Ile	Thr	Gly	Val	Glu	Asp	Ile	Gly	Lys	Gly	Leu	Ile	Arg	Glu	Gly
			85					90						95	
Thr	Gly	Tyr	Val	Thr	Phe	Pro	Xaa	Lys	Tyr	Gln	Cys	Val	Val	Phe	Arg
			100					105					110		
Pro	Phe	Lys	Gly	Glu	Ile	Leu	Glu	Ala	Val	Val	Thr	Met	Val	Asn	Lys
		115					120					125			
Met	Gly	Phe	Phe	Ala	Glu	Ala	Gly	Pro	Val	Gln	Ile	Phe	Val	Ser	Asn
		130				135					140				
His	Leu	Ile	Pro	Asp	Asp	Met	Glu	Phe	Gln	Ser	Xaa	Arg	Cys	Ala	Glu
145				150						155					160
Leu	His	Asn	Phe												

(2) INFORMATION FOR SEQ ID NO:3500:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..130
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577091
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3500:

Met Phe Phe His Ile Val Leu Glu Arg Asn Met Gln Leu His Pro Arg
1 5 10 15
His Phe Gly Pro His Leu Arg Asp Lys Leu Val Ser Lys Leu Ile Lys
 20 25 30
Asp Val Glu Gly Thr Cys Ser Gly Arg His Gly Phe Val Val Ala Ile
 35 40 45
Thr Gly Val Glu Asp Ile Gly Lys Gly Leu Ile Arg Glu Gly Thr Gly
 50 55 60
Tyr Val Thr Phe Pro Xaa Lys Tyr Gln Cys Val Val Phe Arg Pro Phe
65 70 75 80
Lys Gly Glu Ile Leu Glu Ala Val Val Thr Met Val Asn Lys Met Gly
 85 90 95
Phe Phe Ala Glu Ala Gly Pro Val Gln Ile Phe Val Ser Asn His Leu
 100 105 110
Ile Pro Asp Asp Met Glu Phe Gln Ser Xaa Arg Cys Ala Glu Leu His
 115 120 125
Asn Phe
130

(2) INFORMATION FOR SEQ ID NO:3501:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..120
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3501:

Met Gln Leu His Pro Arg His Phe Gly Pro His Leu Arg Asp Lys Leu
1 5 10 15
Val Ser Lys Leu Ile Lys Asp Val Glu Gly Thr Cys Ser Gly Arg His
 20 25 30
Gly Phe Val Val Ala Ile Thr Gly Val Glu Asp Ile Gly Lys Gly Leu
 35 40 45
Ile Arg Glu Gly Thr Gly Tyr Val Thr Phe Pro Xaa Lys Tyr Gln Cys
50 55 60
Val Val Phe Arg Pro Phe Lys Gly Glu Ile Leu Glu Ala Val Val Thr
65 70 75 80
Met Val Asn Lys Met Gly Phe Phe Ala Glu Ala Gly Pro Val Gln Ile
 85 90 95
Phe Val Ser Asn His Leu Ile Pro Asp Asp Met Glu Phe Gln Ser Xaa
 100 105 110
Arg Cys Ala Glu Leu His Asn Phe
 115 120

(2) INFORMATION FOR SEQ ID NO:3502:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 776 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..776

(D) OTHER INFORMATION: / Ceres Seq. ID 1577122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3502:

gggcaactcg	aagaagccgc	gtgcgttatc	ctttgagcag	tttgggcgct	gagcaagtcc	60
agtgagarar	ggagarcggc	gagaggatgg	ctgggatggc	atcgctgcag	ggcgccatGg	120
cgtcgctctc	catctccGcg	ctaggcgcgg	cgacggcgag	cagcagcagc	ttctggggca	180
accggctcgc	cacctaactcc	gcgccgcagc	ctggggtaag	gtttatggtc	aagatatgcc	240
caattgaaat	gagacttaag	agatggggagc	gaaagaagtg	taaaccaaac	agtcttcctg	300
tgctgcacaa	gatgcatgtt	aggatcgggg	acacggtaca	ggttattgca	ggccgtgaga	360
aaggaaaagt	tggagaagtc	acacgccttt	tcaagcacia	cagcacgggt	atcgtgaagg	420
acctgaactt	gaagtcgaag	cacaagaaag	gcacagacga	tgaaccgggt	gaaatcgta	480
tgattgaagg	ccccattcat	agctcaaattg	tgatgctcta	ctctaaggag	aagagtgtgg	540
taagcagggt	tggccacaaa	ttcctggagg	acgggaccaa	gggccgatac	ctggtcaaga	600
ccggtgaagt	aatcgacagt	gttgagaagt	gggtaaaggt	ttttaaggaa	ggaaattcgg	660
agtaacagtt	ttagcatgaa	aacctgcaaa	atgctctgaa	cgctrmtgcg	tcttgcatgt	720
tgaattgagc	ctgtttatcc	ctctatgttg	ttatttacgc	cagtttttcc	ccctgt	

(2) INFORMATION FOR SEQ ID NO:3503:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1577123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3503:

Met	Ala	Gly	Met	Ala	Ser	Leu	Gln	Gly	Ala	Met	Ala	Ser	Leu	Ser	Ile	
1			5					10					15			
Ser	Ala	Leu	Gly	Ala	Ala	Thr	Ala	Ser	Ser	Ser	Ser	Phe	Trp	Gly	Asn	
			20					25					30			
Arg	Leu	Ala	Thr	Tyr	Ser	Ala	Pro	Gln	Pro	Gly	Val	Arg	Phe	Met	Val	
			35					40					45			
Lys	Ile	Cys	Pro	Ile	Glu	Met	Arg	Leu	Lys	Arg	Trp	Glu	Arg	Lys	Lys	
			50					55				60				
Cys	Lys	Pro	Asn	Ser	Leu	Pro	Val	Leu	His	Lys	Met	His	Val	Arg	Ile	
65								70				75			80	
Gly	Asp	Thr	Val	Gln	Val	Ile	Ala	Gly	Arg	Glu	Lys	Gly	Lys	Val	Gly	
			85					90							95	
Glu	Val	Thr	Arg	Leu	Phe	Lys	His	Asn	Ser	Thr	Val	Ile	Val	Lys	Asp	
			100					105						110		
Leu	Asn	Leu	Lys	Ser	Lys	His	Lys	Lys	Gly	Thr	Asp	Asp	Glu	Pro	Gly	
			115					120					125			
Glu	Ile	Val	Met	Ile	Glu	Gly	Pro	Ile	His	Ser	Ser	Asn	Val	Met	Leu	
			130					135				140				
Tyr	Ser	Lys	Glu	Lys	Ser	Val	Val	Ser	Arg	Val	Gly	His	Lys	Phe	Leu	
145																
			150									155			160	
Glu	Asp	Gly	Thr	Lys	Val	Arg	Tyr	Leu	Val	Lys	Thr	Gly	Glu	Val	Ile	
			165									170			175	
Asp	Ser	Val	Glu	Lys	Trp	Val	Lys	Val	Phe	Lys	Glu	Gly	Asn	Ser	Glu	
			180					185							190	

(2) INFORMATION FOR SEQ ID NO:3504:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..189

(D) OTHER INFORMATION: / Ceres Seq. ID 1577124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3504:

Met Ala Ser Leu Gln Gly Ala Met Ala Ser Leu Ser Ile Ser Ala Leu
1 5 10 15
Gly Ala Ala Thr Ala Ser Ser Ser Ser Phe Trp Gly Asn Arg Leu Ala
20 25 30
Thr Tyr Ser Ala Pro Gln Pro Gly Val Arg Phe Met Val Lys Ile Cys
35 40 45
Pro Ile Glu Met Arg Leu Lys Arg Trp Glu Arg Lys Lys Cys Lys Pro
50 55 60
Asn Ser Leu Pro Val Leu His Lys Met His Val Arg Ile Gly Asp Thr
65 70 75 80
Val Gln Val Ile Ala Gly Arg Glu Lys Gly Lys Val Gly Glu Val Thr
85 90 95
Arg Leu Phe Lys His Asn Ser Thr Val Ile Val Lys Asp Leu Asn Leu
100 105 110
Lys Ser Lys His Lys Lys Gly Thr Asp Asp Glu Pro Gly Glu Ile Val
115 120 125
Met Ile Glu Gly Pro Ile His Ser Ser Asn Val Met Leu Tyr Ser Lys
130 135 140
Glu Lys Ser Val Val Ser Arg Val Gly His Lys Phe Leu Glu Asp Gly
145 150 155 160
Thr Lys Val Arg Tyr Leu Val Lys Thr Gly Glu Val Ile Asp Ser Val
165 170 175
Glu Lys Trp Val Lys Val Phe Lys Glu Gly Asn Ser Glu
180 185

(2) INFORMATION FOR SEQ ID NO:3505:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..182

(D) OTHER INFORMATION: / Ceres Seq. ID 1577125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3505:

Met Ala Ser Leu Ser Ile Ser Ala Leu Gly Ala Ala Thr Ala Ser Ser
1 5 10 15
Ser Ser Phe Trp Gly Asn Arg Leu Ala Thr Tyr Ser Ala Pro Gln Pro
20 25 30
Gly Val Arg Phe Met Val Lys Ile Cys Pro Ile Glu Met Arg Leu Lys
35 40 45
Arg Trp Glu Arg Lys Lys Cys Lys Pro Asn Ser Leu Pro Val Leu His
50 55 60
Lys Met His Val Arg Ile Gly Asp Thr Val Gln Val Ile Ala Gly Arg
65 70 75 80
Glu Lys Gly Lys Val Gly Glu Val Thr Arg Leu Phe Lys His Asn Ser
85 90 95
Thr Val Ile Val Lys Asp Leu Asn Leu Lys Ser Lys His Lys Lys Gly
100 105 110
Thr Asp Asp Glu Pro Gly Glu Ile Val Met Ile Glu Gly Pro Ile His
115 120 125
Ser Ser Asn Val Met Leu Tyr Ser Lys Glu Lys Ser Val Val Ser Arg
130 135 140
Val Gly His Lys Phe Leu Glu Asp Gly Thr Lys Val Arg Tyr Leu Val

(2) INFORMATION FOR SEQ ID NO:3506:

(A) LENGTH: 814 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..814

(D) OTHER INFORMATION: / Ceres Seq. ID 1577130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3506:

agtgtaaacc	agccacacct	cctccccgtc	tctctctccct	ccccatgcgc	tgttttgttc	60
tgtattgggt	tgtgcgcggg	ggacaggacg	cctcctgcgc	cgaccgttcc	gttcgtgttt	120
gtgcctgcct	gtgccttcgg	ttgttctctt	gagcgacggc	gagtcggcga	ccgaggggga	180
ccacagacgc	attagctggg	tgaactcttt	caaaaggggc	aggtgcgcga	gtttgaatgg	240
ctgctacaaa	gcttcagggc	ttttggaacc	accctgctgg	ccccaaaacc	attcattttct	300
ggcgcccaac	attcaaatgg	ggatatcagca	ttgccaacat	agccgacttt	gcaaaagccgc	360
ctgaaaagat	atcttaacct	cagcaagttg	ctgttgcatg	cactggaatc	atttggtaa	420
ggtacagctt	ggttatcaca	ccgaaaaaact	ggaacctttt	cagtgttaac	gttgcaatgg	480
cgggtacagg	cctgtatcag	ctttcacgga	agattagsca	agattacNtt	gtctggtgag	540
aaggatgNct	gNctccacaa	ctgNcaagaa	tagataatga	caacacacaa	agaataactg	600
attgagaagt	ctgnocggct	agggatctta	ctcttgattt	ttctgggnca	ggncaaggat	660
atgtctcgat	ccaggacggg	tcatgtttgt	tttctgttct	ttctgaaatc	atgagncagg	720
ttaatgtgaa	aatctctctg	caaaaaaaga	agcccatgaa	gtaatatattt	gtgcattttt	780
gtgggaaaaa	agtcatgncc	aggacatgat	tctgt			

(2) INFORMATION FOR SEQ ID NO:3507:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1577131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3507:

Ser	Val	Asn	Gln	Pro	Thr	Leu	Leu	Pro	Val	Ser	Ser	Pro	Ser	Pro	Cys
1				5					10					15	
Ala	Val	Leu	Phe	Cys	Ile	Gly	Leu	Cys	Ala	Gly	Asp	Arg	Thr	Pro	Pro
		20						25					30		
Ala	Pro	Thr	Val	Pro	Phe	Val	Phe	Val	Pro	Ala	Cys	Ala	Phe	Gly	Cys
		35					40					45			
Ser	Ser	Glu	Arg	Arg	Arg	Val	Gly	Asp	Arg	Gly	Gly	Pro	Gln	Thr	His
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..100
(D) OTHER INFORMATION: / Ceres Seq. ID 1577132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3508:

```
Met Ala Ala Thr Lys Leu Gln Ala Phe Trp Asn His Pro Ala Gly Pro
1      5      10      15
Lys Thr Ile His Phe Trp Ala Pro Thr Phe Lys Trp Gly Ile Ser Ile
      20      25      30
Ala Asn Ile Ala Asp Phe Ala Lys Pro Pro Glu Lys Ile Ser Tyr Pro
      35      40      45
Gln Gln Val Ala Val Ala Cys Thr Gly Ile Ile Trp Ser Arg Tyr Ser
      50      55      60
Leu Val Ile Thr Pro Lys Asn Trp Asn Leu Phe Ser Val Asn Val Ala
      65      70      75      80
Met Ala Gly Thr Gly Leu Tyr Gln Leu Ser Arg Lys Ile Xaa Gln Asp
      85      90      95
Tyr Xaa Val Trp
      100
```

(2) INFORMATION FOR SEQ ID NO:3509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..764
(D) OTHER INFORMATION: / Ceres Seq. ID 1577133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3509:

```
gaaatacccg ccgtacagc ctactgctgg acatctaagg gccacactga aaaaaccctt      60
gcgccgctga gctgagtgccc cttcccttct ctcgtgcgct ccgcctccgc cttcagttta      120
gcctccaagc aggggcgccc cgcggggtat tctgtccgtc gttgaggata gagagtcact      180
tgcaccgggg gagcggagat gaagccgggt gtggggatcg tgggtgctgaa caagatgcag      240
aagtcgggtg tggttgcat ggaccgcctc ttccacaacC Aaaggtatac Aaaccgctac      300
gtcaagcgca cHctCccaag ttcatggcac acgacgatga caacacctgc aacattggcg      360
aCccgggtta ggctggatcc Tttctaggcc cttgagcaga cacaagcact gggttgttgc      420
tgaaattctc cgcagagcta aggtgtacgt tccaccagct gcaacagcgt ccagtgaacg      480
tggtagcaaa tctcaacaag ctgggtgtgc taocaaatga tccatctgaa gttactcaga      540
acaagatgca gtcacggctt gtttttcttt cgtgtatgt ttgtttcctt gtggaatgtg      600
gttgccatgt ttagcatggg agaaaaaata gcaagcagcc agcatctttg cttaattact      660
gttgttcttc tgtggtgtcc ttogtttaac ggtactagcc attaaggatg tagttaccag      720
attcaacaag accaatggat tcatattgta ttggttcact tccg
```

(2) INFORMATION FOR SEQ ID NO:3510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..62
(D) OTHER INFORMATION: / Ceres Seq. ID 1577134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3510:

```
Met Lys Pro Val Val Gly Ile Val Val Ser Asn Lys Met Gln Lys Ser
1      5      10      15
Val Val Val Ala Leu Asp Arg Leu Phe His Asn Gln Arg Tyr Thr Asn
      20      25      30
Arg Tyr Val Lys Arg Xaa Leu Pro Ser Ser Trp His Thr Thr Met Thr
      35      40      45
```

Thr Pro Ala Thr Leu Ala Thr Arg Val Arg Leu Asp Pro Phe
50 55 60

(2) INFORMATION FOR SEQ ID NO:3511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1577135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3511:

Met Gln Lys Ser Val Val Val Ala Leu Asp Arg Leu Phe His Asn Gln
1 5 10 15
Arg Tyr Thr Asn Arg Tyr Val Lys Arg Xaa Leu Pro Ser Ser Trp His
20 25 30
Thr Thr Met Thr Thr Pro Ala Thr Leu Ala Thr Arg Val Arg Leu Asp
35 40 45
Pro Phe
50

(2) INFORMATION FOR SEQ ID NO:3512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1577136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3512:

Met Ile His Leu Lys Leu Leu Arg Thr Arg Cys Ser His Gly Leu Phe
1 5 10 15
Phe Phe Arg Cys Met Phe Val Ser Leu Trp Asn Val Val Ala Met Phe
20 25 30
Ser Met Gly Glu Lys Ile Ala Ser Ser Gln His Leu Cys Leu Ile Thr
35 40 45
Val Val Leu Leu Trp Cys Pro Ser Phe Asn Gly Thr Ser His
50 55 60

(2) INFORMATION FOR SEQ ID NO:3513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 698 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..698

(D) OTHER INFORMATION: / Ceres Seq. ID 1577137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3513:

tgcataatg tccggcgggt aattcatttt gctagctttct cctaacgata cgccgggtggt	60
tcttaattca atgcgtttat acgtgtagct ggagaagctg gccgagatgc tgcacgagcc	120
gccgcagggc aagtactacg gcggcaatgc ggacgacgtg cgctcgggcg gcgtcggcgg	180
cacgaaggag gaggaggagt Cccacagacg cctgcgcgcg ggccgcgctc tactcgtccg	240
agtgcgctgg cggtggcagg ttcacgcgc acttccttggc ggacgacgac gtgggagcag	300
ccctcttccg gccgccgtcg tctccgcagc cgaccgctgg ctactcacg tcgtcggggc	360
cgccggagca ccagccgttc cagttccact ccggctactg ctggccgtcg tcgtcggcgg	420

aGcagacctg cagcggctcg caatggtggg agttcgagtc cctcagcgag tgacgtacga 480
tgatcacaag cggccggggg tcaactcggtt ccaagcacac gtaagggccg ggccaatacg 540
agttcgttcg tagcgggtctc gtcactcgtc agctagccct gcagagcaac ggtgtatgca 600
tagcttcagt agatcgaagt ccaggtccag gactgcccatt caagcagttt cttcttctcg 660
ccatcgatca tcatcatgc atgcaaaaga tttttttt

(2) INFORMATION FOR SEQ ID NO:3514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1577138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3514:

Met Leu His Glu Pro Pro Gln Gly Lys Tyr Tyr Gly Gly Asn Ala Asp
1 5 10 15
Asp Val Arg Ser Gly Gly Val Gly Gly Thr Lys Glu Glu Glu Glu Ser
20 25 30
His Arg Arg Leu Arg Arg Gly Arg Ala Leu Leu Val Arg Val Arg Trp
35 40 45
Arg Trp Gln Val His Arg Ala Leu Leu Gly Gly Arg Arg Arg Gly Ser
50 55 60
Ser Pro Leu Pro Ala Ala Val Val Ser Ala Ala Asp Arg Trp Leu Thr
65 70 75 80
His Val Val Gly Ala Ala Gly Ala Pro Ala Val Pro Val Pro Leu Arg
85 90 95
Leu Leu Leu Ala Val Val Val Gly Gly Ala Asp Leu Gln Arg Leu Ala
100 105 110
Met Val Gly Val Arg Val Pro Gln Arg Val Thr Tyr Asp Asp His Lys
115 120 125
Arg Pro Gly Val Thr Arg Phe Gln Ala His Val Arg Ala Gly Pro Ile
130 135 140
Arg Val Arg Ser
145

(2) INFORMATION FOR SEQ ID NO:3515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1577139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3515:

Met Arg Thr Thr Cys Ala Arg Ala Ala Ser Ala Ala Arg Arg Arg Arg
1 5 10 15
Arg Ser Pro Thr Asp Ala Cys Ala Gly Ala Ala Leu Tyr Ser Ser Glu
20 25 30
Cys Ala Gly Gly Gly Arg Phe Ile Ala His Phe Leu Ala Asp Asp Asp
35 40 45
Val Gly Ala Ala Leu Phe Arg Pro Pro Ser Ser Pro Gln Pro Thr Ala
50 55 60
Gly Leu Leu Thr Ser Ser Gly Pro Pro Glu His Gln Pro Phe Gln Phe
65 70 75 80
His Ser Gly Tyr Cys Trp Pro Ser Ser Ser Ala Glu Gln Thr Cys Ser
85 90 95

Gly Ser Gln Trp Trp Glu Phe Glu Ser Leu Ser Glu
100 105

(2) INFORMATION FOR SEQ ID NO:3516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..570
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3516:

aaagaattag tgggagtgca aactgaagtt gtgtatgaga aatgcccac cgaagctatg	60
attgaaactg gggggttttc ctatgcggtg gtggttggtg gagaggttcc atatgccgaa	120
ttgacaggag atagaactga ccttagtatt cgttttaatg gctctgacct tatcatccgt	180
gttgcaagta aaatccctac cctagtgtatt gttatatctg gaaggccatt aattattgag	240
tcacaagttt tggaaaagat agaagctcta gtcgctgcct ggctgcctgg aagtgagggc	300
atgggaatta ccgattgcct ctttgagat catgattttg tgggcacatt gcctgtgaca	360
tgggtgaagt ctgttgatca attgcctata gatctggag actctaacta tgaccgcgta	420
ttccctgttg gatattgggt aaaaatgttt cgaagcgata atgattcaac ataactttat	480
tattttattg gtacatttga atctttgtga tgttaaatac tctgtattta ttggctattg	540
gGaaactaaa atgaaataat atattgttgt	

(2) INFORMATION FOR SEQ ID NO:3517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3517:

Lys	Glu	Leu	Val	Gly	Val	Gln	Thr	Glu	Val	Tyr	Glu	Lys	Cys	Pro
1			5					10					15	
Thr	Glu	Ala	Met	Ile	Glu	Thr	Gly	Gly	Phe	Ser	Tyr	Ala	Val	Val
		20					25					30		
Val	Gly	Glu	Val	Pro	Tyr	Ala	Glu	Leu	Thr	Gly	Asp	Arg	Thr	Asp
		35					40				45			
Ser	Ile	Pro	Phe	Asn	Gly	Ser	Asp	Leu	Ile	Ile	Arg	Val	Ala	Ser
	50				55					60				Lys
Ile	Pro	Thr	Leu	Val	Ile	Val	Ile	Ser	Gly	Arg	Pro	Leu	Ile	Ile
65				70					75					80
Ser	Gln	Val	Leu	Glu	Lys	Ile	Glu	Ala	Leu	Val	Ala	Ala	Trp	Leu
		85					90						95	Pro
Gly	Ser	Glu	Gly	Met	Gly	Ile	Thr	Asp	Cys	Leu	Phe	Gly	Asp	His
		100					105					110		Asp
Phe	Val	Gly	Thr	Leu	Pro	Val	Thr	Trp	Cys	Lys	Ser	Val	Asp	Gln
		115				120						125		Leu
Pro	Ile	Asp	Ala	Gly	Asp	Ser	Asn	Tyr	Asp	Pro	Leu	Phe	Pro	Val
	130				135					140				Gly
Tyr	Gly	Leu	Lys	Met	Phe	Arg	Ser	Asp	Asn	Asp	Ser	Thr		
145				150						155				

(2) INFORMATION FOR SEQ ID NO:3518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..138
(D) OTHER INFORMATION: / Ceres Seq. ID 1577148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3518:

Met Ile Glu Thr Gly Gly Phe Ser Tyr Ala Val Val Val Val Gly Glu
1 5 10 15
Val Pro Tyr Ala Glu Leu Thr Gly Asp Arg Thr Asp Leu Ser Ile Pro
 20 25 30
Phe Asn Gly Ser Asp Leu Ile Ile Arg Val Ala Ser Lys Ile Pro Thr
 35 40 45
Leu Val Ile Val Ile Ser Gly Arg Pro Leu Ile Ile Glu Ser Gln Val
 50 55 60
Leu Glu Lys Ile Glu Ala Leu Val Ala Ala Trp Leu Pro Gly Ser Glu
65 70 75 80
Gly Met Gly Ile Thr Asp Cys Leu Phe Gly Asp His Asp Phe Val Gly
 85 90 95
Thr Leu Pro Val Thr Trp Cys Lys Ser Val Asp Gln Leu Pro Ile Asp
 100 105 110
Ala Gly Asp Ser Asn Tyr Asp Pro Leu Phe Pro Val Gly Tyr Gly Leu
 115 120 125
Lys Met Phe Arg Ser Asp Asn Asp Ser Thr
 130 135

(2) INFORMATION FOR SEQ ID NO:3519:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1047 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..1047
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3519:

agccacaccc ggacacccca cacaggcacg aggcaaccag ccacgcgagc ggcgaaactg 60
cgggagccaa tcagaacctc cagcgatgca atgatcgccg tcgcatcgtc cttcccctcg 120
cgcgccacag cggctccgtt cggctcgggg acaactgccac cgccgtctac gcggcgcasa 180
cgtccctccg ccacccgcgc gtctcggcgc tcggtggagg cctcgaagga gagccgggga 240
agatactgga tccgcgcgcc acgccgttcc agatccctgg cctcgacgcc gccgcgggct 300
actccgcgcg cgaactcaag gccgcttttc gcgccggggt taaggaattc catcctgatg 360
tttgcaagga cccagaaaaat gcagatttaa taatgaggcg agtgatcgag gcctatcaga 420
tggtatctgg caaccaagaa atgatgtttg aaaggaacaa tgttgacca tttgatgaac 480
ctgagtgtga agctcgtgac atatttgtca atgaacttct atgcattggc actggatgtc 540
catattcttg tgttaaaagg gcaCctcatg tattttcatt ttcagatgat actggtacag 600
ctcgtgcaat atctcaaggt aatggagaag atgatcttgt tcagctcgct gttgggcagt 660
gtccaagaaa gtgcatatac tatgtgacgc cttgccaaac cactattttg gaggatgttc 720
ttgctagtgt gttgatggtg ccttacgata ttgctgaagc agcagttctg gattccctcc 780
tttcaaaagc gaagtctgag aataacagggt ataagaagcc ccaaagagga gcaaaatcat 840
cctccgatta tgttgattgg atgtgatctg atcccagagc acaaagagga tgccagattc 900
agccgaaggc agttcggtag atttatgctg gtttgccctat tctccttggt cagttgcccc 960
atagtttata aaatggaata cgtttacgtg gacagactgc tttgtttgtg gtatacgggt 1020
atgatttcta taatatttct ttctgcc

(2) INFORMATION FOR SEQ ID NO:3520:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 287 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..287

(D) OTHER INFORMATION: / Ceres Seq. ID 1577164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3520:

Pro	His	Pro	Asp	Thr	Pro	His	Arg	His	Glu	Ala	Thr	Ser	His	Ala	Ser	
1				5					10					15		
Gly	Glu	Thr	Ala	Gly	Ala	Asn	Gln	Asn	Leu	Gln	Arg	Cys	Asn	Asp	Arg	
			20					25					30			
Arg	Arg	Ile	Val	Leu	Pro	Leu	Ala	Arg	Pro	Arg	Gly	Ser	Val	Arg	Leu	
			35				40					45				
Gly	Asp	Thr	Ala	Thr	Ala	Val	Tyr	Ala	Ala	Xaa	Thr	Ser	Leu	Arg	His	
	50					55					60					
Pro	Arg	Val	Ser	Ala	Leu	Gly	Gly	Gly	Leu	Glu	Gly	Glu	Pro	Gly	Lys	
65					70					75					80	
Ile	Leu	Asp	Pro	Arg	Ala	Thr	Pro	Phe	Gln	Ile	Leu	Gly	Leu	Asp	Ala	
				85					90					95		
Ala	Ala	Gly	Tyr	Ser	Ala	Ala	Glu	Leu	Lys	Ala	Ala	Phe	Arg	Ala	Arg	
			100					105					110			
Val	Lys	Glu	Phe	His	Pro	Asp	Val	Cys	Lys	Asp	Pro	Glu	Asn	Ala	Asp	
		115					120					125				
Leu	Ile	Met	Arg	Arg	Val	Ile	Glu	Ala	Tyr	Gln	Met	Leu	Ser	Gly	Asn	
	130					135					140					
Gln	Glu	Met	Met	Phe	Glu	Arg	Asn	Asn	Val	Asp	Pro	Phe	Asp	Glu	Pro	
145					150					155					160	
Glu	Cys	Glu	Ala	Arg	Asp	Ile	Phe	Val	Asn	Glu	Leu	Leu	Cys	Ile	Gly	
				165					170					175		
Thr	Gly	Cys	Pro	Tyr	Ser	Cys	Val	Lys	Arg	Ala	Pro	His	Val	Phe	Ser	
			180					185					190			
Phe	Ser	Asp	Asp	Thr	Gly	Thr	Ala	Arg	Ala	Ile	Ser	Gln	Gly	Asn	Gly	
		195					200					205				
Glu	Asp	Asp	Leu	Val	Gln	Leu	Ala	Val	Gly	Gln	Cys	Pro	Arg	Lys	Cys	
	210					215					220					
Ile	Tyr	Tyr	Val	Thr	Pro	Cys	Gln	His	Thr	Ile	Leu	Glu	Asp	Val	Leu	
225					230					235					240	
Ala	Ser	Val	Leu	Met	Val	Pro	Tyr	Asp	Leu	Ala	Glu	Ala	Ala	Val	Leu	
				245					250					255		
Asp	Ser	Leu	Leu	Ser	Lys	Ala	Lys	Phe	Glu	Asn	Asn	Arg	Tyr	Lys	Lys	
		260						265					270			
Pro	Gln	Arg	Gly	Ala	Lys	Ser	Ser	Ser	Asp	Tyr	Val	Asp	Trp	Met		
	275						280						285			

(2) INFORMATION FOR SEQ ID NO:3521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1577165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3521:

Met	Arg	Arg	Val	Ile	Glu	Ala	Tyr	Gln	Met	Leu	Ser	Gly	Asn	Gln	Glu	
1				5				10						15		
Met	Met	Phe	Glu	Arg	Asn	Asn	Val	Asp	Pro	Phe	Asp	Glu	Pro	Glu	Cys	
			20					25					30			
Glu	Ala	Arg	Asp	Ile	Phe	Val	Asn	Glu	Leu	Leu	Cys	Ile	Gly	Thr	Gly	
		35					40					45				
Cys	Pro	Tyr	Ser	Cys	Val	Lys	Arg	Ala	Pro	His	Val	Phe	Ser	Phe	Ser	

50 55 60
Asp Asp Thr Gly Thr Ala Arg Ala Ile Ser Gln Gly Asn Gly Glu Asp
65 70 75 80
Asp Leu Val Gln Leu Ala Val Gly Gln Cys Pro Arg Lys Cys Ile Tyr
85 90 95
Tyr Val Thr Pro Cys Gln His Thr Ile Leu Glu Asp Val Leu Ala Ser
100 105 110
Val Leu Met Val Pro Tyr Asp Leu Ala Glu Ala Ala Val Leu Asp Ser
115 120 125
Leu Leu Ser Lys Ala Lys Phe Glu Asn Asn Arg Tyr Lys Lys Pro Gln
130 135 140
Arg Gly Ala Lys Ser Ser Asp Tyr Val Asp Trp Met
145 150 155

(2) INFORMATION FOR SEQ ID NO:3522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3522:

Met Leu Ser Gly Asn Gln Glu Met Met Phe Glu Arg Asn Asn Val Asp
1 5 10 15
Pro Phe Asp Glu Pro Glu Cys Glu Ala Arg Asp Ile Phe Val Asn Glu
20 25 30
Leu Leu Cys Ile Gly Thr Gly Cys Pro Tyr Ser Cys Val Lys Arg Ala
35 40 45
Pro His Val Phe Ser Phe Ser Asp Asp Thr Gly Thr Ala Arg Ala Ile
50 55 60
Ser Gln Gly Asn Gly Glu Asp Asp Leu Val Gln Leu Ala Val Gly Gln
65 70 75 80
Cys Pro Arg Lys Cys Ile Tyr Tyr Val Thr Pro Cys Gln His Thr Ile
85 90 95
Leu Glu Asp Val Leu Ala Ser Val Leu Met Val Pro Tyr Asp Leu Ala
100 105 110
Glu Ala Ala Val Leu Asp Ser Leu Leu Ser Lys Ala Lys Phe Glu Asn
115 120 125
Asn Arg Tyr Lys Lys Pro Gln Arg Gly Ala Lys Ser Ser Ser Asp Tyr
130 135 140
Val Asp Trp Met
145

(2) INFORMATION FOR SEQ ID NO:3523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..832
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3523:

attttcgtca cccctgacgc tcgacgcctc tctctctctc cdccccacc cgtccatcgc 60
ccctccctcc ggtctgcgct cccacagcct caccctgcg cccccgccga ttgcgctcgc 120
cctttgttg aaggaacgat ggagcagacc ttcacatga tcaagcccga cggcgtccag 180
cggggcctga tcggggacat catcagtcgc ttcgagaaga aagggttcta cctcaagggg 240

atgaagttca tgaacgtgga gaggtccttc ggcagCCag cactacgctg acctttccga 300
caagcctttc ttYCCCCgg gttggtggag tacatcattt cgggccccgt ggtggcgatg 360
gtgtgggagg ggaaggacgt cgtgttgact ggccgcaGga tcattggggc caccaggcct 420
tgggaggcag cccccgtac cattcgtggg gactacgccg tggaagtcgg caggaatgtc 480
atccatggaa gcgactccgt ggagaacggg aagaaggaga tcgctctctg gttccctgaa 540
ggtgtggcac agtgggaagag caaccttcat ccctggatct acgaggcttg agcagttgag 600
cttgatgcc ttgcctgctc catggaaacc agagttttgt ttgagtatta tctgttggt 660
ctggctgaag agtcataatt tagcgtctctg tgtgttacac cagagttaag tctgcctgaa 720
cttatgtggc atttgtttga gtttctgcct tcgtgccttg ttttctaatt taccgtggt 780
gtgaaccggt caatgtgatc tgaaataaaa cattgcgtgc caagtttgtg tc

(2) INFORMATION FOR SEQ ID NO:3524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1577168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3524:

Ile Phe Val Thr Pro Asp Ala Arg Arg Leu Ser Ser Ser Xaa Pro Pro
1 5 10 15
Pro Val His Arg Pro Ser Leu Arg Ser Ala Leu Pro Gln Pro His Pro
20 25 30
Cys Ala Pro Ala Asp Ser Arg Arg Pro Leu Leu Glu Gly Thr Met Glu
35 40 45
Gln Thr Phe Ile Met Ile Lys Pro Asp Gly Val Gln Arg Gly Leu Ile
50 55 60
Gly Asp Ile Ile Ser Arg Phe Glu Lys Lys Gly Phe Tyr Leu Lys Gly
65 70 75 80
Met Lys Phe Met Asn Val Glu Arg Ser Phe Ala Gln Pro Ala Leu Arg
85 90 95

(2) INFORMATION FOR SEQ ID NO:3525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1577169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3525:

Met Val Trp Glu Gly Lys Asp Val Val Leu Thr Gly Arg Arg Ile Ile
1 5 10 15
Gly Ala Thr Arg Pro Trp Glu Ala Ala Pro Gly Thr Ile Arg Gly Asp
20 25 30
Tyr Ala Val Glu Val Gly Arg Asn Val Ile His Gly Ser Asp Ser Val
35 40 45
Glu Asn Gly Lys Lys Glu Ile Ala Leu Trp Phe Pro Glu Gly Val Ala
50 55 60
Gln Trp Lys Ser Asn Leu His Pro Trp Ile Tyr Glu Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:3526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..77
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1577170
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3526:

```
Met Ser Ser Met Glu Ala Thr Pro Trp Arg Thr Gly Arg Arg Arg Ser
1          5          10          15
Leu Ser Gly Ser Leu Lys Val Trp His Ser Gly Arg Ala Thr Phe Ile
20          25          30
Pro Gly Ser Thr Arg Leu Glu Gln Leu Ser Leu Asp Ala Leu Pro Ala
35          40          45
Pro Trp Lys Pro Glu Phe Cys Leu Ser Ile Ile Cys Trp Leu Trp Leu
50          55          60
Lys Ser His Asn Leu Ala Leu Cys Val Leu His Gln Ser
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:3527:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 866 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..866
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1577175
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3527:

```
gttctctcct cctggctcct ggggtctcat tcttcccttc gcttcgcaag gccacaag 60
aactccacca cgcacggccg caccgcacc cgcacccgct ctctgctgcc atggcgctgt 120
ccttcgtcgc gctcaccgtt atgttcgggt tcaccgcagc cctgtgctgc ctccagctcc 180
tcggcgcgga caccacggcc acgaccacga cccagagcgg tctcgcgcg cctggccgcg 240
cctccctggt cccggcggtc ctggscgccc tgacgctgac cccgctgcty gcgttcgcgc 300
gcgtgcacgC ccgtGccggg gcggaggggg cgctcgtgtc gggccttgcc aaggcgacc 360
tcctcgggg gacgggtggc ctcgtcgcgg cgccggtggg gcagctcggc gccgacggc 420
acctcgaccg cggncgcagc acgtcgcgcg cctgaacgtg aagtgaagca agaagcaatc 480
ccccctcct tcttctcctg actataaaaa taacctgcgc caagcgctcg cgtgtcgtcg 540
ctggaggcgt ctggacgacc ggaccactgc taggtcctc gctctgctcg atccgttcgg 600
agctcagcgc gtctgggctt tctgatggcg gcggcgctct aaggagaagg gggtgattaa 660
tgtttgcggt gcccccggtg ccgtgcgggt aaaaaggagg atacttttat tttgttttcc 720
tccgtatatg ttggcctagt sttgcgttc tggatttgtg gtaagctcac tgtctatgta 780
atcccactgg gactgggatt tcagtttgc ctttcacctc ctggacggtc ttgtaaatat 840
atatatatat atactgtgtt tcagtt
```

(2) INFORMATION FOR SEQ ID NO:3528:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 154 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..154
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1577176
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3528:

```
Phe Ser Pro Pro Gly Ser Trp Val Ser Ser Pro Pro Phe Ala Ser Gln
1          5          10          15
Gly Gln Gln Gly Thr Pro Pro Arg Thr Ala Ala Pro Ala Pro Ala Pro
```

20 25 30
Ala Leu Cys Cys His Gly Val Val Leu Arg Arg Ala His Arg Tyr Val
35 40 45
Arg Leu His Arg Ser Pro Val Leu Pro Pro Ala Pro Arg Arg Gly His
50 55 60
His Gly His Asp His Asp Pro Glu Arg Ser Arg Ala Pro Gly Arg Gly
65 70 75 80
Leu Pro Gly Pro Gly Gly Pro Xaa Arg Pro Asp Ala Asp Pro Ala Ala
85 90 95
Xaa Val Arg Ala Arg Ala Arg Pro Cys Arg Gly Gly Gly Gly Ala Arg
100 105 110
Val Gly Pro Cys Gln Gly Asp Pro Pro Arg Gly Asp Gly Gly Ser Arg
115 120 125
Arg Gly Gly Arg Gly Ala Ala Arg Arg Arg Arg Ala Pro Arg Pro Arg
130 135 140
Xaa Asp Asp Val Ala Arg Leu Asn Val Lys
145 150

(2) INFORMATION FOR SEQ ID NO:3529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1577177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3529:

Ser Leu Leu Leu Ala Pro Gly Ser His Leu Leu Pro Ser Leu Arg Lys
1 5 10 15
Ala Asn Lys Glu Leu His His Ala Arg Pro His Pro His Pro His Pro
20 25 30
Leu Ser Ala Ala Met Ala Ser Ser Phe Val Ala Leu Thr Val Met Phe
35 40 45
Gly Phe Thr Ala Ala Leu Cys Cys Leu Gln Leu Leu Gly Ala Asp Thr
50 55 60
Thr Ala Thr Thr Thr Thr Gln Ser Gly Leu Ala Arg Leu Ala Ala Ala
65 70 75 80
Ser Leu Val Pro Ala Val Leu Xaa Ala Leu Thr Leu Thr Pro Leu Xaa
85 90 95
Ala Phe Ala Arg Val His Ala Arg Ala Gly Ala Glu Gly Ala Leu Val
100 105 110
Ser Gly Leu Ala Lys Ala Thr Leu Ala Gly Thr Val Ala Leu Val
115 120 125
Ala Ala Ala Val Val Gln Leu Gly Ala Asp Gly His Leu Asp Arg Xaa
130 135 140
Pro Thr Thr Ser Arg Ala
145 150

(2) INFORMATION FOR SEQ ID NO:3530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1577178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3530:

11/11/2011 11:11:11

Met Ala Ser Ser Phe Val Ala Leu Thr Val Met Phe Gly Phe Thr Ala
1 5 10 15
Ala Leu Cys Cys Leu Gln Leu Leu Gly Ala Asp Thr Thr Ala Thr Thr
20 25 30
Thr Thr Gln Ser Gly Leu Ala Arg Leu Ala Ala Ala Ser Leu Val Pro
35 40 45
Ala Val Leu Xaa Ala Leu Thr Leu Thr Pro Leu Xaa Ala Phe Ala Arg
50 55 60
Val His Ala Arg Ala Gly Ala Glu Gly Ala Leu Val Ser Gly Leu Ala
65 70 75 80
Lys Ala Thr Leu Leu Ala Gly Thr Val Ala Leu Val Ala Ala Ala Val
85 90 95
Val Gln Leu Gly Ala Asp Gly His Leu Asp Arg Xaa Pro Thr Thr Ser
100 105 110
Arg Ala

(2) INFORMATION FOR SEQ ID NO:3531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..782
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3531:

gccttcaacc atcgtttagag tttccttggt agtttttttc cctcttggtca cagcaccoccc 60
caccacacac cacccaaggc cccaactgca gtgcccatcc ggcagacagg tcgatggcgg 120
cggaagcagc ggcagcghng gaaggagaag atgcggacgc tagtcagcag cgacttcaag 180
aagttcgatg tggaggagtc tgtggcgagg gaatcgctga ttatcctgaa cctgatggcg 240
gactgogacg acagtgacat cccgggtcttc aacgtcaacg ccaatatcct cgacaaggtc 300
atcgcgctact gcaggaagca cgccctyggcg ccgcgcscga NTtggcggtg atgcggaGcc 360
aagtgtctgcg agtaacaagg cctcagcggga cgatctcaag tcctttgatg ctgagttcgt 420
cgatgttgac ctgggtcacc tcttggaagt cattaaggct gcagactacc tggagatcaa 480
tgggctgctg gacctgacct gccaggccgt cgcggacatg atcaagggga agactccaga 540
ggagatacgc gagacattcg acatcgagaa tgacttcaca cctgaggaag aggctaaagt 600
gaggagggag aatcagtggt cctttgaatg aagaagctgc aggctagctc taacaaaaca 660
atagcaatat catataacca ggccagagat gaagtgtctg ttcaggatgt tatgagtcga 720
aggtttggtt ggtcgtgagc agactatatt gctgttccag tattttggct ggtttggttc 780
cc

(2) INFORMATION FOR SEQ ID NO:3532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3532:

Pro Ser Thr Ile Val Arg Val Ser Leu Val Val Phe Phe Pro Leu Val
1 5 10 15
Thr Ala Pro Pro Thr His Thr His Pro Arg Pro Gln Leu Gln Cys Pro
20 25 30
Ser Gly Arg Gln Val Asp Gly Gly Gly Ser Ser Gly Ser Xaa Gly Arg
35 40 45
Arg Arg Cys Gly Arg

50

(2) INFORMATION FOR SEQ ID NO:3533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3533:

Met Arg Thr Leu Val Ser Ser Asp Phe Lys Lys Phe Asp Val Glu Glu
1 5 10 15
Ser Val Ala Arg Glu Ser Leu Ile Ile Leu Asn Leu Met Ala Asp Cys
 20 25 30
Asp Asp Ser Asp Ile Pro Val Phe Asn Val Asn Ala Asn Ile Leu Asp
 35 40 45
Lys Val Ile Ala Tyr Cys Arg Lys His Ala Xaa Ala Pro Arg Xaa Xaa
 50 55 60
Trp Arg
65

(2) INFORMATION FOR SEQ ID NO:3534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3534:

Met Arg Ser Gln Val Leu Arg Val Thr Arg Pro Gln Arg Thr Ile Ser
1 5 10 15
Ser Pro Leu Met Leu Ser Ser Ser Met Leu Thr Trp Ser Pro Ser Trp
 20 25 30
Ser Ser Leu Arg Leu Gln Thr Thr Trp Arg Ser Met Gly Cys Trp Thr
 35 40 45

(2) INFORMATION FOR SEQ ID NO:3535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 870 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..870
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3535:

caatgtcgcg tgcggccact agatttttcc tgacgcggtg tctgctccca cttcccctcc 60
tctccccccag gtggcggcag cggcggcgagg gtagcatttg tgctacgagg gcttttgcaa 120
tggcggcttc ggggttcrge ggcggcgagg cgccaaaacc ctaccgccgc cgcgaatccc 180
gcacgacccc aaccatgacc gtgctgagcc gccctacccc gggcacggcc cagtgtctcg 240
ggcggaagaa gaccgccgct gcggtcgcgt acacgaagcc ggggcgcggc ctgatcaagg 300
tgaacggcgt cccgattgar ctgatccgac cggagatgct ccgcctcaag gccttcgagc 360

```
ccatcctgct ggcgggggcg gtcccggttc aaggacatcg acatgcggat ccgcgtccrc 420
ggcgggcgga agacgtcgca gatctacgcc atccgccAag vccgtcgscA aggggctcgt 480
cgctactac cagaagtacg tcgacgaggc cgcyagaag gagatcaagg acatctttac 540
ccgctacgat cgcacctcc tcgtcgctga cccccggcgc tgcgagccga agaagtccg 600
cggacgtggt gcccgcgcca gggtccagaa gtcgtaccgt tgagcggctg cctgctccat 660
ctcgattttt cagatcggtt tgggtgtttt tcgctttatt tcctatcaat ggatctgctt 720
atctggtttt atatctagct gctgctttac cataatgttt agactttaat gcctagcctg 780
aaaccttggt tgcaatgtga aattaatgtg agagattatg aagactatgt tggctagctc 840
ctctattatg attttcatca ttccmgtatt
```

(2) INFORMATION FOR SEQ ID NO:3536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..250

(D) OTHER INFORMATION: / Ceres Seq. ID 1577207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3536:

```
Met Ser Arg Ala Ala Thr Arg Phe Phe Leu Thr Arg Cys Leu Leu Pro
1          5          10          15
Leu Pro Leu Leu Ser Pro Arg Trp Arg Gln Arg Arg Arg Gly Ser Ile
20          25          30
Cys Ala Thr Arg Ala Phe Ala Met Ala Ala Ser Gly Phe Xaa Gly Gly
35          40          45
Glu Ala Pro Lys Pro Tyr Arg Arg Arg Glu Ser Arg Thr Thr Pro Thr
50          55          60
Met Thr Val Leu Ser Arg Pro Thr Pro Gly Thr Ala Gln Cys Phe Gly
65          70          75          80
Arg Lys Lys Thr Ala Val Ala Val Ala Tyr Thr Lys Pro Gly Arg Gly
85          90          95
Leu Ile Lys Val Asn Gly Val Pro Ile Xaa Leu Ile Arg Pro Glu Met
100          105          110
Leu Arg Leu Lys Ala Phe Glu Pro Ile Leu Leu Ala Gly Ala Val Pro
115          120          125
Val Gln Gly His Arg His Ala Asp Pro Arg Xaa Arg Arg Arg Glu Asp
130          135          140
Val Ala Asp Leu Arg His Pro Pro Xaa Pro Ser Xaa Arg Gly Ser Ser
145          150          155          160
Pro Thr Thr Arg Ser Thr Ser Thr Arg Pro Xaa Arg Arg Arg Ser Arg
165          170          175
Thr Ser Leu Pro Ala Thr Ile Ala Pro Ser Ser Ser Leu Thr Pro Gly
180          185          190
Ala Ala Ser Arg Arg Ser Ser Ala Asp Val Val Pro Ala Pro Gly Ser
195          200          205
Arg Ser Arg Thr Val Glu Arg Leu Pro Ala Pro Ser Arg Phe Phe Arg
210          215          220
Ser Leu Trp Val Phe Phe Ala Leu Phe Pro Ile Asn Gly Ser Ala Tyr
225          230          235          240
Leu Val Leu Tyr Leu Ala Ala Ala Leu Pro
245          250
```

(2) INFORMATION FOR SEQ ID NO:3537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..211

(D) OTHER INFORMATION: / Ceres Seq. ID 1577209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3537:

Met Ala Ala Ser Gly Phe Xaa Gly Gly Glu Ala Pro Lys Pro Tyr Arg
1 5 10 15
Arg Arg Glu Ser Arg Thr Thr Pro Thr Met Thr Val Leu Ser Arg Pro
20 25 30
Thr Pro Gly Thr Ala Gln Cys Phe Gly Arg Lys Lys Thr Ala Val Ala
35 40 45
Val Ala Tyr Thr Lys Pro Gly Arg Gly Leu Ile Lys Val Asn Gly Val
50 55 60
Pro Ile Xaa Leu Ile Arg Pro Glu Met Leu Arg Leu Lys Ala Phe Glu
65 70 75 80
Pro Ile Leu Leu Ala Gly Ala Val Pro Val Gln Gly His Arg His Ala
85 90 95
Asp Pro Arg Xaa Arg Arg Arg Glu Asp Val Ala Asp Leu Arg His Pro
100 105 110
Pro Xaa Pro Ser Xaa Arg Gly Ser Pro Thr Thr Arg Ser Thr Ser
115 120 125
Thr Arg Pro Xaa Arg Arg Arg Ser Arg Thr Ser Leu Pro Ala Thr Ile
130 135 140
Ala Pro Ser Ser Ser Leu Thr Pro Gly Ala Ala Ser Arg Arg Ser Ser
145 150 155 160
Ala Asp Val Val Pro Ala Pro Gly Ser Arg Ser Arg Thr Val Glu Arg
165 170 175
Leu Pro Ala Pro Ser Arg Phe Phe Arg Ser Leu Trp Val Phe Phe Ala
180 185 190
Leu Phe Pro Ile Asn Gly Ser Ala Tyr Leu Val Leu Tyr Leu Ala Ala
195 200 205
Ala Leu Pro
210

(2) INFORMATION FOR SEQ ID NO:3538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 790 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..790

(D) OTHER INFORMATION: / Ceres Seq. ID 1577252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3538:

atgctctacc ggagtagcgc aactccgcaa gcaaatacctc ctatctccaa gcctccaatc 60
tgtgaacggg gaaccccaat cgaatgacgc cgacggsagc ctctctctcc cggctcccc 120
attcgtctct atctccgatg tgcgcgcgct ccagctcccc ccgcgcggcg gccaccggcc 180
tcgcccctgc tggaaagggct tggagtgcgg ctccgtacag acgcggatgg tctcttcttt 240
cgttgggagc agaacacgcc gcagaaacgt tatatgtgct tccctgttcg gagttggagc 300
tcccgaagca ctggtcattg gagtagtcgc cttgttggtg ttccggccca agggcttagc 360
agaggtagcc aggaatttg ggaagacttt gcgtgctttc caaccaacca ttagagagat 420
acaggatgta tcaaggagg tcaaggagcac tcttgaacga gaaatcgga ttgatgaggt 480
ttcccagtcg acgaattata caccacgcac catgaataac aaccaacaac ctgctgccga 540
ctcaaatatc aagcctgcac ctgcacctta caccagcgat gaacttgatga aagtAactga 600
agaacaaatt gctgcatcag ctgctgcaga gagTtatcgt cagttggtgc ggtgtgtccg 660
cttaaaacttt atttgtggtt gggttggtact tttgtggtg ttattttttt ggacctcgtg 720
atagtcgggc gggtcaatgt tatcgcggt actggcaaac cttaagtgat acggtattct 780
tcttttcggt

(2) INFORMATION FOR SEQ ID NO:3539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..239
(D) OTHER INFORMATION: / Ceres Seq. ID 1577253
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3539:

Cys Ser Thr Gly Val Ala Gln Leu Arg Lys Gln Ile Leu Leu Ser Pro
1 5 10 15
Ser Leu Gln Ser Val Asn Gly Glu Pro Gln Ser Asn Asp Ala Asp Xaa
20 25 30
Ser Leu Leu Leu Pro Ala Pro Pro Phe Val Ser Ile Ser Asp Val Arg
35 40 45
Arg Leu Gln Leu Pro Pro Arg Gly Gly His Arg Pro Arg Pro Cys Trp
50 55 60
Lys Gly Leu Glu Cys Gly Ser Val Gln Thr Arg Met Val Ser Ser Phe
65 70 75 80
Val Gly Ser Arg Thr Arg Arg Arg Asn Val Ile Cys Ala Ser Leu Phe
85 90 95
Gly Val Gly Ala Pro Glu Ala Leu Val Ile Gly Val Val Ala Leu Leu
100 105 110
Val Phe Gly Pro Lys Gly Leu Ala Glu Val Ala Arg Asn Leu Gly Lys
115 120 125
Thr Leu Arg Ala Phe Gln Pro Thr Ile Arg Glu Ile Gln Asp Val Ser
130 135 140
Arg Glu Phe Arg Ser Thr Leu Glu Arg Glu Ile Gly Ile Asp Glu Val
145 150 155 160
Ser Gln Ser Thr Asn Tyr Thr Pro Thr Thr Met Asn Asn Asn Gln Gln
165 170 175
Pro Ala Ala Asp Ser Asn Ile Lys Pro Ala Pro Ala Pro Tyr Thr Ser
180 185 190
Asp Glu Leu Val Lys Val Thr Glu Glu Gln Ile Ala Ala Ser Ala Ala
195 200 205
Ala Glu Ser Tyr Arg Gln Leu Val Arg Cys Val Arg Leu Asn Phe Ile
210 215 220
Cys Gly Trp Leu Val Leu Trp Trp Leu Phe Phe Trp Thr Ser
225 230 235

(2) INFORMATION FOR SEQ ID NO:3540:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..164
(D) OTHER INFORMATION: / Ceres Seq. ID 1577254
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3540:

Met Val Ser Ser Phe Val Gly Ser Arg Thr Arg Arg Arg Asn Val Ile
1 5 10 15
Cys Ala Ser Leu Phe Gly Val Gly Ala Pro Glu Ala Leu Val Ile Gly
20 25 30
Val Val Ala Leu Leu Val Phe Gly Pro Lys Gly Leu Ala Glu Val Ala
35 40 45
Arg Asn Leu Gly Lys Thr Leu Arg Ala Phe Gln Pro Thr Ile Arg Glu
50 55 60
Ile Gln Asp Val Ser Arg Glu Phe Arg Ser Thr Leu Glu Arg Glu Ile
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:3541:

(A) LENGTH: 859 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..859

(D) OTHER INFORMATION: / Ceres Seq. ID 1577263

agtcttgtct	gctagactgt	cgacagattc	cgctccaacg	cgcacctgca	gtcccgcacg	60
ccctcgccca	ccgtgcctt	tcaaaaagct	ggaggattct	cgagarggag	aagcgcgcct	120
ggcagctccg	ttccatccgc	ccccacgaat	gtccgacgar	gccaggcgcg	ggcccgcggg	180
cgccgcgcag	gcgantgctc	cgggcctcct	ccgaggaccg	caagccggtg	ggcgctgggt	240
ccccggcggc	ggttgcgca	aagatccagc	tcaagagcgc	cgatatgaag	gaggagatgc	300
ggcaggacgc	cttcgaaatt	gcccgcacgc	cgttcgataa	gcacagcatg	gagaaggaca	360
tcgtgtagta	cataaagcag	gagttcgaca	agaaccacgg	cccaaCcttg	gcactgcata	420
gtcggcgcca	acttcggttc	atacgtgacg	cacgagacaa	actactttgt	atatttctac	480
atcgactcta	aagctgtctt	gctattcaag	tctgggtgat	tgctcgcagc	cgacgcaatc	540
adccttgcac	gcctacgttc	cattgctccc	atgtatgcac	cgcacccttc	ccccagggcc	600
cagggtcgtc	tcagcccaag	ctggaagccg	gtaatcttaa	tgagcctgca	tgttgatgta	660
tatcagcaac	ggattattct	tcgtatgcc	attagtgtga	gatcagattg	catcttactt	720
atgtctgata	tatctagcta	ggttaggtgt	tgtgagtaca	ttgtcttggt	gcaatatgat	780
tgccggaaca	ctgggtgaac	tgccctctcg	ctgtttgtga	ttatctcaat	agaagcgtcc	840
ttgctcatgc	qtaatactc					

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1577264

Val	Leu	Ser	Ala	Arg	Leu	Ser	Thr	Asp	Ser	Ala	Pro	Thr	Arg	Thr	Cys
1				5					10					15	
Ser	Pro	Ala	Arg	Pro	Arg	Pro	Pro	Ser	Pro	Phe	Lys	Lys	Leu	Glu	Asp
			20					25					30		
Ser	Arg	Xaa	Gly	Glu	Ala	Arg	Leu	Ala	Ala	Pro	Phe	His	Pro	Pro	Pro
		35					40					45			
Arg	Met	Ser	Asp	Xaa	Ala	Arg	Arg	Gly	Pro	Ala	Gly	Ala	Ala	Gln	Ala
	50					55					60				
Xaa	Ala	Pro	Gly	Leu	Leu	Arg	Gly	Pro	Gln	Ala	Gly	Gly	Arg	Trp	Val
65					70					75					80

Pro Gly Gly Gly Cys Ala Gln Asp Pro Ala Gln Glu Arg Arg Tyr Glu
85 90 95
Gly Gly Asp Ala Ala Gly Arg Leu Arg Asn Cys Pro His Arg Val Arg
100 105 110

(2) INFORMATION FOR SEQ ID NO:3543:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1577265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3543:

Ser Cys Leu Leu Asp Cys Arg Gln Ile Pro Leu Gln Arg Ala Pro Ala
1 5 10 15
Val Pro His Ala Leu Ala His Arg Arg Leu Ser Lys Ser Trp Arg Ile
20 25 30
Leu Glu Xaa Glu Lys Arg Ala Trp Gln Leu Arg Ser Ile Arg Pro His
35 40 45
Glu Cys Pro Thr Xaa Pro Gly Ala Gly Pro Arg Ala Pro Arg Arg Arg
50 55 60
Xaa Leu Arg Ala Ser Ser Glu Asp Arg Lys Pro Val Gly Ala Gly Ser
65 70 75 80
Pro Ala Ala Val Ala His Lys Ile Gln Leu Lys Ser Ala Asp Met Lys
85 90 95
Glu Glu Met Arg Gln Asp Ala Phe Glu Ile Ala Arg Ile Ala Phe Asp
100 105 110
Lys His Ser Met Glu Lys Asp Ile Ala Glu Tyr Ile Lys Lys Glu Phe
115 120 125
Asp Lys Asn His Gly Pro Thr Leu Ala Leu His Arg Arg Pro Gln Leu
130 135 140
Arg Phe Ile Arg Asp Ala Arg Asp Lys Leu Leu Cys Ile Phe Leu His
145 150 155 160
Arg Leu

(2) INFORMATION FOR SEQ ID NO:3544:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 521 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..521

(D) OTHER INFORMATION: / Ceres Seq. ID 1577296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3544:

taagattatt gatgttatcg agaagggaga gaaacagccc aacatcacta ttggcatttt 60
ggtctccggt gtcacgtgtg tcgttacogt tctctgcaag ctctgttttg gtggcaagaa 120
accagtggca cctgtgaaac ctgcagctga ggcgaagaag cccaaggccg cggagacgga 180
cggtgctgga agcagtggtg acaaggatga gaaagaggat gaaaaggagg agacaggccc 240
acgtcggagg acccgaaggr agNacataga cctgtttttg acgtgtttta gctcttctgg 300
cgtctgctta ttttgagaac tcttaatat tgtgagtgtg taataggagc ttatgtcacc 360
tctgcggctt ccccgctgc tgatttggtt ttaattggta gaccaggacc cttcacgagc 420
gtagaattta gttcttggtg gtcatttatg tgctgtgcct gacggtgttc aatcagatag 480
aggatgatggt ttttttggtg gatcaaatca aggaatatatt c

(2) INFORMATION FOR SEQ ID NO:3545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3545:

Lys Ile Ile Asp Val Ile Glu Lys Gly Glu Lys Gln Pro Asn Ile Thr
1 5 10 15
Ile Gly Ile Leu Val Ser Val Val Ile Val Phe Val Thr Val Leu Cys
20 25 30
Lys Leu Leu Phe Gly Gly Lys Lys Pro Val Ala Pro Val Lys Pro Ala
35 40 45
Ala Glu Ala Lys Lys Pro Lys Ala Ala Glu Thr Asp Gly Ala Gly Ser
50 55 60
Ser Gly Asp Lys Asp Glu Lys Glu Asp Glu Lys Glu Glu Thr Gly Pro
65 70 75 80
Arg Arg Arg Thr Arg Arg Xaa Xaa Ile Asp Leu Phe Leu Thr Cys Phe
85 90 95
Ser Ser Ser Gly Val Cys Leu Phe
100

(2) INFORMATION FOR SEQ ID NO:3546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..811
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3546:

aggaagaaag gaaccaccca aagcttcaaa aaaagaaaaa gagctgcaca ctggtcactg 60
gaaaacgaag gcaaacccta atcgctactc caccgcagcg cccactacac cgatcgggct 120
ccgatggact tcgcggastg gaggccgtgg agggcctccg gtggccatgg cactcgtggc 180
cgccgactac ccccgccgcc gcgtccctcg tcgtgccac ctccgtcctc tgctcgccgc 240
tgcagcacc caccgcccgc gacctcctcc cgctgctacc ctacgcgccg ctccgctgcg 300
cctccccggg ttgtggcgcc gcgctcaacc cgttctcgcg cgtgcaccac ggCtccgcgc 360
gctggtcctg cgcttctgt Ggcgcgcgcg ccaaccgcgt ccccgcccta ctggcccccg 420
acgcgctccc cgccgaactc ttccccaccc actocagcgt cgagtacttg ctgcccccg 480
accccgctga gcccggggga ccggggccac ctgcgctcgt gttcgtgatc gatgcggcca 540
cggcggccga ggagctcacc gtgctcaagg acgaggtgcg caggctcatg caggggctgc 600
ctgaggggat caggggtggc ctcgtcaact tcgctgcgtc tgtgtgggtg cacgatcttg 660
gatttgaggg ttgcgctcgg gtggttgtgc ttaatggcga gcgtgagctc gagtctgaca 720
aggtttgtga atttgaata taatccttag gacaccgaat ttgtaatttg gttctgcgcc 780
aatctatgtg acatgatcag cattctagtt c

(2) INFORMATION FOR SEQ ID NO:3547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1577303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3547:

Gly Arg Lys Glu Pro Thr Lys Ala Ser Lys Lys Glu Lys Glu Leu His
1 5 10 15
Thr Gly His Trp Lys Thr Lys Ala Asn Pro Asn Arg Tyr Ser Thr Ala
20 25 30
Ala Pro Thr Thr Pro Ile Gly Leu Arg Trp Thr Ser Arg Xaa Gly Gly
35 40 45
Arg Gly Gly Pro Pro Val Ala Met Ala Leu Val Ala Ala Asp Tyr Pro
50 55 60
Arg Arg Arg Val Pro Arg Arg Ala His Leu Arg Pro Leu Leu Ala Ala
65 70 75 80
Ala Ala Pro His Gly Ala Gly Pro Pro Pro Ala Ala Thr Leu Arg Ala
85 90 95
Ala Pro Leu Arg Leu Pro Gly Leu Trp Arg Arg Ala Gln Pro Val Leu
100 105 110
Ala Arg Ala Pro Arg Leu Arg Ala Leu Val Leu Arg Leu Leu Trp Arg
115 120 125
Arg Arg Gln Pro Val Pro Pro Pro Thr Gly Pro Arg Arg Ala Pro Arg
130 135 140
Arg Thr Leu Pro His Pro Leu Gln Arg Arg Val Leu Ala Ala Pro Gly
145 150 155 160
Pro Arg

(2) INFORMATION FOR SEQ ID NO:3548:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..246

(D) OTHER INFORMATION: / Ceres Seq. ID 1577304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3548:

Glu Glu Arg Asn Pro Lys Leu Gln Lys Lys Lys Ser Cys Thr
1 5 10 15
Leu Val Thr Gly Lys Arg Arg Gln Thr Leu Ile Ala Thr Pro Pro Gln
20 25 30
Arg Pro Leu His Arg Ser Gly Ser Asp Gly Leu Arg Gly Xaa Glu Ala
35 40 45
Val Glu Gly Leu Arg Trp Pro Trp His Ser Trp Pro Pro Thr Thr Pro
50 55 60
Ala Ala Ala Ser Leu Val Val Pro Thr Ser Val Leu Cys Ser Pro Leu
65 70 75 80
Gln His Pro Thr Ala Pro Asp Leu Leu Pro Leu Leu Pro Tyr Ala Pro
85 90 95
Leu Arg Cys Ala Ser Pro Gly Cys Gly Ala Ala Leu Asn Pro Phe Ser
100 105 110
Arg Val His His Gly Ser Ala Arg Trp Ser Cys Ala Phe Cys Gly Ala
115 120 125
Ala Ala Asn Pro Phe Pro Arg Leu Leu Ala Pro Asp Ala Leu Pro Ala
130 135 140
Glu Leu Phe Pro Thr His Ser Ser Val Glu Tyr Leu Leu Pro Pro Asp
145 150 155 160
Pro Ala Glu Pro Gly Gly Pro Gly Pro Pro Ala Leu Val Phe Val Ile
165 170 175
Asp Ala Ala Thr Ala Ala Glu Glu Leu Thr Val Leu Lys Asp Glu Val
180 185 190

Arg Arg Leu Met Gln Gly Leu Pro Glu Gly Ile Arg Val Ala Leu Val
195 200 205
Thr Phe Ala Ala Ser Val Trp Val His Asp Leu Gly Phe Glu Gly Cys
210 215 220
Ala Arg Val Val Val Leu Asn Gly Glu Arg Glu Leu Glu Ser Asp Lys
225 230 235 240
Val Cys Glu Phe Val Ile
245

(2) INFORMATION FOR SEQ ID NO:3549:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1577305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3549:

Met Asp Phe Ala Xaa Trp Arg Pro Trp Arg Ala Ser Gly Gly His Gly
1 5 10 15
Thr Arg Gly Arg Arg Leu Pro Pro Pro Pro Arg Pro Ser Ser Cys Pro
20 25 30
Pro Pro Ser Ser Ala Arg Arg Cys Ser Thr Pro Arg Arg Arg Thr Ser
35 40 45
Ser Arg Cys Tyr Pro Thr Arg Arg Ser Ala Ala Pro Pro Arg Val Val
50 55 60
Ala Pro Arg Ser Thr Arg Ser Arg Ala Cys Thr Thr Ala Pro Arg Ala
65 70 75 80
Gly Pro Ala Pro Ser Val Ala Pro Pro Pro Thr Arg Ser Pro Ala Tyr
85 90 95
Trp Pro Pro Thr Arg Ser Pro Pro Asn Ser Ser Pro Pro Thr Pro Ala
100 105 110
Ser Ser Thr Cys Cys Pro Arg Thr Pro Leu Ser Pro Gly Asp Arg Gly
115 120 125
His Leu Arg Ser Cys Ser
130

(2) INFORMATION FOR SEQ ID NO:3550:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 887 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..887

(D) OTHER INFORMATION: / Ceres Seq. ID 1577310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3550:

acctgacggg ctgcgcatcgc acccgccacc cccaccgcac gcaccctctc gtcctctctg 60
cgccgaccgg gctcttctcc cccaacacaa tctctcttcc ccgatccagt ctgcgggtcg 120
cgccacgct gagggacagc gagaagagac agacacagat cgcgcgcgga gatgtcgtcg 180
gactcgtcgt cgtgggcgcg cgccctggtg cagatctcgc cctacacctt ctccgcaatc 240
ggtatcgccg tctccatcgg cgtctccgtc ctgggcgcgg catgggggat cttcatcacg 300
gggagcagcc tcatcggggc cgccatcaag ggcgccagga tcacttctaa gaacctcatc 360
agtgtcatct tctgtgaggc tgtcgcaatt tatggcgtaa ttgtggcaat catcctccag 420
acaaagcttg aaagtgtgcc aacatctcaa atgtatgata cggagtctct tcgagctggc 480
tatgcaatct ttgcatctgg ccttatcggt ggctttgcta atcttgtttg cgggggatgc 540
Ggtggggata attggaagca Gctgcgcact gtctgatgct cagaactcat cactcttcgt 600
aaagattttg gtgattgaga tcttcggcag cgctctggga ctgttcggtg tcattgtggg 660

catcattatg tcatctcaag cgacatggcc agcaaaagct tgattttcac catttgtagc 720
tctgtaaatt attcagatgg agtgtatcga aatgtgcatg tggcttaact gcattttcat 780
gttcctttta tgtggcgtct tttttggcag aacacgaaat gcggcgcsqt accgccaccg 840
attgtagagt tgctattctt actgccggag tactccatgt gtgttgg

(2) INFORMATION FOR SEQ ID NO:3551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3551:

Pro Asp Gly Leu Ala Ser His Pro Pro Pro Pro His Ala Pro Ser
1 5 10 15
Arg Pro Leu Cys Ala Asp Pro Ala Leu Leu Pro Gln His Asn Pro Pro
20 25 30
Ser Pro Ile Gln Ser Arg Gly Arg Gly His Ala Glu Gly Gln Arg Glu
35 40 45
Glu Thr Asp Thr Asp Arg Ala Arg Arg Cys Arg Arg Thr Arg Arg Arg
50 55 60
Gly Arg Ala Pro Trp Cys Arg Ser Arg Pro Thr Pro Ser Pro Gln Ser
65 70 75 80
Val Ser Pro Ser Pro Ser Ala Ser Pro Ser Ser Ala Arg His Gly Val
85 90 95
Ser Ser Ser Arg Gly Ala Ala Ser Ser Gly Pro Pro Ser Arg Arg Pro
100 105 110
Gly Ser Leu Leu Arg Thr Ser Ser Val Ser Ser Ser Val Arg Leu Ser
115 120 125
Gln Phe Met Ala
130

(2) INFORMATION FOR SEQ ID NO:3552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3552:

Leu Thr Gly Ser His Arg Thr Arg His Pro His Arg Thr His Pro Leu
1 5 10 15
Val Leu Ser Ala Pro Thr Arg Leu Phe Ser Pro Asn Thr Ile Leu Leu
20 25 30
Pro Arg Ser Ser Leu Ala Val Ala Ala Thr Leu Arg Asp Ser Glu Lys
35 40 45
Arg Gln Thr Gln Ile Ala Arg Gly Asp Val Val Gly Leu Val Val Val
50 55 60
Gly Ala Arg Pro Gly Ala Asp Leu Ala Leu His Leu Leu Arg Asn Arg
65 70 75 80
Tyr Arg Arg Leu His Arg Arg Leu Arg Pro Arg Arg Gly Met Gly Tyr
85 90 95
Leu His His Gly Glu Gln Pro His Arg Gly Arg His Gln Gly Ala Gln
100 105 110
Asp His Phe

115

(2) INFORMATION FOR SEQ ID NO:3553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1577313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3553:

Met Ser Ser Asp Ser Ser Ser Trp Ala Arg Ala Leu Val Gln Ile Ser
1 5 10 15
Pro Tyr Thr Phe Ser Ala Ile Gly Ile Ala Val Ser Ile Gly Val Ser
20 25 30
Val Leu Gly Ala Ala Trp Gly Ile Phe Ile Thr Gly Ser Ser Leu Ile
35 40 45
Gly Ala Ala Ile Lys Ala Pro Arg Ile Thr Ser Lys Asn Leu Ile Ser
50 55 60
Val Ile Phe Cys Glu Ala Val Ala Ile Tyr Gly Val Ile Val Ala Ile
65 70 75 80
Ile Leu Gln Thr Lys Leu Glu Ser Val Pro Thr Ser Gln Met Tyr Asp
85 90 95
Pro Glu Ser Leu Arg Ala Gly Tyr Ala Ile Phe Ala Ser Gly Leu Ile
100 105 110
Val Gly Phe Ala Asn Leu Val Cys Gly Val Cys Gly Gly Asp Asn Trp
115 120 125
Lys Gln Leu Arg Thr Val
130

(2) INFORMATION FOR SEQ ID NO:3554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..876

(D) OTHER INFORMATION: / Ceres Seq. ID 1577318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3554:

atccgaaacc agagcgaaga atcgccatca cagcaagcta cgcgcactga aatcctccaa 60
tccacaggac acagctctac ttccgcagtt cgcactcgca cgcaccaagc cgctagcaac 120
gaagcagaaa tgtcgtctggt gaggcgcasa gcgtgttcga cccattctcc gtggacctct 180
tcgaccctgt cgacagcatg ttccgctcca tcgtgccgtc gtcgtcgtcg tcgggctccg 240
agaccgccgc cttcgccagc gcccgcatcg actggaagga gacgcccag ggcacagtgt 300
tcaaggccga cctccccggc gtgaagaaag aggaggtcaa ggtggaggtg gaggacggca 360
acgtgctgct catcagcggg cagcgcaGca gggagaagga ggacaagggc gacaagtggc 420
accgcgtgga gcgcagcagc ggccagttcg tgcggcgctt ccgcctgccg gagaacgcca 480
agacggagga ggtgagggcc gcgctggaga acggcggtgct cacggtcacc gtgcccgaag 540
ccgaggtcaa gaagcccag gtgaagagca tccagatctc cggctgaaga agacatggac 600
gggaggtgaa tggntcgcgt cgcgttcgcg tcgcggcgct ggatcttggg ttccagcgac 660
gcgactcgtg tgtgtgtgct gtgtgttgct tctgctttgg tatgtttggt gtgtacgtgt 720
gctgttcagt gtttcctggt cctcgtctgt actttgcgct gttcggtgag cttcctggct 780
cagtatgttg tgttgtgcga gtgaataaat aaawacaaac cagctgtagt atattcacct 840
actactatcg tgtttcaaaa agaagaaaga acgctt

(2) INFORMATION FOR SEQ ID NO:3555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..107
(D) OTHER INFORMATION: / Ceres Seq. ID 1577319
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3555:

Ile Arg Asn Gln Ser Glu Glu Ser Pro Ser Gln Gln Ala Thr Arg Thr
1 5 10 15
Glu Ile Leu Gln Ser Thr Gly His Ser Ser Thr Ser Ala Val Arg Thr
20 25 30
Arg Thr His Gln Ala Ala Ser Asn Glu Ala Glu Met Ser Leu Val Arg
35 40 45
Arg Xaa Ala Cys Ser Thr His Ser Pro Trp Thr Ser Ser Thr Arg Ser
50 55 60
Thr Ala Cys Ser Ala Pro Ser Cys Arg Arg Arg Arg Arg Ala Pro
65 70 75 80
Arg Pro Pro Pro Ser Pro Ala Pro Ala Ser Thr Gly Arg Arg Arg Pro
85 90 95
Arg Arg Thr Cys Ser Arg Pro Thr Ser Pro Ala
100 105

(2) INFORMATION FOR SEQ ID NO:3556:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..64
(D) OTHER INFORMATION: / Ceres Seq. ID 1577320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3556:

Met Ser Leu Val Arg Arg Xaa Ala Cys Ser Thr His Ser Pro Trp Thr
1 5 10 15
Ser Ser Thr Arg Ser Thr Ala Cys Ser Ala Pro Ser Cys Arg Arg Arg
20 25 30
Arg Arg Arg Ala Pro Arg Pro Pro Pro Ser Pro Ala Pro Ala Ser Thr
35 40 45
Gly Arg Arg Arg Pro Arg Arg Thr Cys Ser Arg Pro Thr Ser Pro Ala
50 55 60

(2) INFORMATION FOR SEQ ID NO:3557:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..129
(D) OTHER INFORMATION: / Ceres Seq. ID 1577321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3557:

Met Phe Arg Ser Ile Val Pro Ser Ser Ser Ser Gly Ser Glu Thr
1 5 10 15
Ala Ala Phe Ala Ser Ala Arg Ile Asp Trp Lys Glu Thr Pro Glu Ala
20 25 30

(2) INFORMATION FOR SEQ ID NO:3558:

acggccaatc	aggagtcCaa	aggccCacat	gtatcMagag	cacgtccgtc	gccccctgga	60
ccacgcagcc	Cggcagccca	gagccggaga	gcccagtgaa	acagagccgg	tgaacgcagc	120
ccagtcagtg	acccccccga	tcccgactcc	ggcgatctcc	ccaaccccat	ggcctccgcc	180
ggcgaggccc	ccagcacgct	cctccgcttc	ctctacttcc	tccgcgccgg	agtaatctgc	240
accaaggcca	tcaacaccta	tccgcactac	gagcacaaga	aggagtccac	cgcgcgcctc	300
gccgccgcgc	aatcggCgtG	tggctgctgc	cgcggcgggc	gagcccgcct	ctgcaaccgc	360
cgcgcgcgaag	ccCtgattgt	ggacagagggc	ctgtcttcgg	cggttagggt	tctcggaatg	420
ttgctctcca	taggggagat	agatattttc	ttttgtttct	gatgtttcag	ctacgtgtat	480
gtgctctttt	ggcttgaatc	aatcagtaat	aatactttct	ttcctgtct		

Arg	Pro	Ile	Arg	Ser	Pro	Lys	Ala	His	Met	Tyr	Xaa	Glu	His	Val	Arg
1				5					10					15	
Arg	Pro	Leu	Asp	His	Ala	Ala	Arg	Gln	Pro	Arg	Ala	Gly	Glu	Pro	Ser
			20					25					30		
Glu	Thr	Glu	Pro	Val	Asn	Ala	Ala	Gln	Ser	Val	Thr	Pro	Pro	Ile	Pro
			35				40					45			
Thr	Pro	Ala	Ile	Ser	Pro	Thr	Pro	Trp	Pro	Pro	Pro	Ala	Arg	Pro	Pro
	50					55					60				
Ala	Arg	Ser	Ser	Ala	Ser	Ser	Thr	Ser	Ser	Ala	Pro	Glu			
65					70				75						

(B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..68
(D) OTHER INFORMATION: / Ceres Seq. ID 1577348
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3560:

Met Tyr Xaa Glu His Val Arg Arg Pro Leu Asp His Ala Ala Arg Gln
1 5 10 15
Pro Arg Ala Gly Glu Pro Ser Glu Thr Glu Pro Val Asn Ala Ala Gln
20 25 30
Ser Val Thr Pro Pro Ile Pro Thr Pro Ala Ile Ser Pro Thr Pro Trp
35 40 45
Pro Pro Pro Ala Arg Pro Pro Ala Arg Ser Ser Ala Ser Ser Thr Ser
50 55 60
Ser Ala Pro Glu
65

(2) INFORMATION FOR SEQ ID NO:3561:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..97
(D) OTHER INFORMATION: / Ceres Seq. ID 1577349
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3561:

Met Ala Ser Ala Gly Glu Ala Pro Ser Thr Leu Leu Arg Phe Leu Tyr
1 5 10 15
Phe Val Gly Ala Gly Val Ile Cys Thr Lys Ala Ile Asn Thr Tyr Arg
20 25 30
Asp Tyr Glu His Lys Lys Glu Ser Thr Ala Ala Leu Ala Ala Glu
35 40 45
Ser Ala Cys Gly Cys Cys Arg Gly Gly Arg Ala Arg Ser Cys Asn Arg
50 55 60
Arg Arg Glu Ala Leu Ile Val Asp Glu Gly Leu Ser Ser Ala Val Arg
65 70 75 80
Val Leu Gly Met Leu Leu Ser Ile Gly Glu Ile Asp Ile Phe Phe Cys
85 90 95
Phe

(2) INFORMATION FOR SEQ ID NO:3562:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 737 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..737
(D) OTHER INFORMATION: / Ceres Seq. ID 1577353
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3562:

aaaaaattaa aatcctcccg gaaatcagag acgcgaatcc ctgcgccag gccccgaaac 60
ctccgagttc tctcgccaat tcgatccgcc tcaccgccgc cgcccgtcg ccggtcggcc 120
ttgactgctc cgtcgcacgt ggcggttcgc agcgcggaat ctaccttggtg ttgagagatc 180
cggggaaacc cttgttcccg gtcgttcggg ctcgaaatctt ctgcggactg gcaatgtaag 240
cgttctccat cggaggggcga cgatctacgg ggcggttggt ggcggggttk agggaaatgga 300

(2) INFORMATION FOR SEQ ID NO:3563:

(A) LENGTH: 57 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 1577354

Lys	Lys	Leu	Lys	Ser	Ser	Arg	Lys	Ser	Glu	Thr	Arg	Ile	Pro	Arg	Pro
1				5					10					15	
Arg	Pro	Arg	Asn	Leu	Arg	Val	Leu	Ser	Pro	Ile	Arg	Ser	Ala	Ser	Pro
			20					25					30		
Pro	Pro	Pro	Val	Arg	Arg	Ser	Ala	Leu	Thr	Ala	Pro	Ser	His	Val	Ala
		35					40					45			
Val	Arg	Ser	Ala	Glu	Ser	Thr	Leu	Cys							
	50					55									

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1577355

Lys	Ile	Lys	Ile	Leu	Pro	Glu	Ile	Arg	Asp	Ala	Asn	Pro	Ser	Pro	Gln
1				5					10					15	
Ala	Pro	Lys	Pro	Pro	Ser	Ser	Leu	Ala	Asn	Ser	Ile	Arg	Leu	Thr	Ala
			20					25					30		
Ala	Ala	Arg	Pro	Pro	Val	Gly	Leu	Asp	Cys	Ser	Val	Ala	Arg	Gly	Gly
		35				40						45			
Ser	Gln	Arg	Gly	Ile	Tyr	Leu	Val	Leu	Arg	Asp	Pro	Gly	Lys	Pro	Leu
	50					55				60					
Phe	Pro	Val	Val	Pro	Ala	Arg	Ile	Phe	Cys	Gly	Leu	Ala	Met		
65					70				75						

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..42

(D) OTHER INFORMATION: / Ceres Seq. ID 1577356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3565:

Met Glu His Val Phe Gly Gly Lys Phe Lys Leu Gly Lys Lys Ile Gly
1 5 10 15
Ser Gly Ser Phe Arg Arg Ala Leu Ser Arg Arg Gln His Thr Glu Arg
20 25 30
Arg Gly Gly Gly Tyr Gln Val Gly Met Arg
35 40

(2) INFORMATION FOR SEQ ID NO:3566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..667
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3566:

cgggccacct cgagctgctg aaccgcgacc ccgacgacaa cccgctggtg acgttcaact 60
acttctcgca ccccgaggac ctccgcgcgt gcgtggccgg cttgtcggtc atcgagcgcg 120
tcatccactc ccaggccttc aagaacttca cgtacccoga cttctccatg gagacgctgc 180
tcaacatgtc gacgggggttc cccgtcaacc tgetgccccg gcacgacaaac gactccacgt 240
cgcttgagat gttctgcaag gacaccgtca tgaccatctg gcaactaccac ggtggctgcc 300
aggtcggcag ggtcgtcgac gctgaatacc gagtgcctcg catcgaCGcg ctgcgcgtca 360
ttgacggctc cactttcaac gcctcgccag gaaccaaccc gcaggcaacc gtcgatgatgc 420
tcggcaggta tatgggagtc agaatacaca acgaaagggt ggcagctgaa ggattagagg 480
gaacaaaacc gtgatgatcc tataatccaa gacagtaggc gaggcgtaTt taagaatctc 540
tattgaacta tgtaatgctg gattcaatat tgttggtgtg attctgatat tgataggttg 600
cacatatatt cggagttgta tcatgttggt tgttgttact atgtggacta ttatgagtga 660
aatctgc

(2) INFORMATION FOR SEQ ID NO:3567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3567:

Gly His Leu Glu Leu Arg Asn Arg Asp Pro Asp Asp Asn Pro Leu Val
1 5 10 15
Thr Phe Asn Tyr Phe Ser His Pro Glu Asp Leu Arg Arg Cys Val Ala
20 25 30
Gly Leu Ser Val Ile Glu Arg Val Ile His Ser Gln Ala Phe Lys Asn
35 40 45
Phe Thr Tyr Pro Asp Phe Ser Met Glu Thr Leu Leu Asn Met Ser Thr
50 55 60
Gly Phe Pro Val Asn Leu Leu Pro Arg His Asp Asn Asp Ser Thr Ser
65 70 75 80
Leu Glu Met Phe Cys Lys Asp Thr Val Met Thr Ile Trp His Tyr His
85 90 95
Gly Gly Cys Gln Val Gly Arg Val Val Asp Ala Glu Tyr Arg Val Leu
100 105 110
Gly Ile Asp Ala Leu Arg Val Ile Asp Gly Ser Thr Phe Asn Ala Ser
115 120 125
Pro Gly Thr Asn Pro Gln Ala Thr Val Met Met Leu Gly Arg Tyr Met
130 135 140

Gly Val Arg Ile Thr Asn Glu Arg Leu Ala Ala Glu Gly Leu Glu Gly
145 150 155 160
Thr Lys Pro

(2) INFORMATION FOR SEQ ID NO:3568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3568:

Met Glu Thr Leu Leu Asn Met Ser Thr Gly Phe Pro Val Asn Leu Leu
1 5 10 15
Pro Arg His Asp Asn Asp Ser Thr Ser Leu Glu Met Phe Cys Lys Asp
 20 25 30
Thr Val Met Thr Ile Trp His Tyr His Gly Gly Cys Gln Val Gly Arg
 35 40 45
Val Val Asp Ala Glu Tyr Arg Val Leu Gly Ile Asp Ala Leu Arg Val
50 55 60
Ile Asp Gly Ser Thr Phe Asn Ala Ser Pro Gly Thr Asn Pro Gln Ala
65 70 75 80
Thr Val Met Met Leu Gly Arg Tyr Met Gly Val Arg Ile Thr Asn Glu
 85 90 95
Arg Leu Ala Ala Glu Gly Leu Glu Gly Thr Lys Pro
 100 105

(2) INFORMATION FOR SEQ ID NO:3569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3569:

Met Ser Thr Gly Phe Pro Val Asn Leu Leu Pro Arg His Asp Asn Asp
1 5 10 15
Ser Thr Ser Leu Glu Met Phe Cys Lys Asp Thr Val Met Thr Ile Trp
 20 25 30
His Tyr His Gly Gly Cys Gln Val Gly Arg Val Val Asp Ala Glu Tyr
 35 40 45
Arg Val Leu Gly Ile Asp Ala Leu Arg Val Ile Asp Gly Ser Thr Phe
50 55 60
Asn Ala Ser Pro Gly Thr Asn Pro Gln Ala Thr Val Met Met Leu Gly
65 70 75 80
Arg Tyr Met Gly Val Arg Ile Thr Asn Glu Arg Leu Ala Ala Glu Gly
 85 90 95
Leu Glu Gly Thr Lys Pro
 100

(2) INFORMATION FOR SEQ ID NO:3570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3570:

(2) INFORMATION FOR SEQ ID NO:3571:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1577379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3571:

[illegible]

(2) INFORMATION FOR SEQ ID NO:3572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1577380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3572:

Leu Ser Ser Gly Ser Ser Arg Gly Ser Thr Ser Ala Ser Pro Thr Trp
1 5 10 15
Ser Arg Ser Arg Ala Arg Thr Pro Ser Ala Arg Pro Ala Ala Ser Pro
20 25 30
Ser Ser Ser Ala Ser Thr Thr Ser Leu Asp Pro Ala Ala Pro Thr Arg
35 40 45
Thr Trp Thr Pro Pro Thr Ala Ala Arg Ser Thr His Ser Ala Pro Arg
50 55 60
Ala Ala Thr Arg Arg Ser Arg Glu Ala Trp Thr Pro Pro His Ala Ser
65 70 75 80
Ser Thr Thr Ser Thr Ser Arg Thr Ser Xaa Arg Ser Ala Ala Ser Ser
85 90 95
Thr Pro Thr Arg Arg Ser Ser Leu Thr Thr Pro Gly Pro Val Gly Ser
100 105 110
Ser Ser Gly Ser Ala Arg Thr Arg Thr Pro Ser Ser Gly Pro Ser Ser
115 120 125
Arg Gly
130

(2) INFORMATION FOR SEQ ID NO:3573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1577381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3573:

Ser His Pro Ala Leu Arg Gly Ala Gln Pro Gln Arg His Arg Pro Gly
1 5 10 15
Arg Ala Leu Gly Leu Ala Leu His Arg Arg Gly Pro Leu Leu His
20 25 30
Arg Leu Pro Pro Leu Gln Pro Val Trp Ile Arg Pro Pro Arg Pro Ala
35 40 45
His Gly His Arg Leu Pro Pro Leu Ala Arg Arg Thr Leu Pro Gln Gly
50 55 60
Arg Arg Arg Gly Gly His Gly Arg Pro Gly Arg His Pro Thr His Leu
65 70 75 80
Arg Gln Pro Val Leu Arg Gly Pro Arg Xaa Ala Pro Arg Leu Pro Gln
85 90 95
Leu Arg Pro Asp Ala Leu Leu
100

(2) INFORMATION FOR SEQ ID NO:3574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 761 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..761

(D) OTHER INFORMATION: / Ceres Seq. ID 1577382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3574:

catttctcgt gcagggtggtt gaggttaatg ttaaggtgga aagtgcaggc acacataaca 60
tgcacaataa tgatttctat gctaaagaga agttgctcaa atcaatgcgt gattgtgatc 120

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cttcgtcttt gcgccattgg attgtaagag ttgttttctt gttttatatt ttttttgta 180
ttcctaccat tgaattgggc attcaatacc tgtycattat ctttatgctt atgcaatcca 240
ataatgatgg aaaataactg acttggtgc tctcttgagt tgtggcaacC ggaagttcca 300
ggccccattg cagcacYtac actgcgctaa tggaccttca ggactattct gagaatggaa 360
ctgtaaccgt ggtatatcga gtgatactta aaggaactga tggagaggca tatagagatg 420
ccacgggcac aacacagttG ccatgagggg cgcagggaag atgctgttgc agccgcagag 480
gaagctgcat tcagcaaagc ttgcgcatgg ttcggttttg gctgtatct gtaccaccag 540
gatgaatctc attacgacga ccacttccat tgaggctcaa tctgcaaaag agttgatcat 600
aagttgtaac atgcgttga tatgccctta gaaaattcgt atctagaatc aatttttggt 660
ctttgcgtag tatcatactc ataacacaaa gaagtgaacc tatgtagatg ctatttgaaa 720
ccddkttatt aatattataa ttcttattaa tattattgta t

(2) INFORMATION FOR SEQ ID NO:3575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3575:

Phe Leu Val Gln Val Val Glu Val Asn Val Lys Val Glu Ser Ala Gly
1 5 10 15
Thr His Asn Met His Asn Asn Asp Phe Tyr Ala Lys Glu Lys Leu Leu
20 25 30
Lys Ser Met Arg Asp Cys Asp Pro Ser Ser Leu Arg His Trp Ile Val
35 40 45
Arg Val Val Phe Leu Phe Tyr Ile Phe Phe Val Ile Pro Thr Ile Glu
50 55 60
Leu Gly Ile Gln Tyr Leu Xaa Ile Ile Phe Met Leu Met Gln Ser Asn
65 70 75 80
Asn Asp Gly Lys

(2) INFORMATION FOR SEQ ID NO:3576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3576:

Met His Asn Asn Asp Phe Tyr Ala Lys Glu Lys Leu Leu Lys Ser Met
1 5 10 15
Arg Asp Cys Asp Pro Ser Ser Leu Arg His Trp Ile Val Arg Val Val
20 25 30
Phe Leu Phe Tyr Ile Phe Phe Val Ile Pro Thr Ile Glu Leu Gly Ile
35 40 45
Gln Tyr Leu Xaa Ile Ile Phe Met Leu Met Gln Ser Asn Asn Asp Gly
50 55 60
Lys
65

(2) INFORMATION FOR SEQ ID NO:3577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid

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- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..62
(D) OTHER INFORMATION: / Ceres Seq. ID 1577385
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3577:

Met	Arg	Gly	Ala	Gly	Lys	Met	Leu	Leu	Gln	Pro	Gln	Arg	Lys	Leu	His
1				5					10					15	
Ser	Ala	Lys	Leu	Ala	His	Gly	Ser	Val	Leu	Ala	Cys	Ile	Cys	Thr	Thr
			20					25					30		
Arg	Met	Asn	Leu	Ile	Thr	Thr	Thr	Ser	Ile	Glu	Ala	Gln	Ser	Ala	
		35					40					45			
Lys	Glu	Leu	Ile	Ile	Ser	Cys	Asn	Met	Arg	Trp	Ile	Cys	Pro		
	50					55					60				

- (2) INFORMATION FOR SEQ ID NO:3578:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..780
(D) OTHER INFORMATION: / Ceres Seq. ID 1577401

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3578:

gagctcgctg	cgccgtcttt	caatgctccc	cgccgccttc	cccgtataa	agcacctgcc	60
ttgccacctc	tctctcctca	cgaccacaca	ccaccgctcc	acacacaaga	agagagccga	120
gagctagcta	cctagcgctc	gatggcgatg	tccgcttcca	agatgatggc	ggtcgccgcc	180
gctngccctg	ctagccctgg	tcctggccgc	gtcgaccgcg	naggcgagga	acatcaagac	240
gacgacgacg	acgacggaga	agaaggacga	tgcggtggtg	bagccgcaga	ccttcccgcc	300
cttcgamcgc	ctcgccggcg	gNcgcgCcc	cggcggtccg	gtggcctccc	cggcacctcg	360
tcgggcgcca	gcagcattcc	agcgttcagc	atgccgggca	gcggcagcag	cctccccggc	420
gggtcgttct	tgcccggcag	cagcggcagc	atcggcagca	tgcccctctt	cagcggcggc	480
tccccggcct	tcagcggctt	cggcggcatg	cccgggtccc	ncgccgccgg	ctccgtctcc	540
gtcgtccccg	tgcacggcag	caagccctga	aaatccgtcc	gtcgccggag	cccgggaagtc	600
tgtcgggcca	acttggtccc	tagtactcct	ttgcctgcat	tgtattggag	agttggtatc	660
gcgtttcggt	tggtgtttgc	tttgttatta	taggccgcct	atctaccgag	acatgtgatg	720
tttggtgcgg	taaattaaaa	tcggttgat	tcattgctgt	gctgttgtct	ttaatttgct	780

- (2) INFORMATION FOR SEQ ID NO:3579:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..142
(D) OTHER INFORMATION: / Ceres Seq. ID 1577402

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3579:

Met	Ala	Met	Ser	Ala	Ser	Lys	Met	Met	Ala	Val	Ala	Ala	Xaa	Pro	
1				5					10				15		
Ala	Ser	Pro	Gly	Pro	Gly	Arg	Val	Asp	Arg	Xaa	Gly	Glu	Glu	His	Gln
			20					25					30		
Asp	Asp	Asp	Asp	Asp	Asp	Gly	Glu	Glu	Gly	Arg	Cys	Gly	Gly	Xaa	Ala
		35					40					45			
Ala	Asp	Leu	Pro	Ala	Leu	Arg	Xaa	Pro	Arg	Arg	Arg	Xaa	Arg	Pro	Pro

50 55 60
Ala Ser Gly Gly Leu Pro Gly Thr Ser Ser Gly Gly Ser Ser Ile Pro
65 70 75 80
Ala Phe Ser Met Pro Gly Ser Gly Ser Ser Leu Pro Gly Gly Ser Phe
85 90 95
Leu Pro Gly Ser Ser Gly Ser Ile Gly Ser Met Pro Leu Phe Ser Gly
100 105 110
Gly Ser Pro Ala Phe Ser Gly Phe Gly Gly Met Pro Gly Ser Xaa Ala
115 120 125
Ala Gly Ser Val Ser Val Val Pro Val His Gly Ser Lys Pro
130 135 140

(2) INFORMATION FOR SEQ ID NO:3580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1577403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3580:

Met Ser Ala Ser Lys Met Met Ala Val Ala Ala Ala Xaa Pro Ala Ser
1 5 10 15
Pro Gly Pro Gly Arg Val Asp Arg Xaa Gly Glu Glu His Gln Asp Asp
20 25 30
Asp Asp Asp Asp Gly Glu Glu Gly Arg Cys Gly Gly Xaa Ala Ala Asp
35 40 45
Leu Pro Ala Leu Arg Xaa Pro Arg Arg Arg Xaa Arg Pro Pro Ala Ser
50 55 60
Gly Gly Leu Pro Gly Thr Ser Ser Gly Gly Ser Ser Ile Pro Ala Phe
65 70 75 80
Ser Met Pro Gly Ser Gly Ser Ser Leu Pro Gly Gly Ser Phe Leu Pro
85 90 95
Gly Ser Ser Gly Ser Ile Gly Ser Met Pro Leu Phe Ser Gly Gly Ser
100 105 110
Pro Ala Phe Ser Gly Phe Gly Gly Met Pro Gly Ser Xaa Ala Ala Gly
115 120 125
Ser Val Ser Val Val Pro Val His Gly Ser Lys Pro
130 135 140

(2) INFORMATION FOR SEQ ID NO:3581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1577404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3581:

Met Met Ala Val Ala Ala Ala Xaa Pro Ala Ser Pro Gly Pro Gly Arg
1 5 10 15
Val Asp Arg Xaa Gly Glu Glu His Gln Asp Asp Asp Asp Asp Asp Gly
20 25 30
Glu Glu Gly Arg Cys Gly Gly Xaa Ala Ala Asp Leu Pro Ala Leu Arg
35 40 45
Xaa Pro Arg Arg Arg Xaa Arg Pro Pro Ala Ser Gly Gly Leu Pro Gly
50 55 60

Thr Ser Ser Gly Gly Ser Ser Ile Pro Ala Phe Ser Met Pro Gly Ser
65 70 75 80
Gly Ser Ser Leu Pro Gly Gly Ser Phe Leu Pro Gly Ser Ser Gly Ser
85 90 95
Ile Gly Ser Met Pro Leu Phe Ser Gly Gly Ser Pro Ala Phe Ser Gly
100 105 110
Phe Gly Gly Met Pro Gly Ser Xaa Ala Ala Gly Ser Val Ser Val Val
115 120 125
Pro Val His Gly Ser Lys Pro
130 135

(2) INFORMATION FOR SEQ ID NO:3582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..837
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3582:

accctctcca	cttcggtttc	cggatcccgt	ttccagctcc	gatccaaccc	agcatctgta	60
ccgcgcgcgc	gagcacgtcc	ggcgccggtg	cggcaggcga	aatccgagag	cactcctmcc	120
ccgctacgcc	gcaccgccc	tggccgcagc	tagccgcaga	tagagagagg	cgcaggcgag	180
ggcgtgcaga	tccagatccg	gtgggcggga	aggacttgat	cgccccacc	accatggccg	240
gcccgggtgc	ggcgctcttc	ctgctggaca	tgaagggccg	cgttctcgtc	tggcgcgact	300
accgcggcga	tgtctccgcg	ctccaggccg	agcgcttctt	caccaagctc	ctcgacaagg	360
agggcgattc	ggaagtgcac	tcgctgtgg	tctacgacga	cgctggcgtc	acttacatgt	420
tcattccagca	caacaatgtc	ttcctcctca	ccgcgcgtcg	ccagaactgt	aacgcggCcc	480
agcactctcc	tcttctctcca	ccgtgtaata	gatgtgttta	agcactactt	cgaggagctg	540
gaggaggagt	cgctcagaga	taacttcgtc	gttggtgatg	agttgctcga	tgagatgatg	600
gattttgggt	accacaata	cacggaggcg	aagatattga	gtgagttcat	caagacagat	660
gcatacagga	tggaggtcac	acagcgtcca	cccatggccg	tgacaaatgc	tgtgtcatgg	720
aggagcgagg	ggatccggta	caagaagaat	gaagtcttct	tggatgtagt	ggagagtgtt	780
aacattctag	ttaacagcaa	tggccagatt	gtgagatcag	atgtggttgg	ggcactg	

(2) INFORMATION FOR SEQ ID NO:3583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..172
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3583:

Pro Leu His Phe Arg Phe Arg Ile Pro Phe Pro Ala Pro Ile Gln Pro
1 5 10 15
Ser Ile Cys Thr Ala Pro Xaa Ser Thr Ser Gly Ala Gly Ala Ala Gly
20 25 30
Glu Ile Arg Glu His Ser Xaa Pro Ala Thr Pro His Arg Pro Trp Pro
35 40 45
Gln Leu Ala Ala Asp Arg Glu Arg Arg Arg Arg Gly Arg Ala Asp Pro
50 55 60
Asp Pro Val Gly Gly Lys Asp Leu Ile Ala Pro Thr Thr Met Ala Gly
65 70 75 80
Pro Val Ser Ala Leu Phe Leu Leu Asp Met Lys Gly Arg Val Leu Val
85 90 95
Trp Arg Asp Tyr Arg Gly Asp Val Ser Ala Leu Gln Ala Glu Arg Phe

(2) INFORMATION FOR SEO ID NO:3584:

(A) LENGTH: 176 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1577407

Met	Ser	Pro	Arg	Ser	Arg	Pro	Ser	Ala	Ser	Ser	Pro	Ser	Ser	Ser	Thr
1				5					10					15	
Arg	Arg	Ala	Ile	Arg	Lys	Cys	Thr	Arg	Leu	Trp	Ser	Thr	Thr	Thr	Leu
			20					25					30		
Ala	Ser	Leu	Thr	Cys	Ser	Ser	Ser	Thr	Thr	Met	Ser	Ser	Ser	Ser	Pro
			35				40					45			
Pro	Leu	Ala	Arg	Thr	Val	Thr	Arg	Pro	Ser	Ile	Leu	Leu	Phe	Leu	His
	50					55					60				
Arg	Val	Ile	Asp	Val	Phe	Lys	His	Tyr	Phe	Glu	Glu	Leu	Glu	Glu	Glu
65					70				75					80	
Ser	Leu	Arg	Asp	Asn	Phe	Val	Val	Val	Tyr	Glu	Leu	Leu	Asp	Glu	Met
				85					90				95		
Met	Asp	Phe	Gly	Tyr	Pro	Gln	Tyr	Thr	Glu	Ala	Lys	Ile	Leu	Ser	Glu
			100					105					110		
Phe	Ile	Lys	Thr	Asp	Ala	Tyr	Arg	Met	Glu	Val	Thr	Gln	Arg	Pro	Pro
			115				120					125			
Met	Ala	Val	Thr	Asn	Ala	Val	Ser	Trp	Arg	Ser	Glu	Gly	Ile	Arg	Tyr
	130					135				140					
Lys	Lys	Asn	Glu	Val	Phe	Leu	Asp	Val	Val	Glu	Ser	Val	Asn	Ile	Leu
145					150				155					160	
Val	Asn	Ser	Asn	Gly	Gln	Ile	Val	Arg	Ser	Asp	Val	Val	Gly	Ala	Leu
				165					170				175		

(A) LENGTH: 134 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1577408

Met Ser Ser Ser Ser Pro Pro Leu Ala Arg Thr Val Thr Arg Pro Ser
1 5 10 15
Ile Leu Leu Phe Leu His Arg Val Ile Asp Val Phe Lys His Tyr Phe
20 25 30

Glu Glu Leu Glu Glu Glu Ser Leu Arg Asp Asn Phe Val Val Val Tyr
35 40 45
Glu Leu Leu Asp Glu Met Met Asp Phe Gly Tyr Pro Gln Tyr Thr Glu
50 55 60
Ala Lys Ile Leu Ser Glu Phe Ile Lys Thr Asp Ala Tyr Arg Met Glu
65 70 75 80
Val Thr Gln Arg Pro Pro Met Ala Val Thr Asn Ala Val Ser Trp Arg
85 90 95
Ser Glu Gly Ile Arg Tyr Lys Lys Asn Glu Val Phe Leu Asp Val Val
100 105 110
Glu Ser Val Asn Ile Leu Val Asn Ser Asn Gly Gln Ile Val Arg Ser
115 120 125
Asp Val Val Gly Ala Leu
130

(2) INFORMATION FOR SEQ ID NO:3586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..886
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3586:

aaaatttccc	ccccaatttc	cctccaccga	agcatcaccc	aatcagatcc	gatttcgtag	60
agatgaagcc	ggcagtagag	gcggaggctg	acgagcgagc	ggcggaggag	atggcaccta	120
agaaggcagc	ggctgccaag	aaagcngccg	aggaagttga	ggtggaggad	gtggtggacg	180
gggacgaggc	ggtcgatggg	gagggcgacg	gtgacgagga	cgacgatggg	gaaggcggtg	240
acgaggagga	tgatgatgab	gaggtggatg	gggaggagaa	ggangcggca	ggggttgtgg	300
agatctccga	cGgaagacga	cgacgacggt	gacggggakg	cggacgacga	cgacgacgat	360
gacggggatg	acgacgacga	cgacgacgag	gactcagacg	acgaggaaga	ggtcgacggt	420
gaagacgatc	aggaggagga	gctgggaacc	gagtatctgg	ttcagcctct	tgggcgggct	480
gaagacgaag	agcactcgag	cgactttgaa	cgggaagaaa	acggtgaggg	tgccgacgat	540
gaggagatcg	atgaagagga	cgatgacggt	gaggactctg	tgaaggcgca	gacctctacg	600
aagaggaaga	ggtcaggcga	cgaagaagaa	gaagacgacg	acgatgggga	tgatgatggt	660
gacgatgatg	acgatgggag	gccaccatca	aagcgatagt	atggttagct	ctagttttgt	720
agctgtgtcc	ttgggtgttt	ggtaggtagg	tagtgctgct	gatgttggtt	tagaagaact	780
catcatcacc	tgggatatgt	gtgtgatttg	gcttggccga	tggatgaatg	atgaaggtct	840
tgtacttggt	gctgottott	tcatgttgat	gaactcgcac	tgattc		

(2) INFORMATION FOR SEQ ID NO:3587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3587:

Met Gly Arg Ala Thr Val Thr Arg Thr Met Gly Lys Ala Val Thr	
1 5 10 15	
Arg Arg Met Met Met Xaa Arg Trp Met Gly Arg Arg Arg Xaa Arg Gln	
20 25 30	
Gly Leu Trp Arg Ser Pro Thr Glu Asp Asp Asp Asp Gly Asp Gly Xaa	
35 40 45	
Ala Asp Asp Asp Asp Asp Asp Asp Gly Asp Asp Asp Asp Asp Asp	
50 55 60	

Glu Asp Ser Asp Asp Glu Glu Glu Val Asp Gly Glu Asp Asp Gln Glu
65 70 75 80
Glu Glu Leu Gly Thr Glu Tyr Leu Val Gln Pro Leu Gly Arg Ala Glu
85 90 95
Asp Glu Glu His Ser Ser Asp Phe Glu Pro Glu Glu Asn Gly Glu Gly
100 105 110
Ala Asp Asp Glu Glu Ile Asp Glu Glu Asp Asp Asp Gly Glu Asp Ser
115 120 125
Val Lys Ala Gln Thr Ser Thr Lys Arg Lys Arg Ser Gly Asp Glu Glu
130 135 140
Glu Glu Asp Asp Asp Asp Gly Asp Asp Asp Asp Asp Asp
145 150 155 160
Gly Arg Pro Pro Ser Lys Arg
165

(2) INFORMATION FOR SEQ ID NO:3588:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1577458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3588:

Met Gly Lys Ala Val Thr Arg Arg Met Met Met Xaa Arg Trp Met Gly
1 5 10 15
Arg Arg Arg Xaa Arg Gln Gly Leu Trp Arg Ser Pro Thr Glu Asp Asp
20 25 30
Asp Asp Gly Asp Gly Xaa Ala Asp Asp Asp Asp Asp Asp Gly Asp
35 40 45
Asp Asp Asp Asp Asp Asp Glu Asp Ser Asp Asp Glu Glu Glu Val Asp
50 55 60
Gly Glu Asp Asp Gln Glu Glu Leu Gly Thr Glu Tyr Leu Val Gln
65 70 75 80
Pro Leu Gly Arg Ala Glu Asp Glu Glu His Ser Ser Asp Phe Glu Pro
85 90 95
Glu Glu Asn Gly Glu Gly Ala Asp Asp Glu Glu Ile Asp Glu Glu Asp
100 105 110
Asp Asp Gly Glu Asp Ser Val Lys Ala Gln Thr Ser Thr Lys Arg Lys
115 120 125
Arg Ser Gly Asp Glu Glu Glu Asp Asp Asp Asp Gly Asp Asp Asp
130 135 140
Gly Asp Asp Asp Asp Asp Gly Arg Pro Pro Ser Lys Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:3589:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1577459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3589:

Met Met Met Xaa Arg Trp Met Gly Arg Arg Arg Xaa Arg Gln Gly Leu
1 5 10 15
Trp Arg Ser Pro Thr Glu Asp Asp Asp Asp Gly Asp Gly Xaa Ala Asp

20 25 30
Asp Asp Asp Asp Asp Gly Asp Asp Asp Asp Asp Asp Asp Glu Asp
35 40 45
Ser Asp Asp Glu Glu Glu Val Asp Gly Glu Asp Asp Gln Glu Glu Glu
50 55 60
Leu Gly Thr Glu Tyr Leu Val Gln Pro Leu Gly Arg Ala Glu Asp Glu
65 70 75 80
Glu His Ser Ser Asp Phe Glu Pro Glu Glu Asn Gly Glu Gly Ala Asp
85 90 95
Asp Glu Glu Ile Asp Glu Glu Asp Asp Asp Gly Glu Asp Ser Val Lys
100 105 110
Ala Gln Thr Ser Thr Lys Arg Lys Arg Ser Gly Asp Glu Glu Glu Glu
115 120 125
Asp Asp Asp Asp Gly Asp Asp Asp Gly Asp Asp Asp Asp Asp Gly Arg
130 135 140
Pro Pro Ser Lys Arg
145

(2) INFORMATION FOR SEQ ID NO:3590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..620
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3590:

accggacagc	tccccacaaa	acogtcagtt	ctctttttccc	ctgtaaatacg	caaattcgtc	60
ttccctgccc	atctatcgct	tggacacctc	tgcaagggag	cacatggctc	tcgagaaggc	120
caaggagatc	atcgcgctcct	ccccggtcga	cctagctctc	cgaaaggcca	aggagaccgt	180
cgcctcccac	cccgctgctcg	tcttcagcaa	aacttactgc	cctttctgca	cccgagtga	240
acaattgcta	gcaaagttgg	gggcaagtta	caaggctatt	gagttKggat	gtggaaagt	300
atggcgctga	gctgcagtca	gctctcgctg	aatggactgg	ccagagaact	gttcccaatg	360
tcttcgtgaa	aggggagcgg	attgggtggct	gtgacgcaac	catggcaatg	cacgacgggtg	420
aagctGggtg	cctctgctca	ccgaggctgg	agcaattgtc	actgccaggg	ctactgcaac	480
tactaccact	ccgtctttKg	tagacatgtt	ttacagcgct	gttccgctcg	cttcgtggct	540
atatgcaaat	gcaagtgttg	tacggagtag	taaactcata	cgtggcaaaa	gatgaataaa	600
gacttaaaca	tttcttcgcc					

(2) INFORMATION FOR SEQ ID NO:3591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3591:

Thr Gly Gln Leu Pro Thr Lys Pro Ser Val Leu Phe Ser Pro Val Asn
1 5 10 15
Arg Lys Phe Val Phe Pro Ala His Leu Ser Leu Gly His Leu Cys Lys
20 25 30
Gly Ala His Gly Ser Arg Glu Gly Gln Gly Asp His Arg Val Leu Pro
35 40 45
Gly Arg Pro Ser Ser Pro Lys Gly Gln Gly Asp Arg Arg Leu Pro Pro
50 55 60
Arg Arg Arg Leu Gln Gln Asn Leu Leu Pro Phe Leu His Pro Ser Glu

65 70 75 80
Thr Ile Ala Ser Lys Val Gly Gly Lys Leu Gln Gly Tyr
 85 90

(2) INFORMATION FOR SEQ ID NO:3592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3592:

Arg Thr Ala Pro His Lys Thr Val Ser Ser Leu Phe Pro Cys Lys Ser
1 5 10 15
Gln Ile Arg Leu Pro Cys Pro Ser Ile Ala Trp Thr Pro Leu Gln Gly
 20 25 30
Ser Thr Trp Leu Ser Arg Arg Pro Arg Arg Ser Ser Arg Pro Pro Arg
 35 40 45
Ser Thr
50

(2) INFORMATION FOR SEQ ID NO:3593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3593:

Met Ala Leu Glu Lys Ala Lys Glu Ile Ile Ala Ser Ser Pro Val Asp
1 5 10 15
Leu Ala Leu Arg Lys Ala Lys Glu Thr Val Ala Ser His Pro Val Val
 20 25 30
Val Phe Ser Lys Thr Tyr Cys Pro Phe Cys Thr Arg Val Lys Gln Leu
 35 40 45
Leu Ala Lys Leu Gly Ala Ser Tyr Lys Ala Ile Glu Xaa Gly Cys Gly
 50 55 60
Lys
65

(2) INFORMATION FOR SEQ ID NO:3594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..923
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3594:

tgagtatcar gaggcactac agtggaggat gcgggagcca aatttgggtg caaagctctt 60
ccttggtggt gttggagtgc agaagacagg tgaggagatt gcgactgcac tgaacaacat 120
tgacattagc tctgagtatg ttctgaagct ccgtcatgag attgaggagc tctgcgtgga 180
ggtttttcat actccagctg atcgagagaa gatcaagtcc tgtttatcag agctaggaga 240

ggtcagtgc tcatttaaga agatccttca ttctgcactg gagcatttgg tggcatctgt 300
ggtaccacgc attcgtccag tccttgacac tgttgctact gtcagttatg agttggatga 360
tactgaatat ggggaaaatg aggtgaacga tccatgggtg cagaagctta tacttacagt 420
waacagtaat gttgcttggc tccagccagt tatgacatta aacaactacg attcctttgt 480
gcacttgatc attgacttca ttgtcaagag gctcgaggtg attatgatgc agaagagggtt 540
cagccagctc ggcggtctcc agctcgataa ggaggtccgc tctctgatca accatttctc 600
agagatgtCc cagagaccag tcagagacaa gttctctagg ctttcgcaga tgtcgaccat 660
tttgaacttc gagcgggtat cggagatatt ggatttcttg ggtgacaatg ctggccatct 720
gacgtggctg ttgacacctg cagaggtgcg gagagtgtta ggacttagga ttgacttcag 780
gcctgaagct attgctgctt tgaggctctg aatcgtgcat ttatttgtac ttgttaattc 840
attatatgtg atatatagca acgagatgcc ttagaaattt ttgttgtaat gacgaaagac 900
ctgcattgta gaagaaatct gcg

(2) INFORMATION FOR SEQ ID NO:3595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..269
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3595:

Glu Tyr Xaa Glu Ala Leu Gln Trp Arg Met Arg Glu Pro Asn Leu Gly
1 5 10 15
Ala Lys Leu Phe Leu Gly Gly Val Gly Val Gln Lys Thr Gly Glu Glu
20 25 30
Ile Ala Thr Ala Leu Asn Asn Ile Asp Ile Ser Ser Glu Tyr Val Leu
35 40 45
Lys Leu Arg His Glu Ile Glu Glu Leu Cys Val Glu Val Phe His Thr
50 55 60
Pro Ala Asp Arg Glu Lys Ile Lys Ser Cys Leu Ser Glu Leu Gly Glu
65 70 75 80
Val Ser Ala Ser Phe Lys Lys Ile Leu His Ser Ala Leu Glu His Leu
85 90 95
Val Ala Ser Val Val Pro Arg Ile Arg Pro Val Leu Asp Thr Val Ala
100 105 110
Thr Val Ser Tyr Glu Leu Asp Asp Thr Glu Tyr Gly Glu Asn Glu Val
115 120 125
Asn Asp Pro Trp Val Gln Lys Leu Ile Leu Thr Xaa Asn Ser Asn Val
130 135 140
Ala Trp Leu Gln Pro Val Met Thr Leu Asn Asn Tyr Asp Ser Phe Val
145 150 155 160
His Leu Ile Ile Asp Phe Ile Val Lys Arg Leu Glu Val Ile Met Met
165 170 175
Gln Lys Arg Phe Ser Gln Leu Gly Gly Leu Gln Leu Asp Lys Glu Val
180 185 190
Arg Ser Leu Ile Asn His Phe Ser Glu Met Ser Gln Arg Pro Val Arg
195 200 205
Asp Lys Phe Ser Arg Leu Ser Gln Met Ser Thr Ile Leu Asn Phe Glu
210 215 220
Arg Val Ser Glu Ile Leu Asp Phe Trp Gly Asp Asn Ala Gly His Leu
225 230 235 240
Thr Trp Leu Leu Thr Pro Ala Glu Val Arg Arg Val Leu Gly Leu Arg
245 250 255
Ile Asp Phe Arg Pro Glu Ala Ile Ala Ala Leu Arg Leu
260 265

(2) INFORMATION FOR SEQ ID NO:3596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids

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- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..260
(D) OTHER INFORMATION: / Ceres Seq. ID 1577490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3596:

Met Arg Glu Pro Asn Leu Gly Ala Lys Leu Phe Leu Gly Gly Val Gly
1 5 10 15
Val Gln Lys Thr Gly Glu Glu Ile Ala Thr Ala Leu Asn Asn Ile Asp
20 25 30
Ile Ser Ser Glu Tyr Val Leu Lys Leu Arg His Glu Ile Glu Glu Leu
35 40 45
Cys Val Glu Val Phe His Thr Pro Ala Asp Arg Glu Lys Ile Lys Ser
50 55 60
Cys Leu Ser Glu Leu Gly Glu Val Ser Ala Ser Phe Lys Lys Ile Leu
65 70 75 80
His Ser Ala Leu Glu His Leu Val Ala Ser Val Val Pro Arg Ile Arg
85 90 95
Pro Val Leu Asp Thr Val Ala Thr Val Ser Tyr Glu Leu Asp Asp Thr
100 105 110
Glu Tyr Gly Glu Asn Glu Val Asn Asp Pro Trp Val Gln Lys Leu Ile
115 120 125
Leu Thr Xaa Asn Ser Asn Val Ala Trp Leu Gln Pro Val Met Thr Leu
130 135 140
Asn Asn Tyr Asp Ser Phe Val His Leu Ile Ile Asp Phe Ile Val Lys
145 150 155 160
Arg Leu Glu Val Ile Met Met Gln Lys Arg Phe Ser Gln Leu Gly Gly
165 170 175
Leu Gln Leu Asp Lys Glu Val Arg Ser Leu Ile Asn His Phe Ser Glu
180 185 190
Met Ser Gln Arg Pro Val Arg Asp Lys Phe Ser Arg Leu Ser Gln Met
195 200 205
Ser Thr Ile Leu Asn Phe Glu Arg Val Ser Glu Ile Leu Asp Phe Trp
210 215 220
Gly Asp Asn Ala Gly His Leu Thr Trp Leu Leu Thr Pro Ala Glu Val
225 230 235 240
Arg Arg Val Leu Gly Leu Arg Ile Asp Phe Arg Pro Glu Ala Ile Ala
245 250 255
Ala Leu Arg Leu
260

(2) INFORMATION FOR SEQ ID NO:3597:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 760 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..760
(D) OTHER INFORMATION: / Ceres Seq. ID 1577513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3597:

accaaagcct cccccctt ccctgacacc ctgcgccg cgcaagcag cacgaaccag 60
cgaagagatg ggcgtctaca ccttcgtgtg ccgcacrc ccggcgsgcga ngtggaccgc 120
caagcagcac tccggcgaga tggaggcctc cgcgccacc ccctacgagc tgcagcgccg 180
cctcgtcgcc gCgcctccg cGgccgactc cgcgtccggc gtccagtcgt ccttctCcca 240
tggtcacc cc caGctccgcc gtcttcagg tgatcgtcgg tgggtggcgcg atgatggtta 300
gtgGAngcgg cgCgcggcgg tGcggccgAy ngccgCdckg gktgNgcgct gcggccgaag 360

ctcccaaGgg aggagaagaa ggaagaggag aaggaagaga gcgacgacga catggggattc 420
tccctgttcg actagagtta agctgcgtgt gcatgggttc gggttcGggtc gtgtcgcgcg 480
aaacgtgaag agctcaagcg gcctttttgt tccagtccca catgtgagag ctttgatacg 540
ttgtctggaa tgaaaaaatt tccccttgac accttgtctg caccgagggg ggagtaggcg 600
tgggggaaaa actgtagaac ctgtgggatg caaaatctat ctagtctagt tttgggatcg 660
gttacgaatt tgtcttcaac aaatagtttg gatgagacga gtggaaaaca tgggtggtgt 720
tgatttcaga aacgaatggc gatatgacat gtgttgtggc

(2) INFORMATION FOR SEQ ID NO:3598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90

(D) OTHER INFORMATION: / Ceres Seq. ID 1577514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3598:

Thr Lys Ala Ser Xaa Pro Phe Pro Asp Thr Leu Ala Ala Ala His Ala
1 5 10 15
Arg Thr Asn Gln Arg Arg Asp Gly Arg Leu His Leu Arg Val Pro Xaa
20 25 30
Xaa Arg Arg Xaa Xaa Val Asp Arg Gln Ala Ala Leu Arg Arg Asp Gly
35 40 45
Gly Leu Arg Arg His Pro Leu Arg Ala Ala Ala Pro Pro Arg Arg Arg
50 55 60
Arg Leu Arg Gly Arg Leu Arg Val Arg Arg Pro Val Val Leu Leu Pro
65 70 75 80
Trp Ser Pro Pro Ala Pro Pro Ser Ser Arg
85 90

(2) INFORMATION FOR SEQ ID NO:3599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1577515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3599:

Pro Lys Pro Xaa Pro Pro Ser Leu Thr Pro Ser Pro Pro Arg Thr His
1 5 10 15
Ala Arg Thr Ser Glu Glu Met Gly Val Tyr Thr Phe Val Cys Arg Xaa
20 25 30
Xaa Gly Xaa Ala Xaa Trp Thr Ala Lys Gln His Ser Gly Glu Met Glu
35 40 45
Ala Ser Ala Ala Thr Pro Tyr Glu Leu Gln Arg Arg Leu Val Ala Ala
50 55 60
Ala Ser Ala Ala Asp Ser Ala Ser Gly Val Gln Ser Ser Phe Ser His
65 70 75 80
Gly His Pro Gln Leu Arg Arg Leu Pro Gly Asp Arg Arg Trp Trp Arg
85 90 95
Asp Asp Gly

(2) INFORMATION FOR SEQ ID NO:3600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..82
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1577516
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3600:

Met	Val	Thr	Pro	Ser	Ser	Ala	Val	Phe	Gln	Val	Ile	Val	Gly	Gly	Gly
1				5					10					15	
Ala	Met	Met	Val	Ser	Gly	Xaa	Gly	Ala	Arg	Arg	Cys	Gly	Arg	Xaa	Pro
			20					25					30		
Xaa	Arg	Xaa	Xaa	Ala	Ala	Ala	Glu	Ala	Pro	Lys	Gly	Gly	Glu	Glu	Gly
		35					40					45			
Arg	Gly	Glu	Gly	Arg	Glu	Arg	Arg	Arg	His	Gly	Ile	Leu	Pro	Val	Arg
	50				55				60						
Leu	Glu	Leu	Ser	Cys	Val	Cys	Met	Val	Ala	Val	Arg	Val	Val	Ser	Arg
65				70					75					80	
Glu	Thr														

- (2) INFORMATION FOR SEQ ID NO:3601:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1006 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1006
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1577517
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3601:

ctagggttta	catcccttat	aaaatctcgt	cttccacccc	tgcctccctc	agtcgcactt	60
cctccggcgg	cggcaactcg	acggccaacc	gcgccaccct	gccgcggcag	ccatggtgca	120
tgtaacttc	taccgcaact	atgggaagac	tttcaagaag	ccaaggcggc	cgtatgagaa	180
ggagcgcta	gatgctgagc	tgaagctggt	tgggtgagat	ggcctgcggt	gcaagcgcca	240
gctgtggcgc	gtgcagtatg	ccctgagccg	tatcaggaat	gcagccaggg	agctgctcac	300
cctggatgag	aagaaccac	gcggtatctt	tgagggcgag	gcgctccctc	gccgcatgaa	360
cagatatggt	cttcttggtg	agggacagaa	caagcttgat	tacgtgcttg	ctctcactgt	420
tgagaacttc	ctccagcgcc	gcctccagac	catcgtcttc	aagaatggca	tggccaagtc	480
catccaccat	gctcgtgtcc	tgatcaggca	gcgcCacatc	aggggtggga	ggcagctcgt	540
caacatcccc	tcgttcatgg	tcagggtcga	atcagagaag	cacatcgact	tctccctcac	600
cagccctctg	ggtggtggtc	ctgcccgaag	ggtgaagcgg	aagaaccaga	agaaggcctc	660
agggggcggc	gacgctgagg	aggacgagga	gtaaaggggg	ggggggcacg	taggattctg	720
ggacggcaat	tggtttaaat	gtgaggtgga	cactttagtt	gttgtgcctg	agtgtgtttg	780
tggtgtaatg	aatacaaatt	ctactgtggt	agacaatttt	gcacccccac	tactgacact	840
cgtgtttaaa	tttaaacatt	ggcatcgtgt	ctggacacga	tgaattgtat	tctggtttgg	900
gtggctattt	gctagtttgg	tctttaggcc	aatgtttaag	actgaaacaa	attggtagcc	960
aactttacta	tcttatgctc	tgctggtctg	tttggtgatt	tttttt		

- (2) INFORMATION FOR SEQ ID NO:3602:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..193
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1577518
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3602:

Met	Val	His	Val	Asn	Phe	Tyr	Arg	Asn	Tyr	Gly	Lys	Thr	Phe	Lys	Lys
1				5					10					15	
Pro	Arg	Arg	Pro	Tyr	Glu	Lys	Glu	Arg	Leu	Asp	Ala	Glu	Leu	Lys	Leu
			20					25					30		
Val	Gly	Glu	Tyr	Gly	Leu	Arg	Cys	Lys	Arg	Glu	Leu	Trp	Arg	Val	Gln
		35					40					45			
Tyr	Ala	Leu	Ser	Arg	Ile	Arg	Asn	Ala	Ala	Arg	Glu	Leu	Leu	Thr	Leu
	50				55					60					
Asp	Glu	Lys	Asn	Pro	Arg	Arg	Ile	Phe	Glu	Gly	Glu	Ala	Leu	Leu	Arg
65					70				75						80
Arg	Met	Asn	Arg	Tyr	Gly	Leu	Leu	Gly	Glu	Gly	Gln	Asn	Lys	Leu	Asp
			85					90					95		
Tyr	Val	Leu	Ala	Leu	Thr	Val	Glu	Asn	Phe	Leu	Gln	Arg	Arg	Leu	Gln
			100					105					110		
Thr	Ile	Val	Phe	Lys	Asn	Gly	Met	Ala	Lys	Ser	Ile	His	His	Ala	Arg
		115				120						125			
Val	Leu	Ile	Arg	Gln	Arg	His	Ile	Arg	Val	Gly	Arg	Gln	Leu	Val	Asn
	130					135					140				
Ile	Pro	Ser	Phe	Met	Val	Arg	Val	Glu	Ser	Glu	Lys	His	Ile	Asp	Phe
145					150					155					160
Ser	Leu	Thr	Ser	Pro	Leu	Gly	Gly	Gly	Pro	Ala	Gly	Arg	Val	Lys	Arg
				165				170						175	
Lys	Asn	Gln	Lys	Lys	Ala	Ser	Gly	Gly	Gly	Asp	Ala	Glu	Glu	Asp	Glu
			180					185					190		
Glu															

(2) INFORMATION FOR SEQ ID NO:3603:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1577519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3603:

Met	Asn	Arg	Tyr	Gly	Leu	Leu	Gly	Glu	Gly	Gln	Asn	Lys	Leu	Asp	Tyr
1				5					10					15	
Val	Leu	Ala	Leu	Thr	Val	Glu	Asn	Phe	Leu	Gln	Arg	Arg	Leu	Gln	Thr
			20					25					30		
Ile	Val	Phe	Lys	Asn	Gly	Met	Ala	Lys	Ser	Ile	His	His	Ala	Arg	Val
		35				40					45				
Leu	Ile	Arg	Gln	Arg	His	Ile	Arg	Val	Gly	Arg	Gln	Leu	Val	Asn	Ile
	50					55				60					
Pro	Ser	Phe	Met	Val	Arg	Val	Glu	Ser	Glu	Lys	His	Ile	Asp	Phe	Ser
65					70				75						80
Leu	Thr	Ser	Pro	Leu	Gly	Gly	Gly	Pro	Ala	Gly	Arg	Val	Lys	Arg	Lys
				85				90					95		
Asn	Gln	Lys	Lys	Ala	Ser	Gly	Gly	Gly	Asp	Ala	Glu	Glu	Asp	Glu	Glu
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:3604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 851 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(D) OTHER INFORMATION: / Ceres Seq. ID 1577526

aagagctccc	caacctcgccc	cccccatcc	agctccgacc	ctagggtttc	catccggctc	60
ttccggaagc	ttccgaaat	ggccaccgac	gagctcgccc	acgccgtcgc	ccccgccccg	120
gccgggggag	accactcccc	ggcctttctcg	ttcagcatct	ggccgccgac	gcagcgcaag	180
cgnhgacgsg	ntggtgcggc	gcctcgtgga	gacgctcgcg	ggagacca	tcctctgcaa	240
gcgctacggt	gcggtgcggc	ccgccgacgc	cgagcccgcg	gcgcgcgcca	tcgaggccga	300
ggccttcgac	gcccgggcct	ccacgggagg	cgccgcgcgc	gcctccgtgg	aggaggggat	360
cgaggcgctg	cagttcCtac	tccaaaggagg	tgagccgcgc	cctcctyvcg	ttcgtcaagt	420
yccGctccgc	ggacgccaag	gcgggtgaca	cgccgtcgga	ggagccccgg	gccctaggcg	480
cgcccgaggc	cgaggccgcc	cagcccgcgg	cgtgagcgcc	gdacagccat	tcgttcogtt	540
ttgtattttc	tgcagcctgt	gtttggcttg	ggtctgagtt	tgtatgactt	gaacgttagc	600
tgtttgcaca	tctatgcaat	tcttgttctt	ccatgaatag	ccccgttcta	gtgcgtgttc	660
ctgtttttct	gggaatccct	gcccgatcct	gaggttgta	aaccatcgca	gcattgacct	720
ctgtctgtgt	gcagcttcga	gtgatggctg	aattgttcgc	gagaccgaat	tgacaagcaa	780
ttaaagatttc	tcccatcttt	caagccacat	ttatatgtat	aataataatc	tgaccgttga	840
tttgaaatttc	t					

(D) OTHER INFORMATION: / Ceres Seq. ID 1577527

[illegible]

(D) OTHER INFORMATION: / Ceres Seq. ID 1577528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3606:

Arg Ala Pro His Leu Ala Pro Pro His Pro Ala Pro Thr Leu Gly Phe
1 5 10 15
Pro Ser Gly Ser Ser Gly Ser Phe Arg Lys Trp Pro Pro Thr Ser Ser
20 25 30
Pro Thr Pro Ser Pro Pro Pro Arg Pro Gly Glu Thr Thr Pro Arg Pro
35 40 45
Ser Arg Ser Ala Ser Gly Arg Arg Arg Ser Ala Arg Xaa Asp Xaa Xaa
50 55 60
Val Arg Arg Leu Val Glu Thr Leu Ala Gly Asp Thr Ile Leu Cys Lys
65 70 75 80
Arg Tyr Gly Ala Val Pro Ala Ala Asp Ala Glu Pro Ala Ala Arg Ala
85 90 95
Ile Glu Ala Glu Ala Phe Asp Ala Ala Ala Ser Thr Gly Gly Ala Ala
100 105 110
Ala Ala Ser Val Glu Glu Gly Ile Glu Ala Leu Gln Phe Leu Leu Gln
115 120 125
Gly Gly Glu Pro Pro Pro Pro Xaa Leu Arg Gln Xaa Pro Leu Arg Gly
130 135 140
Arg Gln Gly Arg
145

(2) INFORMATION FOR SEQ ID NO:3607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3607:

Met Ala Thr Asp Glu Leu Ala His Ala Val Ala Pro Ala Pro Ala Gly
1 5 10 15
Gly Asp His Ser Pro Ala Phe Ser Phe Ser Ile Trp Pro Pro Thr Gln
20 25 30
Arg Thr Arg Xaa Xaa Xaa Gly Ala Ala Pro Arg Gly Asp Ala Arg Gly
35 40 45
Arg His His Pro Leu Gln Ala Leu Arg Cys Gly Ala Gly Arg Arg Arg
50 55 60
Arg Ala Arg Gly Ala Arg His Arg Gly Arg Gly Leu Arg Arg Arg Gly
65 70 75 80
Leu His Gly Arg Arg Arg Arg Arg Leu Arg Gly Gly Gly Asp Arg Gly
85 90 95
Ala Ala Val Pro Thr Pro Arg Arg
100

(2) INFORMATION FOR SEQ ID NO:3608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..842
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3608:

agtgttggtgt cctagcgccg cgcgcgcccc aactcgctt gcgtgactga aagctcgctg 60
gcttcgctcc acgcgagaag cgagagcatg gacacccagg tgaagcttgc tgttggtgtg 120

aaggtgatgg gcaggaccgg ctccaggggt caggtgaccc aggtcagagt taagttcttg 180
gatgaccaga accggctcat catgaggaat gtcaaggcac ttgtcaccac ttgacgagaa 240
gaacccccgt cgtatctttg aggggtgaggc gcttcttcgc cgcatagaacc gctatgggct 300
gcttgctgag ggtcagaaca agcttgatta tgttcttgcc ctcaccgctg agaacttcct 360
cgcaaggcgg cttcaaacac ttgtcttcaa ggctggcatg gccaaagtcca ttcaccatgc 420
tcgtgtcttg atcaagcagc gtcacatcag gggtggcagg caaattgtca acgtcccatc 480
attcatggtg aggggtggagt ctgagaagca cattgacttt tcaactgtcaa gccattcgg 540
tgaggagcccc gcaGgaaggg tgaagagaaa gaatcagaag aaggcaagcg gtggcggcga 600
tgctggcgat gaggatgagg agtgaggatg gacaagtagc gttacccaat ataataatat 660
tatctagttt tcttgaactt gttcgaatga tgagtgttta gctgtgtgat ctgacgcaga 720
gttcctgtg ctgactctgt gtcatggatg gtccatttta tcttgtggta ttatcagcct 780
ttacataact gctatgtttg gatatgttca attctgttgc aattttatgt ggttgttttt 840
tg

(2) INFORMATION FOR SEQ ID NO:3609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3609:

Met Ser Arg His Leu Leu Thr Leu Asp Glu Lys Asn Pro Arg Arg Ile
1 5 10 15
Phe Glu Gly Glu Ala Leu Leu Arg Arg Met Asn Arg Tyr Gly Leu Leu
20 25 30
Ala Glu Gly Gln Asn Lys Leu Asp Tyr Val Leu Ala Leu Thr Ala Glu
35 40 45
Asn Phe Leu Ala Arg Arg Leu Gln Thr Leu Val Phe Lys Ala Gly Met
50 55 60
Ala Lys Ser Ile His His Ala Arg Val Leu Ile Lys Gln Arg His Ile
65 70 75 80
Arg Val Gly Arg Gln Ile Val Asn Val Pro Ser Phe Met Val Arg Val
85 90 95
Glu Ser Glu Lys His Ile Asp Phe Ser Leu Ser Ser Pro Phe Gly Gly
100 105 110
Gly Pro Ala Gly Arg Val Lys Arg Lys Asn Gln Lys Lys Ala Ser Gly
115 120 125
Gly Gly Asp Ala Gly Asp Glu Asp Glu Glu
130 135

(2) INFORMATION FOR SEQ ID NO:3610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3610:

Met Asn Arg Tyr Gly Leu Leu Ala Glu Gly Gln Asn Lys Leu Asp Tyr
1 5 10 15
Val Leu Ala Leu Thr Ala Glu Asn Phe Leu Ala Arg Arg Leu Gln Thr
20 25 30
Leu Val Phe Lys Ala Gly Met Ala Lys Ser Ile His His Ala Arg Val
35 40 45

Leu Ile Lys Gln Arg His Ile Arg Val Gly Arg Gln Ile Val Asn Val
50 55 60
Pro Ser Phe Met Val Arg Val Glu Ser Glu Lys His Ile Asp Phe Ser
65 70 75 80
Leu Ser Ser Pro Phe Gly Gly Gly Pro Ala Gly Arg Val Lys Arg Lys
85 90 95
Asn Gln Lys Lys Ala Ser Gly Gly Gly Asp Ala Gly Asp Glu Asp Glu
100 105 110
Glu

(2) INFORMATION FOR SEQ ID NO:3611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1577542

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3611:

Met Ala Lys Ser Ile His His Ala Arg Val Leu Ile Lys Gln Arg His
1 5 10 15
Ile Arg Val Gly Arg Gln Ile Val Asn Val Pro Ser Phe Met Val Arg
20 25 30
Val Glu Ser Glu Lys His Ile Asp Phe Ser Leu Ser Ser Pro Phe Gly
35 40 45
Gly Gly Pro Ala Gly Arg Val Lys Arg Lys Asn Gln Lys Lys Ala Ser
50 55 60
Gly Gly Gly Asp Ala Gly Asp Glu Asp Glu Glu
65 70 75

(2) INFORMATION FOR SEQ ID NO:3612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 569 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..569

(D) OTHER INFORMATION: / Ceres Seq. ID 1577548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3612:

aaaacagaca ggaagcccg cgaacatcac aaggctgcga acctcctaga agctcgagga 60
gatgctctcc aagctgtcgg cgtggttcgt gaacccgcgg aggaatygb tcgcgcgtct 120
ccaccggaac gccgtgcgct ccgcctccg caaatacggg ctccaggtatg acgacctcta 180
cgaccggtac cagcacctag acatcaagga ggcgCtgggc cggctgccgc gggaggtggt 240
ggacgcccgt aaccagcgcc tcaagcgggc catggacctc tccatgaagc accagtacct 300
acccgacgac gtccaggcta tacagacgcc attcaggagc tacctttttg acatgcttgc 360
tcttgtagaa aaggagagcg cagagcgtga agcattggga gcgcttccac tctaccagag 420
aaccatccca taaagtgcct ctttgcatga tccaatcaat agtgcacgcg atgatcagca 480
gaggctgata ctgtaatgtg tattgtgttt ttccgaggaa atctctacta cttattaaga 540
cgataagggt agcctgccgt tctgacgtc

(2) INFORMATION FOR SEQ ID NO:3613:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1577549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3613:

Met Leu Ser Lys Leu Ser Ala Trp Phe Val Asn Pro Arg Arg Asn Xaa
1 5 10 15
Xaa Ala Arg Leu His Arg Asn Ala Val Ala Ser Arg Leu Arg Lys Tyr
20 25 30
Gly Leu Arg Tyr Asp Asp Leu Tyr Asp Pro Tyr His Asp Leu Asp Ile
35 40 45
Lys Glu Ala Leu Ala Arg Leu Pro Arg Glu Val Val Asp Ala Arg Asn
50 55 60
Gln Arg Leu Lys Arg Ala Met Asp Leu Ser Met Lys His Gln Tyr Leu
65 70 75 80
Pro Asp Asp Val Gln Ala Ile Gln Thr Pro Phe Arg Ser Tyr Leu Phe
85 90 95
Asp Met Leu Ala Leu Val Lys Lys Glu Ser Ala Glu Arg Glu Ala Leu
100 105 110
Gly Ala Leu Pro Leu Tyr Gln Arg Thr Ile Pro
115 120

(2) INFORMATION FOR SEQ ID NO:3614:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 704 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..704

(D) OTHER INFORMATION: / Ceres Seq. ID 1577550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3614:

gtgctttctt agaggtgggt tggcttctcc tccccctccg gttcgggttc gggttcgtga 60
ggttctccgg ggttcgggtt cgtgggtgav cggatcgaga tggcggcgtc ggatgttgag 120
taccgctgct tcgctcggcag ctacagcvgt ggcggcgggc gctacgggtg cggcggcgcc 180
accacttgct cgccttcgcc ccttctgtct cccttcgtcc gtagcagacc aggaacgcc 240
aaggcgctaG cgtctccaag atggtgctgc aaaacgacat tgacttactc aatccaccgg 300
cagagcttga gaagctaaag cacaagaaga agcggctagt ccagtcccc aactccttct 360
tcatggatgt caagtgccag ggctgtttca gcataaccac tgtgttcagc cactcccaga 420
ctgtggttgt gtgccaggc tgccaaactg ttctgtgcc acctaccggt gggaaggcca 480
ggctcaccga ggggtgctcc ttccgtcgca agggcgatta ggtCctgctt ctcttaacgt 540
gagaagagat aaatttggtg ttttgcaact ttctcaggat atgtactgta ctcggtgagg 600
attttgttaa ttattatggc tgtttagcgtg gcttgacaat gcttgtgtgt maacctgcac 660
tttgtttgag cgtagtgaca tctaatatgg tgctgtttgg cttt

(2) INFORMATION FOR SEQ ID NO:3615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1577551

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3615:

Cys Phe Leu Arg Gly Gly Leu Ala Ser Pro Pro Pro Pro Val Arg Val
1 5 10 15
Arg Val Arg Glu Val Leu Arg Gly Ser Val Ser Trp Val Xaa Gly Ser
20 25 30

20250904 14:33:50

Arg Trp Arg Arg Arg Met Leu Ser Thr Ala Ala Ser Ser Ala Ala Thr
35 40 45
Xaa Val Ala Ala Ala Ala Thr Val Ala Ala Ala Pro Pro Leu Ala Arg
50 55 60
Leu Arg Pro Phe Cys Leu Pro Ser Ser Val Ala Asp Gln Glu Arg Pro
65 70 75 80
Arg Arg

(2) INFORMATION FOR SEQ ID NO:3616:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1577552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3616:

Met Ala Ala Ser Asp Val Glu Tyr Arg Cys Phe Val Gly Ser Tyr Ser
1 5 10 15
Xaa Gly Gly Gly Gly Tyr Gly Gly Gly Gly Ala Thr Thr Cys Ser Pro
20 25 30
Ser Pro Leu Leu Ser Pro Phe Val Arg Ser Arg Pro Gly Thr Pro Lys
35 40 45
Ala Leu Ala Ser Pro Arg Trp Cys Cys Lys Thr Thr Leu Thr Tyr Ser
50 55 60
Ile His Arg Gln Ser Leu Arg Ser
65 70

(2) INFORMATION FOR SEQ ID NO:3617:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1577553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3617:

Met Val Leu Gln Asn Asp Ile Asp Leu Leu Asn Pro Pro Ala Glu Leu
1 5 10 15
Glu Lys Leu Lys His Lys Lys Lys Arg Leu Val Gln Ser Pro Asn Ser
20 25 30
Phe Phe Met Asp Val Lys Cys Gln Gly Cys Phe Ser Ile Thr Thr Val
35 40 45
Phe Ser His Ser Gln Thr Val Val Val Cys Pro Gly Cys Gln Thr Val
50 55 60
Leu Cys Gln Pro Thr Gly Gly Lys Ala Arg Leu Thr Glu Gly Cys Ser
65 70 75 80
Phe Arg Arg Lys Gly Asp
85

(2) INFORMATION FOR SEQ ID NO:3618:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 941 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..941

(D) OTHER INFORMATION: / Ceres Seq. ID 1577582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3618:

aggccagggc	acttgcaaag	gatttatcct	cccaaagagc	aacgagagat	agggattttg	60
cttttgcattg	gttcatttgt	ttgcggcgctc	aaagagctcg	ttaaataatgg	acgtntctgga	120
tcactcggac	gatgaggagg	agcagcagga	cgggtgcggc	accagcagcg	gcagatcagg	180
ctccaggctc	ggcgcgcggg	csggcggcag	aagcggaggt	caggcggcag	cgccagaacc	240
tgctgctcat	ggactgcgtc	ggcggcaacg	gcggcgacgg	ggacggcgcg	ttggaggaca	300
ccgcgccgct	gccagactac	gagctcttgt	cccagtcggc	ccgcctccac	gacgacgcca	360
agaatccgcc	tccggcgctg	ctggttgcag	avgaggagga	gcagcagaag	gcgccggcca	420
agcaggggaa	gCggtccccc	ccacagcctc	cgcccggtgc	actgccacag	cggcagcaga	480
agccggcgctg	gaggctgata	gagtagctga	ggtaaggaa	cagktcgggc	ggcgcagggc	540
cgggggtcgg	tgggtgcggc	gcctggtctg	acggcgactc	caagagctcc	gaggacggcg	600
aggacggggg	cggcgaaggg	aagaaagata	agaagaagaa	gcggtcgtcc	tggctgccgg	660
accccgaccg	cgggtggccg	gtgcagggat	tctactagcg	cgttcatcgt	cttcgcagtc	720
tagtaaaacc	gtgtagtca	tgatgcgcct	ctgactcatg	cgttggtttg	gttgctccgg	780
gccctgtttg	gaagtgaagt	ttttttcata	gtttttgaga	aatactatag	tatccgttaa	840
tattagagta	ttctggacta	ttaatagatt	attagaaaat	agagtttcta	atatcatggt	900
ttttttaagt	atttgatata	tagttctgga	cctaagtttt	t		

(2) INFORMATION FOR SEQ ID NO:3619:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1577583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3619:

Met	Val	His	Trp	Phe	Ala	Ala	Ser	Lys	Ser	Ser	Leu	Asn	Met	Asp	Xaa
1				5					10					15	
Leu	Asp	His	Ser	Asp	Asp	Glu	Glu	Glu	Gln	Gln	Asp	Arg	Cys	Gly	Thr
			20					25					30		
Ser	Ser	Gly	Arg	Ser	Gly	Ser	Arg	Leu	Gly	Ala	Arg	Xaa	Gly	Gly	Arg
		35					40					45			
Ser	Gly	Gly	Gln	Ala	Ala	Ala	Pro	Glu	Pro	Ala	Ala	His	Gly	Leu	Arg
	50					55				60					
Arg	Arg	Gln	Arg	Arg	Arg	Arg	Gly	Arg	Arg	Val	Gly	Gly	His	Arg	Ala
65				70					75					80	
Ala	Ala	Arg	Leu	Arg	Ala	Leu	Val	Pro	Val	Arg	Pro	Pro	Pro	Arg	Arg
			85					90					95		
Arg	Gln	Glu	Ser	Ala	Ser	Gly	Ala	Ala	Gly	Cys	Arg	Xaa	Gly	Gly	Ala
		100						105					110		
Ala	Glu	Gly	Ala	Gly	Gln	Ala	Gly	Glu	Gly	Val	Pro	Ala	Thr	Ala	Ser
	115					120						125			
Ala	Arg	Ala	Thr	Ala	Thr	Ala	Ala	Ala	Glu	Ala	Gly	Val	Glu	Ala	Asp
	130					135					140				
Arg	Val	Arg	Glu	Val	Lys	Glu	Gln	Xaa	Gly	Arg	Arg	Arg	Ala	Gly	Gly
145					150					155					160
Arg	Trp	Val	Arg	Arg	Leu	Val									
					165										

(2) INFORMATION FOR SEQ ID NO:3620:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1577584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3620:

Met Asp Xaa Leu Asp His Ser Asp Asp Glu Glu Glu Gln Gln Asp Arg
1 5 10 15
Cys Gly Thr Ser Ser Gly Arg Ser Gly Ser Arg Leu Gly Ala Arg Xaa
20 25 30
Gly Gly Arg Ser Gly Gly Gln Ala Ala Pro Glu Pro Ala Ala His
35 40 45
Gly Leu Arg Arg Arg Gln Arg Arg Arg Arg Gly Arg Arg Val Gly Gly
50 55 60
His Arg Ala Ala Ala Arg Leu Arg Ala Leu Val Pro Val Arg Pro Pro
65 70 75 80
Pro Arg Arg Arg Gln Glu Ser Ala Ser Gly Ala Ala Gly Cys Arg Xaa
85 90 95
Gly Gly Ala Ala Glu Gly Ala Gly Gln Ala Gly Glu Gly Val Pro Ala
100 105 110
Thr Ala Ser Ala Arg Ala Thr Ala Ala Ala Glu Ala Gly Val
115 120 125
Glu Ala Asp Arg Val Arg Glu Val Lys Glu Gln Xaa Gly Arg Arg Arg
130 135 140
Ala Gly Gly Arg Trp Val Arg Arg Leu Val
145 150

(2) INFORMATION FOR SEQ ID NO:3621:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..188

(D) OTHER INFORMATION: / Ceres Seq. ID 1577585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3621:

Met Arg Arg Ser Ser Arg Thr Gly Ala Ala Pro Ala Ala Asp Gln
1 5 10 15
Ala Pro Gly Ser Ala Arg Gly Xaa Ala Ala Glu Ala Glu Val Arg Arg
20 25 30
Gln Arg Gln Asn Leu Leu Leu Met Asp Cys Val Gly Gly Asn Gly Gly
35 40 45
Asp Gly Asp Gly Ala Leu Glu Asp Thr Ala Pro Leu Pro Asp Tyr Glu
50 55 60
Leu Leu Ser Gln Ser Ala Arg Leu His Asp Asp Ala Lys Asn Pro Pro
65 70 75 80
Pro Ala Leu Leu Val Ala Xaa Glu Glu Glu Gln Gln Lys Ala Pro Ala
85 90 95
Lys Gln Gly Lys Ala Ser Pro Pro Gln Pro Pro Pro Val Pro Leu Pro
100 105 110
Gln Arg Gln Gln Lys Pro Ala Trp Arg Leu Ile Glu Tyr Val Arg Ser
115 120 125
Arg Asn Xaa Ser Gly Gly Ala Gly Pro Gly Val Gly Gly Cys Gly Ala
130 135 140
Trp Ser Asp Gly Asp Ser Lys Ser Ser Glu Asp Gly Glu Asp Gly Gly
145 150 155 160
Gly Glu Gly Lys Lys Asp Lys Lys Lys Lys Arg Ser Ser Trp Leu Pro
165 170 175
Asp Pro Asp Arg Arg Trp Pro Val Gln Gly Phe Tyr

180 185
(2) INFORMATION FOR SEQ ID NO:3622:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 854 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..854
(D) OTHER INFORMATION: / Ceres Seq. ID 1577601
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3622:
acttgctcca tatcccatcc atcacagcta gctagcgtag agacgaataa tctctttcttc 60
acctcactag ctaacaccag ctagcagctc gatcgctctg tcctgcaata atggccgctc 120
gctcctcctc ccagcagctg gtcgcgggcg cggtcctggc agcggcgcts ctgctgctgg 180
cgggcgggggc cgggacggcg tcggcgggcg tgagctgcgg cgaggtgacg tcgtcggtgg 240
cgccgtgcct cgggtacggc atgggcagcg cggcgctgcc ctccgcgggc tgctgcagcg 300
gggtgcgctc gctcaacagc cgcgcgtcgt cggcgggcga ccgncaggcc acctgcaact 360
gcctcaagag catgacgggc cggctcggcg gcggcgctcag Catggccaac gccgccaaca 420
tcccgggcaa atgcggcgct ccgctcggcg tgcccatcag cccaccgctc gactgcacca 480
agatcaactg atcgatggaa ccatagtggg ggtagctcgc tcgttggtat gcagcgtagc 540
tggccatcag cagcatgcag tcgtcgtcgt agcagagatg tcctagctac gtgtgtgtca 600
tgcacagac tggcacataa taaagaagta gatcatgcac ccactagtga tcacttcgtc 660
tagtgtccct ccgttcgtcg ttgtcgtcgt cgtcgtcgtg gtgtacctcg tacgtgacat 720
gccgtagcac gtacgctagc agagcagcac ctcaatgtcc ttgggtttgc tttgctggct 780
ctctgttttc gtctcgtgtt gcttttaatc tggcacaggt ttctaaatta taataatgaa 840
tacttttttg tcct

(2) INFORMATION FOR SEQ ID NO:3623:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..126
(D) OTHER INFORMATION: / Ceres Seq. ID 1577602
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3623:
Met Ala Ala Arg Ser Ser Ser Gln Gln Leu Val Ala Ala Ala Val Leu
1 5 10 15
Ala Ala Ala Xaa Leu Leu Leu Ala Ala Gly Ala Gly Thr Ala Ser Ala
20 25 30
Ala Val Ser Cys Gly Glu Val Thr Ser Ser Val Ala Pro Cys Leu Gly
35 40 45
Tyr Ala Met Gly Ser Ala Ala Ser Pro Ser Ala Ala Cys Cys Ser Gly
50 55 60
Val Arg Ser Leu Asn Ser Arg Ala Ser Ser Ala Ala Asp Xaa Gln Ala
65 70 75 80
Thr Cys Asn Cys Leu Lys Ser Met Thr Gly Arg Leu Gly Gly Gly Val
85 90 95
Ser Met Ala Asn Ala Ala Asn Ile Pro Gly Lys Cys Gly Val Ser Val
100 105 110
Gly Val Pro Ile Ser Pro Thr Val Asp Cys Thr Lys Ile Asn
115 120 125

(2) INFORMATION FOR SEQ ID NO:3624:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..76
(D) OTHER INFORMATION: / Ceres Seq. ID 1577603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3624:

Met Gly Ser Ala Ala Ser Pro Ser Ala Ala Cys Cys Ser Gly Val Arg
1 5 10 15
Ser Leu Asn Ser Arg Ala Ser Ser Ala Ala Asp Xaa Gln Ala Thr Cys
20 25 30
Asn Cys Leu Lys Ser Met Thr Gly Arg Leu Gly Gly Gly Val Ser Met
35 40 45
Ala Asn Ala Ala Asn Ile Pro Gly Lys Cys Gly Val Ser Val Gly Val
50 55 60
Pro Ile Ser Pro Thr Val Asp Cys Thr Lys Ile Asn
65 70 75

(2) INFORMATION FOR SEQ ID NO:3625:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 572 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..572
(D) OTHER INFORMATION: / Ceres Seq. ID 1577610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3625:

aagaaaagcc tccattcccg agtctccagc caaccgcatc cagtcaccc catccccctc 60
gacccccgaca accccgagtc ccgaccgat ggcgcccaag gccgagaaga agccagcgga 120
gaagaagccg gcggccgagg agaaggcgga gaagacgacc gcagGtaaga ggctttggct 180
ttgtgaacta ctccgacagt gatgctgcc aggaagctat ttctgcaatg gatggcaagg 240
aaattgatgg gcggcaggta cgtgtcaaca tggctaata gagacctgct gggaaccgtg 300
gtggtggcgg ctatggtggc ggcggctatg gaggtggtg ctacggaggt ggtggcggct 360
acggaggtgg tggctatggt ggtggcagcc aaagctatga tgcttgaagg gggcaggatc 420
ctattaagtc attatcaacc aagatatattg aaataatgaa ctttaggact tggatatgac 480
ttttatgta agcattgtca ggttttgcta ttcgtgttat gctgaattgt tggaactcct 540
agatgcagaa tattacgtat tggttttggt cc

(2) INFORMATION FOR SEQ ID NO:3626:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..134
(D) OTHER INFORMATION: / Ceres Seq. ID 1577611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3626:

Glu Lys Pro Pro Phe Pro Ser Leu Gln Pro Thr Ala Ser Ser Pro Pro
1 5 10 15
His Pro Pro Arg Pro Arg Gln Pro Arg Val Pro Thr Arg Trp Arg Pro
20 25 30
Arg Pro Arg Arg Ser Gln Arg Arg Arg Ser Arg Arg Pro Arg Arg Arg
35 40 45
Arg Arg Arg Arg Pro Gln Val Arg Gly Phe Gly Phe Val Asn Tyr Ser
50 55 60
Asp Ser Asp Ala Ala Lys Glu Ala Ile Ser Ala Met Asp Gly Lys Glu
65 70 75 80

Ile Asp Gly Arg Gln Val Arg Val Asn Met Ala Asn Glu Arg Pro Ala
85 90 95
Gly Asn Arg Gly Gly Gly Tyr Gly Gly Gly Tyr Gly Gly Gly
100 105 110
Gly Tyr Gly Gly Gly Gly Tyr Gly Gly Gly Tyr Gly Gly Gly
115 120 125
Ser Gln Ser Tyr Asp Ala
130

(2) INFORMATION FOR SEQ ID NO:3627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1577612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3627:

Met Leu Pro Arg Lys Leu Phe Leu Gln Trp Met Ala Arg Lys Leu Met
1 5 10 15
Gly Gly Arg Tyr Val Ser Thr Trp Leu Met Arg Asp Leu Leu Gly Thr
20 25 30
Val Val Val Ala Ala Met Val Ala Ala Ala Met Glu Val Val Ala Thr
35 40 45
Glu Val Val Ala Ala Thr Glu Val Val Ala Met Val Val Ala Ala Lys
50 55 60
Ala Met Met Leu Glu Gly Arg Ile Leu Leu Ser His Tyr Gln Pro
65 70 75 80
Arg Tyr Leu Lys

(2) INFORMATION FOR SEQ ID NO:3628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1577613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3628:

Met Ala Arg Lys Leu Met Gly Gly Arg Tyr Val Ser Thr Trp Leu Met
1 5 10 15
Arg Asp Leu Leu Gly Thr Val Val Val Ala Ala Met Val Ala Ala Ala
20 25 30
Met Glu Val Val Ala Thr Glu Val Val Ala Ala Thr Glu Val Val Ala
35 40 45
Met Val Val Ala Ala Lys Ala Met Met Leu Glu Gly Gly Arg Ile Leu
50 55 60
Leu Ser His Tyr Gln Pro Arg Tyr Leu Lys
65 70

(2) INFORMATION FOR SEQ ID NO:3629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..731

(D) OTHER INFORMATION: / Ceres Seq. ID 1577614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3629:

aaaaacccta	gcagccaccc	ggttctccct	cgctccaggt	ggcggcgcg	ccccctcggt	60
ttgtttcttac	tccctccggt	tccctcacta	gtcgttactg	acttctcgct	tgccctgctcc	120
agatctccct	tgcagccgg	ccagggaccc	cttcacagcg	cgggagatgg	ctgatcagga	180
ggccccagtt	gcagttgagg	caccaacccc	agttcttgga	gagccaatgg	acttgatgac	240
tgcgctgcag	ctggtgatga	agaagtcaag	tgctcatgat	ggacttggtga	agggctcttcg	300
cgaggctgcc	aaggccattg	agaagcatgc	tgctcagctt	tgcgttcttg	ctgaggactg	360
tgaccagcca	gattatgtca	agctggtgaa	ggcgctctgt	gctgaacaca	atgttcaoct	420
tgctactggt	cctgctgcta	agactcttgg	cgagtgggct	gggctttgca	agattgactc	480
cgagggcaag	gcaaggaagg	ttgtaggctg	ctcctgtgtc	gttgtcaagg	actacggtga	540
agaatctgag	ggccttaaca	tagtgcagga	gtatgtcaag	tcgcactaga	tgtAacacgt	600
ttcagtaata	ctctacattt	ggatctgggc	ttaatattat	gcttgcgtct	tgggcttgct	660
aggagattag	gacaatttac	tacaagagcc	catgaggata	tgagcaattt	ggaattctaa	720
atgttttggt	t					

(2) INFORMATION FOR SEQ ID NO:3630:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1577615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3630:

Met	Ala	Asp	Gln	Glu	Ala	Pro	Val	Ala	Val	Glu	Ala	Pro	Thr	Pro	Val	
1			5						10					15		
Leu	Gly	Glu	Pro	Met	Asp	Leu	Met	Thr	Ala	Leu	Gln	Leu	Val	Met	Lys	
			20					25					30			
Lys	Ser	Ser	Ala	His	Asp	Gly	Leu	Val	Lys	Gly	Leu	Arg	Glu	Ala	Ala	
			35				40					45				
Lys	Ala	Ile	Glu	Lys	His	Ala	Ala	Gln	Leu	Cys	Val	Leu	Ala	Glu	Asp	
	50					55					60					
Cys	Asp	Gln	Pro	Asp	Tyr	Val	Lys	Leu	Val	Lys	Ala	Leu	Cys	Ala	Glu	
65					70					75				80		
His	Asn	Val	His	Leu	Val	Thr	Val	Pro	Ala	Ala	Lys	Thr	Leu	Gly	Glu	
			85					90					95			
Trp	Ala	Gly	Leu	Cys	Lys	Ile	Asp	Ser	Glu	Gly	Lys	Ala	Arg	Lys	Val	
			100					105					110			
Val	Gly	Cys	Ser	Cys	Val	Val	Val	Lys	Asp	Tyr	Gly	Glu	Glu	Ser	Glu	
			115				120					125				
Gly	Leu	Asn	Ile	Val	Gln	Glu	Tyr	Val	Lys	Ser	His					
	130					135					140					

(2) INFORMATION FOR SEQ ID NO:3631:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1577616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3631:

Met Asp Leu Met Thr Ala Leu Gln Leu Val Met Lys Lys Ser Ser Ala

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1 5 10 15
His Asp Gly Leu Val Lys Gly Leu Arg Glu Ala Ala Lys Ala Ile Glu
20 25 30
Lys His Ala Ala Gln Leu Cys Val Leu Ala Glu Asp Cys Asp Gln Pro
35 40 45
Asp Tyr Val Lys Leu Val Lys Ala Leu Cys Ala Glu His Asn Val His
50 55 60
Leu Val Thr Val Pro Ala Ala Lys Thr Leu Gly Glu Trp Ala Gly Leu
65 70 75 80
Cys Lys Ile Asp Ser Glu Gly Lys Ala Arg Lys Val Val Gly Cys Ser
85 90 95
Cys Val Val Val Lys Asp Tyr Gly Glu Ser Glu Gly Leu Asn Ile
100 105 110
Val Gln Glu Tyr Val Lys Ser His
115 120

(2) INFORMATION FOR SEQ ID NO:3632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1577617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3632:

Met Thr Ala Leu Gln Leu Val Met Lys Lys Ser Ser Ala His Asp Gly
1 5 10 15
Leu Val Lys Gly Leu Arg Glu Ala Ala Lys Ala Ile Glu Lys His Ala
20 25 30
Ala Gln Leu Cys Val Leu Ala Glu Asp Cys Asp Gln Pro Asp Tyr Val
35 40 45
Lys Leu Val Lys Ala Leu Cys Ala Glu His Asn Val His Leu Val Thr
50 55 60
Val Pro Ala Ala Lys Thr Leu Gly Glu Trp Ala Gly Leu Cys Lys Ile
65 70 75 80
Asp Ser Glu Gly Lys Ala Arg Lys Val Val Gly Cys Ser Cys Val Val
85 90 95
Val Lys Asp Tyr Gly Glu Glu Ser Glu Gly Leu Asn Ile Val Gln Glu
100 105 110
Tyr Val Lys Ser His
115

(2) INFORMATION FOR SEQ ID NO:3633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..790

(D) OTHER INFORMATION: / Ceres Seq. ID 1577622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3633:

aaaggccaaa atcatcgctg crogccagt rgacggttc gactccggcc gccgcccctg	60
ctcctcctgc ccacccgcac cggccattgc cctgcctgc totgccacc gcaccttcca	120
ccgccccgc gtgctcctcc gcagtctggc cggtgcacc acctgcwccc caccaccgcc	180
gccccacca cttatccacc gttgcmggtc gtgcmccam ctgctcccc actgacaccg	240
gtcgaggtat aatctcacc tgggtgaagc ttcaccgcac tgctccgac acaccgaacc	300
aaacccatcc gagcgcatat acccagcaaa aaagtggaca cattttttac agcctaggtt	360

tNtccgCtgc gccccctgtt ttcgaaatcc tttccctagc gatcataact gacgccccga 420
atcgCcgcgcg ggcgggggag gagattcatc acgttttctg ctagggtttt gtatttggac 480
tagacagagc ggaaatctgg tgggtggtgat tctgtaacca gaagatcaga aactacggag 540
gagtgggggtt ttgtgattgg ttaccgatag gggttttgat tcatcggcac ccaaattgct 600
gttgattttt tcctgcagtt tctctcaatg tatttatggt catggtagta ctggattatg 660
gatacatttt tttcaagtga ttcataatct gcatcactcc tttttaaaaa agatcatcaa 720
tgaggagtga tgatatgatg atttttttat ttatctgtta acatcagtaa catcataata 780
gttttttttc

(2) INFORMATION FOR SEQ ID NO:3634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577623

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3634:

Lys Gly Gln Asn His Arg Cys Xaa Ala Ser Xaa Arg Val Arg Leu Arg
1 5 10 15
Pro Pro Pro Leu Leu Leu Leu Pro Thr Arg Thr Gly His Cys Pro Arg
20 25 30
Leu Leu Cys His Pro His Leu Pro Pro Pro Pro Arg Ala Pro Pro Gln
35 40 45
Ser Gly Arg Cys Thr His Leu Xaa Pro Thr Thr Ala Ala Pro Pro Thr
50 55 60
Tyr Pro Pro Leu Xaa Val Val Xaa Pro Xaa Ala Pro Pro Leu Thr Pro
65 70 75 80
Val Glu Val

(2) INFORMATION FOR SEQ ID NO:3635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3635:

Lys Ala Lys Ile Ile Ala Xaa Pro Pro Xaa Asp Ala Phe Asp Ser Gly
1 5 10 15
Arg Arg Pro Cys Ser Ser Cys Pro Pro Ala Pro Ala Ile Ala Leu Ala
20 25 30
Cys Ser Ala Thr Arg Thr Phe His Arg Pro Arg Val Leu Leu Arg Ser
35 40 45
Leu Ala Val Ala Pro Thr Cys Xaa Pro Pro Pro Pro Pro His Pro Leu
50 55 60
Ile His Arg Cys Xaa Ser Ser Xaa Xaa Leu Leu Pro His
65 70 75

(2) INFORMATION FOR SEQ ID NO:3636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1577625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3636:

```
Arg Pro Lys Ser Ser Leu Xaa Arg Gln Xaa Thr Arg Ser Thr Pro Ala
1          5          10          15
Ala Ala Pro Ala Pro Pro Ala His Pro His Arg Pro Leu Pro Ser Pro
20          25          30
Ala Leu Pro Pro Ala Pro Ser Thr Ala Pro Ala Cys Ser Ser Ala Val
35          40          45
Trp Pro Leu His Pro Pro Xaa Pro His His Arg Arg Pro Thr His Leu
50          55          60
Ser Thr Val Xaa Gly Arg Arg Xaa Xaa Cys Ser Pro Thr Asp Thr Gly
65          70          75          80
Arg Gly Ile Ile Ser Pro Trp Val Lys Leu His Pro Thr Ala Pro Ile
85          90          95
Thr Pro Asn Gln Thr His Pro Ser Ala Tyr Thr Gln Gln Lys Ser Gly
100         105         110
His Ile Phe Tyr Ser Leu Gly Xaa Ser Ala Ala Pro Pro Val Phe Glu
115         120         125
Ile Leu Ser Leu Ala Ile Ile Thr Asp Ala Pro Asn Arg Arg Ala Ala
130         135         140
Gly Glu Glu Ile His His Val Phe Cys
145         150
```

(2) INFORMATION FOR SEQ ID NO:3637:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 798 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..798

(D) OTHER INFORMATION: / Ceres Seq. ID 1577634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3637:

```
aacctcgctg tgtctcggt tggcttggt tcctctccc cgacgaccac cccgcgcttc      60
tcctctcccc ccgtcccacc ttccgagagg ctcgagccct gatcccacgc tgagggcggc      120
ggtgttagga gtttagcgat ggcgaggtgg cggccggcgg cgctgctggt agtggcgctg      180
acagcgggtt tgtcgggrgc gcr gcgggcg gatgcgctct cagtgcggt gaccgacacc      240
gagtgcaccc accgcctcg cgcacccggt tccgcgtgcc tttccccacc tactctcgcg      300
Gctctcgcca gccagctctag ggtttcgggtc ccggcggtgt tatccgcccc cgccggccat      360
gtcgaagcaa ggaggggaagg ccaagccgct gaaggcgccc aaggccgaca agaaggagta      420
cgacgagact gatcttgcac atctgcagaa gaagaaagat gaggaaaaag cactgaagga      480
gcttaaggcc aaggcacaga agggcgcgat tgggggctcg ggtctgaaga aaagtggaaa      540
gaaatgagac tggtcacccg tctccaatac ctagaggatg ataaggcagc tgtctatctg      600
tggtgcgctt cactaagtgt gattgtaaca gtggtacctc ttgtgttctg tgttccgcga      660
tggtgcagtt ggttgcttga tcgaaagatg tttcaacctc ccactctgcta gctatgatac      720
agatggtccc ctgataataa tgatgacata ttctgtgatg gatgccacag cattttttgt      780
ttttgttttt gcattcag
```

(2) INFORMATION FOR SEQ ID NO:3638:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1577635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3638:

Met Ala Arg Trp Arg Pro Ala Ala Leu Val Val Ala Leu Thr Ala
1 5 10 15
Val Leu Ser Xaa Ala Xaa Arg Ala Asp Ala Leu Ser Val Thr Val Thr
20 25 30
Asp Thr Glu Cys Ile His Pro Pro Arg Ala Pro Gly Ser Ala Cys Leu
35 40 45
Ser Pro Pro Thr Leu Ala Ala Leu Ala Ser Gln Ser Arg Val Ser Val
50 55 60
Pro Ala Cys Leu Ser Ala Pro Ala Gly His Val Glu Ala Arg Arg Glu
65 70 75 80
Gly Gln Ala Ala Glu Gly Ala Gln Gly Arg Gln Glu Gly Val Arg Arg
85 90 95
Asp

(2) INFORMATION FOR SEQ ID NO:3639:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1577636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3639:

Met Ser Lys Gln Gly Gly Lys Ala Lys Pro Leu Lys Ala Pro Lys Ala
1 5 10 15
Asp Lys Lys Glu Tyr Asp Glu Thr Asp Leu Ala Tyr Leu Gln Lys Lys
20 25 30
Lys Asp Glu Glu Lys Ala Leu Lys Glu Leu Lys Ala Lys Ala Gln Lys
35 40 45
Gly Ala Ile Gly Gly Ser Gly Leu Lys Lys Ser Gly Lys Lys
50 55 60

(2) INFORMATION FOR SEQ ID NO:3640:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..55

(D) OTHER INFORMATION: / Ceres Seq. ID 1577637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3640:

Met Arg Leu Val Thr Arg Leu Gln Tyr Leu Glu Asp Asp Lys Ala Ala
1 5 10 15
Val Tyr Leu Cys Cys Ala Ser Leu Ser Val Ile Val Thr Val Val Pro
20 25 30
Leu Val Phe Cys Val Pro Arg Cys Cys Ser Trp Leu Leu Asp Arg Lys
35 40 45
Met Phe Gln Pro Pro Ile Cys
50 55

(2) INFORMATION FOR SEQ ID NO:3641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 810 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..810
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3641:

gtogagttcg accctggatt tggcgatgrg ccccggcgcc ctcctcccc gcagcgcgctc	60
ccgtacgcct ccttcgctcc aggaagggga aggagcgcga sgggaacgag gagcaggaat	120
ctggcgctct cgcgttcctc ctccaacggt gcagcagtgat catccctgac aacagattcG	180
ggagaagaag ggcccagtga taatggaaat tccactggac caaatccgga ggccactgat	240
gcgaacgcgg gccaatgata cagtcaaggt gcaagaactc atgggcagta tccgtgtcat	300
cggcctccaa gtacctattg atgtgttggg ggtcgatggg gtctattatg gcttctctgg	360
atgccaccgc tacgaggtc accagcgcct tgggtctcca accatccgct gcaaagttcg	420
ccgtgggaca aaggaaacac tgaggcacca tatgcgatga gttatatattt attcagttac	480
aaagtgatct gtgtatctag agctaaaaca gaagcttcca tgggtcttttc gtogtctcgt	540
ctgcaattct ccatacctgt aaatgttgct caaacagagt ggtgaatagt acttctgtac	600
ccagcagcat cagaaaatgt taattttgcc tacaacactc ttttcgatca gtggatggat	660
gagtaaccacc cgtcagtag atcattccat ttctacgaga tttttgtaaa aaaagaaaaa	720
tgcagcagca gtcggcacgc tgtgtcattt agatcatcta gaaaaccaga aaaacagagt	780
catgtaactt gtttggtcgc tgcaaaaaat	

(2) INFORMATION FOR SEQ ID NO:3642:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..85
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3642:

Val	Glu	Phe	Asp	Pro	Gly	Phe	Gly	Asp	Xaa	Pro	Arg	Arg	Pro	Pro	Pro
1				5				10					15		
Pro	Gln	Arg	Val	Pro	Tyr	Ala	Ser	Phe	Ala	Pro	Gly	Arg	Gly	Arg	Ser
			20				25					30			
Ala	Xaa	Gly	Thr	Arg	Ser	Arg	Asn	Leu	Ala	Leu	Ser	Ala	Ser	Ser	Ser
		35				40				45					
Asn	Gly	Ala	Ala	Val	Pro	Ser	Leu	Thr	Thr	Asp	Ser	Gly	Glu	Glu	Gly
	50					55				60					
Pro	Ser	Asp	Asn	Gly	Asn	Ser	Thr	Gly	Pro	Asn	Pro	Glu	Ala	Thr	Asp
65					70				75					80	
Ala	Asn	Ala	Gly	Gln											
				85											

(2) INFORMATION FOR SEQ ID NO:3643:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..85
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3643:

Met	Glu	Ile	Pro	Leu	Asp	Gln	Ile	Arg	Arg	Pro	Leu	Met	Arg	Thr	Arg
1				5				10					15		
Ala	Asn	Asp	Pro	Val	Lys	Val	Gln	Glu	Leu	Met	Gly	Ser	Ile	Arg	Val
			20					25				30			

Ile Gly Leu Gln Val Pro Ile Asp Val Leu Glu Val Asp Gly Val Tyr
35 40 45
Tyr Gly Phe Ser Gly Cys His Arg Tyr Glu Ala His Gln Arg Leu Gly
50 55 60
Leu Pro Thr Ile Arg Cys Lys Val Arg Arg Gly Thr Lys Glu Thr Leu
65 70 75 80
Arg His His Met Arg
85

(2) INFORMATION FOR SEQ ID NO:3644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3644:

Met Pro Pro Leu Arg Gly Ser Pro Ala Pro Trp Ser Pro Asn His Pro
1 5 10 15
Leu Gln Ser Ser Pro Trp Asp Lys Gly Asn Thr Glu Ala Pro Tyr Ala
20 25 30
Met Ser Tyr Ile Leu Phe Ser Tyr Lys Val Ile Cys Val Ser Arg Ala
35 40 45
Lys Thr Glu Ala Ser Met Val Phe Ser Ser Ser Arg Leu Gln Phe Ser
50 55 60
Ile Pro Val Asn Val Val Gln Thr Glu Trp
65 70

(2) INFORMATION FOR SEQ ID NO:3645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 770 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..770
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3645:

atgttatgta ataatgtatg aagttatgaa gtccgaccca taccaccgcg cctagactgt	60
gcctgcaccc ctcacgcgtc ggctcgatcg ctgatcagtt ctgcrgccgg cgacgtgtgc	120
tagctcacga cgacgacatg ggctcggcgg tgaagatcgg gacgtggggc ggcgacggcG	180
ggagccccgt cgacatcacg gtggcgccgc ggcggctgga gagcatcacc atccgctgga	240
accagaggtg ggctgacaaa gcatacaaga agagccactt gggcaatgag tggaaaaaac	300
cttttgctgg atcatctcac gccaaaggga tcgttctgga gaagattggt attgaggcca	360
agcagccaaa ttccggccatc cgtaagtgtg cccgtgttca gctggtgaag aatggaaaga	420
agattgctgc ctttgtgccc aatgatggtt gcctaaacta catcgaggag aatgatgagg	480
tgttgattgc tggatttggt cgtaagggtc atgctgtggg agacattcct ggtgtcagggt	540
tcaaggttgt taagggtgtc ggtgtgtcgc tgcttgact cttcaaggag aagaaggaga	600
agCcaaggtc ttagatcact ttccgtagtc aagaatggtg taaactgccc aaggctctat	660
tgttaaagtt ctgctagcaa cagagctggt aattctgagc tgtacctttt tgtaaacatt	720
gttacagtct tacagagttc tgtttccatt ttgaagatat taatattgcg	

(2) INFORMATION FOR SEQ ID NO:3646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..158
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577662
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3646:

Met Gly Ser Ala Val Lys Ile Gly Thr Trp Gly Gly Asp Gly Gly Ser
1 5 10 15
Pro Cys Asp Ile Thr Val Ala Pro Arg Arg Leu Glu Ser Ile Thr Ile
 20 25 30
Arg Trp Asn Gln Arg Trp Ala Asp Lys Ala Tyr Lys Lys Ser His Leu
 35 40 45
Gly Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser Ser His Ala Lys Gly
50 55 60
Ile Val Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala
65 70 75 80
Ile Arg Lys Cys Ala Arg Val Gln Leu Val Lys Asn Gly Lys Lys Ile
 85 90 95
Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Tyr Ile Glu Glu Asn
 100 105 110
Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His Ala Val Gly
 115 120 125
Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser Gly Val Ser
130 135 140
Leu Leu Ala Leu Phe Lys Glu Lys Lys Glu Lys Pro Arg Ser
145 150 155

- (2) INFORMATION FOR SEQ ID NO:3647:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 969 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..969
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577663

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3647:

acataaccgc ccatamccac nccctcgcc gctgcrctcc acctccgccc cccgccctcc 60
ccgcgtcccc cctctcctac gcagatcgtc caggtaagat gtcgtccgag gcggtgaagg 120
tggcggtgcc ggagtcggta ctccgcaagc ggaagcgcn aggagcagtg gcccgccgag 180
aagaaggaga agtccctggc cgagaggaag aagtccatcg agaaccggaa gtcctcttc 240
acccgcgcca agcagtagc cgaggagtac gatgccagg agaaggaact ggtacagctt 300
aagcgtgagg cccgtttgaa ggggtggttc tatgtcagtc ctgagGcaaa gctgctattt 360
gtgatccgca tccgtggtat caatgccatg catcctaaga ccaggaagat attgcagctt 420
ctgcgtttga ggcagatatt caatggcgtg ttcctgaaag tcaacaaggc taccattaac 480
atgCttcgca gggttgagcc ttatgttgca tatgggtacc Cgaacttgaa gagtgtcagg 540
gagttgatct acaagagggg ctacggaaaa ctgaacaagc agaggatccc tctgtctaac 600
aaccaagtca tcgaggaggg cttgggcaag cacaacatca tttgcattga ggatcttggt 660
catgagatca tgactgtcgg ccacacttc aaggaggcga acaacttcct ttggccattt 720
aagctgaagg caccgctggg aggtctgaag aagaagagga accactatgt ggagggtggt 780
gatgccggtg accgtgagaa ttacatcaac gagctcatca aaaggatgaa ttaggttcac 840
gatcaagctc tattgtgttc taagaaactt tctgtgctct cccaatttta cattattagg 900
aagcggatga atatgcatgc agttttgttg tttggaacta gatgtgtatg gaagaaacat 960
gatcttttc

- (2) INFORMATION FOR SEQ ID NO:3648:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..99
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1577664
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3648:

Ile Thr Arg His Xaa His Xaa Pro Arg Arg Leu Xaa Pro Pro Pro Pro
1 5 10 15
Pro Ala Leu Pro Ala Ser Pro Leu Ser Tyr Ala Asp Arg Pro Gly Lys
20 25 30
Met Ser Ser Glu Ala Val Lys Val Ala Val Pro Glu Ser Val Leu Arg
35 40 45
Lys Arg Lys Arg Xaa Gly Ala Val Gly Arg Arg Glu Glu Gly Glu Val
50 55 60
Pro Gly Arg Glu Glu Glu Val His Arg Glu Pro Glu Ala His Leu His
65 70 75 80
Pro Arg Gln Ala Val Arg Arg Gly Val Arg Cys Pro Gly Glu Gly Thr
85 90 95
Gly Thr Ala

- (2) INFORMATION FOR SEQ ID NO:3649:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..148
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1577665
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3649:

Met His Pro Lys Thr Arg Lys Ile Leu Gln Leu Leu Arg Leu Arg Gln
1 5 10 15
Ile Phe Asn Gly Val Phe Leu Lys Val Asn Lys Ala Thr Ile Asn Met
20 25 30
Leu Arg Arg Val Glu Pro Tyr Val Ala Tyr Gly Tyr Pro Asn Leu Lys
35 40 45
Ser Val Arg Glu Leu Ile Tyr Lys Arg Gly Tyr Gly Lys Leu Asn Lys
50 55 60
Gln Arg Ile Pro Leu Ser Asn Asn Gln Val Ile Glu Glu Gly Leu Gly
65 70 75 80
Lys His Asn Ile Ile Cys Ile Glu Asp Leu Val His Glu Ile Met Thr
85 90 95
Val Gly Pro His Phe Lys Glu Ala Asn Asn Phe Leu Trp Pro Phe Lys
100 105 110
Leu Lys Ala Pro Leu Gly Gly Leu Lys Lys Lys Arg Asn His Tyr Val
115 120 125
Glu Gly Gly Asp Ala Gly Asn Arg Glu Asn Tyr Ile Asn Glu Leu Ile
130 135 140
Lys Arg Met Asn
145

- (2) INFORMATION FOR SEQ ID NO:3650:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1577666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3650:

Met Leu Arg Arg Val Glu Pro Tyr Val Ala Tyr Gly Tyr Pro Asn Leu
1 5 10 15
Lys Ser Val Arg Glu Leu Ile Tyr Lys Arg Gly Tyr Gly Lys Leu Asn
20 25 30
Lys Gln Arg Ile Pro Leu Ser Asn Asn Gln Val Ile Glu Glu Gly Leu
35 40 45
Gly Lys His Asn Ile Ile Cys Ile Glu Asp Leu Val His Glu Ile Met
50 55 60
Thr Val Gly Pro His Phe Lys Glu Ala Asn Asn Phe Leu Trp Pro Phe
65 70 75 80
Lys Leu Lys Ala Pro Leu Gly Gly Leu Lys Lys Lys Arg Asn His Tyr
85 90 95
Val Glu Gly Gly Asp Ala Gly Asn Arg Glu Asn Tyr Ile Asn Glu Leu
100 105 110
Ile Lys Arg Met Asn
115

(2) INFORMATION FOR SEQ ID NO:3651:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..433

(D) OTHER INFORMATION: / Ceres Seq. ID 1577678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3651:

atcattggtc tgctagcaga aacctcagag atatgttaca gagaaataaa ggacatcaag 60
tgcatacact gccctcacia gccagaaggt tccatgtttg tcatggtgaa attaaatttg 120
tatcttttgg aggggattca tgacgatatt gatttttgct gcaagCtggc aaaagaagag 180
tctgtgattt tgtgtccagg gagtgttttg ggaatggaaa actggatccg catcactttc 240
gchattgatt catcttctct tcttgatggg cttgagagga tcaaattctt ctgccaaagg 300
cataagaaga agaatttgct taatggccat taactgtatc tacgttcaaa gttacccagt 360
tccattgttt ttcattgtat catcaacaaa tgtggaactt tgaaatccct ctgaattaat 420
aaagttttcc ttg

(2) INFORMATION FOR SEQ ID NO:3652:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1577679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3652:

Ile Ile Gly Leu Leu Ala Glu Thr Ser Glu Ile Cys Tyr Arg Glu Ile
1 5 10 15
Lys Asp Ile Lys Cys Ile Thr Cys Pro His Lys Pro Glu Gly Ser Met
20 25 30
Phe Val Met Val Lys Leu Asn Leu Tyr Leu Leu Glu Gly Ile His Asp
35 40 45
Asp Ile Asp Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile Leu
50 55 60
Cys Pro Gly Ser Val Leu Gly Met Glu Asn Trp Ile Arg Ile Thr Phe
65 70 75 80

Xaa Ile Asp Ser Ser Ser Leu Leu Asp Gly Leu Glu Arg Ile Lys Ser
85 90 95
Phe Cys Gln Arg His Lys Lys Lys Asn Leu Leu Asn Gly His
100 105 110

(2) INFORMATION FOR SEQ ID NO:3653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3653:

Met Phe Val Met Val Lys Leu Asn Leu Tyr Leu Leu Glu Gly Ile His
1 5 10 15
Asp Asp Ile Asp Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile
20 25 30
Leu Cys Pro Gly Ser Val Leu Gly Met Glu Asn Trp Ile Arg Ile Thr
35 40 45
Phe Xaa Ile Asp Ser Ser Ser Leu Leu Asp Gly Leu Glu Arg Ile Lys
50 55 60
Ser Phe Cys Gln Arg His Lys Lys Lys Asn Leu Leu Asn Gly His
65 70 75

(2) INFORMATION FOR SEQ ID NO:3654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3654:

Met Val Lys Leu Asn Leu Tyr Leu Leu Glu Gly Ile His Asp Asp Ile
1 5 10 15
Asp Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile Leu Cys Pro
20 25 30
Gly Ser Val Leu Gly Met Glu Asn Trp Ile Arg Ile Thr Phe Xaa Ile
35 40 45
Asp Ser Ser Ser Leu Leu Asp Gly Leu Glu Arg Ile Lys Ser Phe Cys
50 55 60
Gln Arg His Lys Lys Lys Asn Leu Leu Asn Gly His
65 70 75

(2) INFORMATION FOR SEQ ID NO:3655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1045 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1045
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3655:

atcaagtcgg ctatcttctc cggccatcgg tcgcaccccc acgtgggggc ggcggcggtc

```
ccgcagcagc agcagctggg gagcacgcgt tcgttccact cgacacccat tctgcagcgg 120
aagcacaaga cccagtggca caacagattc aactattata cgagacgtag gaggaaccga 180
gaaactaaaa ggtcaatgct acggaacatg tcagaatatg cagagtctct ctttcagagt 240
tggcgtgatg aagatgagaa aaatgctgca tctgctgggc cttcatgggt tagaggacat 300
cgttgggtca gaaattcaag caacaatggt ttccgtacac acgattttta ttacgggaat 360
ttcaaaagca aaggaggatt tgagttttgc acaagtgatg aggatgaacc agagaatctg 420
tttcgtaatg tttttcgaga ccagcacaca tattattggt ctttttcatc tgataatttt 480
cagagGaact ccaaactgtc tcgctcacia aaatccagaa actggagttt tgaaacagac 540
gaggaggatg aagtatcagc tccatcagag gtatctttgg cacgacaagc tcttgggttg 600
agcactttctg gtccgcttaa acttgaagat gttaaaagcg cataccgagc atgtgcactt 660
agatggcatc cagatcgcca caatggatca tctaagtcta cagcggagga gaaattcaag 720
cattgcagtg cagcatataca gaccttatgt gatagtttgg ccgctgcata gataattttg 780
aatgaagatg gactctggat gagccccctc caaactttct agctgcaaat tctgaagagc 840
tgccacatgc ttgtggtagc tccgaccatc ccaatcccaa gaggcgggag tgcattttct 900
tggttattga ggcgattgag tcaattcaaa attgaccgga taatatatgt actgtaccgt 960
gtaaaatttt ttgtcacagc tcattgttgt attattttta tagatatgaa gatattgttc 1020
acaccactca ataaattttc ttggc
```

(2) INFORMATION FOR SEQ ID NO:3656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..256
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3656:

```
Ile Lys Ser Ala Ile Phe Ser Gly His Arg Ser His Pro His Val Gly
1           5           10           15
Ala Ala Ala Val Pro Gln Gln Gln Gln Leu Gly Ser Thr Ala Ser Phe
20           25           30
His Ser Thr Pro Ile Leu Gln Arg Lys His Lys Thr Gln Trp His Asn
35           40           45
Arg Phe Asn Tyr Tyr Thr Arg Arg Arg Arg Asn Arg Glu Thr Lys Arg
50           55           60
Ser Met Leu Arg Asn Met Ser Glu Tyr Ala Glu Ser Leu Phe Gln Ser
65           70           75           80
Trp Arg Asp Glu Asp Glu Lys Asn Ala Ala Ser Ala Gly Pro Ser Trp
85           90           95
Phe Arg Gly His Arg Trp Val Arg Asn Ser Ser Asn Asn Gly Phe Arg
100          105          110
Thr His Asp Phe Tyr Tyr Gly Asn Phe Lys Ser Lys Gly Gly Phe Glu
115          120          125
Phe Cys Thr Ser Asp Glu Asp Glu Pro Glu Asn Leu Phe Arg Asn Val
130          135          140
Phe Arg Asp Gln His Thr Tyr Tyr Trp Ser Phe Ser Ser Asp Asn Phe
145          150          155          160
Gln Arg Asn Ser Lys Arg Ala Arg Ser Gln Lys Ser Arg Asn Trp Ser
165          170          175
Phe Glu Thr Asp Glu Glu Asp Glu Val Ser Ala Pro Ser Glu Val Ser
180          185          190
Leu Ala Arg Gln Ala Leu Gly Leu Ser Thr Ser Gly Pro Leu Lys Leu
195          200          205
Glu Asp Val Lys Ser Ala Tyr Arg Ala Cys Ala Leu Arg Trp His Pro
210          215          220
Asp Arg His Asn Gly Ser Ser Lys Ser Thr Ala Glu Glu Lys Phe Lys
225          230          235          240
His Cys Ser Ala Ala Tyr Lys Thr Leu Cys Asp Ser Leu Ala Ala Ala
245          250          255
```

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(2) INFORMATION FOR SEQ ID NO:3657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..199

(D) OTHER INFORMATION: / Ceres Seq. ID 1577690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3657:

Ser Ser Arg Leu Ser Ser Pro Ala Ile Gly Arg Thr Pro Thr Trp Gly
1 5 10 15
Arg Arg Arg Ser Arg Ser Ser Ser Ser Trp Gly Ala Pro Leu Arg Ser
20 25 30
Thr Arg His Pro Phe Cys Ser Gly Ser Thr Arg Pro Ser Gly Thr Thr
35 40 45
Asp Ser Thr Ile Ile Arg Asp Val Gly Gly Thr Glu Lys Leu Lys Gly
50 55 60
Gln Cys Tyr Gly Thr Cys Gln Asn Met Gln Ser Leu Ser Phe Arg Val
65 70 75 80
Gly Val Met Lys Met Arg Lys Met Leu His Leu Leu Gly Leu His Gly
85 90 95
Leu Glu Asp Ile Val Gly Ser Glu Ile Gln Ala Thr Met Val Ser Val
100 105 110
His Thr Ile Phe Ile Thr Gly Ile Ser Lys Ala Lys Glu Asp Leu Ser
115 120 125
Phe Ala Gln Val Met Arg Met Asn Gln Arg Ile Cys Phe Val Met Phe
130 135 140
Phe Glu Thr Ser Thr His Ile Ile Gly Leu Phe His Leu Ile Ile Phe
145 150 155 160
Arg Gly Thr Pro Asn Val Leu Ala His Lys Asn Pro Glu Thr Gly Val
165 170 175
Leu Lys Gln Thr Arg Arg Met Lys Tyr Gln Leu His Gln Arg Tyr Leu
180 185 190
Trp His Asp Lys Leu Leu Gly
195

(2) INFORMATION FOR SEQ ID NO:3658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1577691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3658:

Met Leu Arg Asn Met Ser Glu Tyr Ala Glu Ser Leu Phe Gln Ser Trp
1 5 10 15
Arg Asp Glu Asp Glu Lys Asn Ala Ala Ser Ala Gly Pro Ser Trp Phe
20 25 30
Arg Gly His Arg Trp Val Arg Asn Ser Ser Asn Asn Gly Phe Arg Thr
35 40 45
His Asp Phe Tyr Tyr Gly Asn Phe Lys Ser Lys Gly Gly Phe Glu Phe
50 55 60
Cys Thr Ser Asp Glu Asp Glu Pro Glu Asn Leu Phe Arg Asn Val Phe

65 70 75 80
Arg Asp Gln His Thr Tyr Tyr Trp Ser Phe Ser Ser Asp Asn Phe Gln
85 90 95
Arg Asn Ser Lys Arg Ala Arg Ser Gln Lys Ser Arg Asn Trp Ser Phe
100 105 110
Glu Thr Asp Glu Glu Asp Glu Val Ser Ala Pro Ser Glu Val Ser Leu
115 120 125
Ala Arg Gln Ala Leu Gly Leu Ser Thr Ser Gly Pro Leu Lys Leu Glu
130 135 140
Asp Val Lys Ser Ala Tyr Arg Ala Cys Ala Leu Arg Trp His Pro Asp
145 150 155 160
Arg His Asn Gly Ser Ser Lys Ser Thr Ala Glu Glu Lys Phe Lys His
165 170 175
Cys Ser Ala Ala Tyr Lys Thr Leu Cys Asp Ser Leu Ala Ala Ala
180 185 190

(2) INFORMATION FOR SEQ ID NO:3659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 875 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..875
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3659:

atcgggtgcc	cattggccac	tggcccctag	ccctcgccct	cccttttcta	ttgctccgaa	60
gcccagagttg	cgagctgtct	cctccactct	tctccttcac	tgtcgagacc	gccccttgta	120
gaagcttcga	ggctgtgct	gctgcgcca	tggcgcgga	aggcaagacg	ccgtccctcg	180
ccgaggagta	ttcacttcca	ccacaggaag	ttccagtggg	aaaggcagct	gaggagaagc	240
cctctagtgg	tactgagtct	gaagctgctc	cctcaaccCa	atgatgaaac	tcctccatct	300
gtagaagaca	agaatggaac	ttctgaagta	caagatgctg	ctgaaaatcc	agaggcagaa	360
gaaactaaca	ctgctgcaga	ggaaacacct	gctgtagagg	aagcaagtga	gactaccgag	420
gaggaagagg	ctgagaaacc	tgagatcaag	atcgaaacag	ctccagcaga	ttttcgtttc	480
ccaacaacaa	accaaacaag	gcattgtttc	acacgcctatg	ttgaatatca	caggtgtgtg	540
gctgcaaaaag	gtgaggatgc	acctgagtgt	gataagttcg	ccaagtacta	tcgatccctg	600
tgcccaggtg	aatgggttga	tcgctggaac	gagcaacgcg	aaaacggcac	cttccctgga	660
cctctgtaat	cctacaatgc	aaaagaagta	tgaactcacg	atgttggtgcc	ggctttctctt	720
ccttggtaac	tggcgccaag	ttaccttttt	tggagctctc	tacagaataa	gaaatccctt	780
ttggcttgaa	gaatgccctg	ttgctcttcc	taacggtcat	gttggtgcgct	gctgagaaac	840
tagcgtcaca	gttaacaatt	ttctttatac	agttc			

(2) INFORMATION FOR SEQ ID NO:3660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3660:

Arg Val Pro Ile Gly His Trp Pro Leu Ala Leu Pro Phe Leu
1 5 10 15
Leu Leu Arg Ser Pro Ser Cys Glu Leu Ser Pro Pro Leu Phe Ser Phe
20 25 30
Thr Val Ala Ala Ala Pro Cys Arg Ser Phe Glu Ala Ala Ala Ala
35 40 45
Pro Met Ala Ala Glu Gly Lys Thr Pro Ser Leu Ala Glu Glu Tyr Ser

(2) INFORMATION FOR SEQ ID NO:3661:

(A) LENGTH: 105 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1577700

Met Leu Asn Ile Thr Gly Val Trp Leu Gln Lys Val Arg Met His Leu
1 5 10 15

Ser Val Ile Ser Ser Pro Ser Thr Ile Asp Pro Cys Ala Gln Val Asn
20 25 30

Gly Leu Ile Ala Gly Thr Ser Asn Ala Lys Thr Ala Pro Ser Leu Asp

Leu Cys Asn Pro Thr Met Gln Lys Lys Tyr Glu Leu Thr Met Leu Cys

Arg Leu Leu Phe Leu Gly Asn Trp Arg Gln Val Thr Phe Phe Gly Ala
65 70 75 80

Leu Tyr Arg Ile Arg Asn Pro Phe Trp Leu Glu Glu Cys Pro Val Ala

Leu Pro Asn Gly His Val Val Arg Cys
100 105

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1577701

Met	His	Leu	Ser	Val	Ile	Ser	Ser	Pro	Ser	Thr	Ile	Asp	Pro	Cys	Ala
1				5				10						15	

Gln Val Asn Gly Leu Ile Ala Gly Thr Ser Asn Ala Lys Thr Ala Pro
20 25 30

Ser Leu Asp Leu Cys Asn Pro Thr Met Gln Lys Lys Tyr Glu Leu Thr
35 40 45

Met Leu Cys Arg Leu Leu Phe Leu Gly Asn Trp Arg Gln Val Thr Phe

Phe Gly Ala Leu Tyr Arg Ile Arg Asn Pro Phe Trp Leu Glu Glu Cys
65 70 75 80

Pro Val Ala Leu Pro Asn Gly His Val Val Arg Cys
85 90

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1009 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1009

(D) OTHER INFORMATION: / Ceres Seq. ID 1577714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3663:

gtcgtctctcc gaactctgat tgaggaggag tgaagcttct tttctttcttc ctccagtcac	60
cccattgcaa aagtagaagc agggaaggaa ttggaagcat gaacaagcag cagcaggcgt	120
acgggtacgg aaatgggcag caggccgacg tcccaggcta ctgctgtttc catccccggg	180
aggtcggcgt cggcgtctgc gctcaactgcc tcaaggatcg cctcctcctc ctccctcgccg	240
ctgccaacaa caataagatc gacgacgacg cccgccgcaa aagcaggagc aggagcagga	300
gcatctccct ccccaaggtc ttccgcgtcg gctctctcct cctccagcgc ctcgactccc	360
gccaccaccg gggacgaggc cgggacaaca actgctactc cgacgacgac gacgccaccg	420
cctccgtcgc aagcctcgat gattccttca tctccatcaa attcgaggac aacggcaagg	480
cgacgtggga cagccagagc cagcacaagg cggcagCtcc cgcgaggtct cgtcgacgac	540
gaccatggta gcggtggagc acgtcaagcg tktcggcgct acccggtggc gcaaacaggt	600
gggtgggccc atgtctcagc tggcgcgctg gaggaggtcg tccgctgctg cgggtgggct	660
ggacggcaag aaggcgcgcg cggcgcgcg ctagcggtcc aaggccagag ggagaggctg	720
gatccggagc ctactctgga ggcgcgcgca cggggaccgg gcgtggtagg tcgccgtcgt	780
cggtaaggag gcccggtcgg tcggggggcg ggcagcccat gcatgcatgc atggtgtccg	840
atggatgatg gcatctcgca gcttcccccc ttgctttgga tggagacgta gtaattgctt	900
gcttgtgctt tgtaccaagt gagatgagtg agtgccctct ttacactact ataggctact	960
atacgtacag ttaatagcag ctagctgttg gtgtggattg ctatgcgtg	

(2) INFORMATION FOR SEQ ID NO:3664:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1577715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3664:

Met Asn Lys Gln Gln Gln Ala Tyr Gly Tyr Gly Asn Gly Gln Gln Ala	
1 5 10 15	
Asp Val Pro Gly Tyr Cys Cys Phe His Pro Arg Glu Val Gly Val Gly	
20 25 30	
Val Cys Ala His Cys Leu Lys Asp Arg Leu Leu Leu Leu Ala Ala	
35 40 45	
Ala Asn Asn Asn Lys Ile Asp Asp Asp Ala Arg Arg Lys Ser Arg Ser	
50 55 60	
Arg Ser Arg Ser Ile Ser Leu Pro Lys Val Phe Ala Leu Gly Ser Ser	
65 70 75 80	
Phe Leu Gln Arg Leu Asp Ser Arg His His Arg Gly Arg Gly Arg Asp	
85 90 95	
Asn Asn Cys Tyr Ser Asp Asp Asp Asp Ala Thr Ala Ser Val Ala Ser	
100 105 110	
Leu Asp Asp Ser Phe Ile Ser Ile Lys Phe Glu Asp Asn Gly Lys Ala	
115 120 125	
Thr Trp Asp Ser Gln Ser Gln His Lys Ala Ala Ala Pro Ala Arg Ser	
130 135 140	
Arg Arg Arg Arg Pro Trp	
145 150	

(2) INFORMATION FOR SEQ ID NO:3665:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..186
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3665:

Met Gly Ser Arg Pro Thr Ser Gln Ala Thr Ala Val Ser Ile Pro Gly
1 5 10 15
Arg Ser Ala Ser Ala Ser Ala Leu Thr Ala Ser Arg Ile Ala Ser Ser
 20 25 30
Ser Ser Ser Pro Leu Pro Thr Thr Thr Thr Thr Thr Thr Thr Ala
 35 40 45
Ala Lys Ala Gly Ala Gly Ala Gly Ala Ser Pro Ser Pro Arg Ser Ser
 50 55 60
Arg Ser Ala Pro Pro Ser Ser Ser Ala Ser Thr Pro Ala Thr Thr Gly
65 70 75 80
Asp Glu Gly Gly Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Pro Pro
 85 90 95
Pro Pro Ser Gln Ala Ser Met Ile Pro Ser Ser Pro Ser Asn Ser Arg
 100 105 110
Thr Thr Ala Arg Arg Arg Gly Thr Ala Arg Ala Ser Thr Arg Arg Gln
 115 120 125
Leu Pro Arg Gly Leu Val Asp Asp Asp His Gly Ser Gly Gly Ala Arg
 130 135 140
Gln Ala Xaa Arg Arg His Pro Val Ala Gln Thr Gly Gly Gly Pro His
145 150 155 160
Ala Ala Ala Gly Ala Leu Glu Glu Val Val Arg Cys Cys Gly Trp Ala
 165 170 175
Gly Arg Gln Glu Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 180 185

(2) INFORMATION FOR SEQ ID NO:3666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..588
(D) OTHER INFORMATION: / Ceres Seq. ID 1577717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3666:

aactaggcaa ctactccgtc tcacgcctct cctgtcccct ctgcgcgCtc tcgccccgcc 60
tctgctcccg cctcctccat cgcacccagc tttcctcccc accccaccac cactcctacc 120
ccgccacgtc gtgtagtcgc ggcgggcgat atgcaggccg ccgccgcctt caaccaggca 180
gccttcaccg cccgctcgct gcacgcgccc ccgaggcccc tccacctagc tgttgcgag 240
gatgcttttg cggggataag aggcgcgcct tttacacggc cccggtgctg cgggagcctc 300
tctgtcggcg tcggcagcta caacagcgag cacactccag tatttccaag acaacaatca 360
tgggatccct acaagcttct tgggtgtgat caagatgcat ctgaagaaga ggtccggagt 420
gcacggaatt ttcttctaaa acaatacgcc ggatatgaag aaagtgaaga ggccattgaa 480
ggtgcttatg acaagataat aatgaatagc tacacagacc gtaagaaatc caaattcaat 540
ctgaaaagca agctaaaaga gcaagttgaa ggatccccat catggcct

(2) INFORMATION FOR SEQ ID NO:3667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

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(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1577718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3667:

Leu	Gly	Asn	Tyr	Ser	Val	Ser	Arg	Leu	Ser	Cys	Pro	Leu	Ser	Pro	Leu	
1				5				10						15		
Ser	Pro	Arg	Leu	Cys	Leu	Arg	Leu	Leu	His	Arg	Thr	Gln	Leu	Ser	Ser	
			20					25					30			
Pro	Pro	His	His	His	Ser	Tyr	Pro	Ala	Thr	Ser	Cys	Ser	Arg	Gly	Gly	
			35					40					45			
Gly	Tyr	Ala	Gly	Arg	Arg	Arg	Leu	Gln	Pro	Gly	Ser	Leu	His	Arg	Pro	
	50					55					60					
Leu	Ala	Ala	Ser	Pro	Pro	Glu	Ala	Pro	Pro	Pro	Ser	Cys	Cys	Gly	Gly	
65					70					75					80	
Cys	Phe	Cys	Gly	Asp	Lys	Arg	Arg	Ala	Phe	Tyr	Thr	Ala	Pro	Val	Leu	
				85					90					95		
Arg	Glu	Pro	Leu	Cys	Arg	Arg	Arg	Gln	Leu	Gln	Gln	Arg	Ala	His	Ser	
			100					105					110			
Ser	Ile	Ser	Lys	Thr	Thr	Ile	Met	Gly	Ser	Leu	Gln	Ala	Ser	Trp	Cys	
			115				120					125				

(2) INFORMATION FOR SEQ ID NO:3668:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1577719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3668:

Met	Gln	Ala	Ala	Ala	Ala	Phe	Asn	Gln	Ala	Ala	Phe	Thr	Ala	Arg	Ser	
1				5				10						15		
Leu	His	Arg	Pro	Pro	Arg	Pro	Leu	His	Leu	Ala	Val	Ala	Glu	Asp	Ala	
			20					25					30			
Phe	Ala	Gly	Ile	Arg	Gly	Ala	Pro	Phe	Thr	Arg	Pro	Arg	Cys	Cys	Gly	
		35				40						45				
Ser	Leu	Ser	Val	Gly	Val	Gly	Ser	Tyr	Asn	Ser	Glu	His	Thr	Pro	Val	
	50					55				60						
Phe	Pro	Arg	Gln	Gln	Ser	Trp	Asp	Pro	Tyr	Lys	Leu	Leu	Gly	Val	Asp	
65					70				75						80	
Gln	Asp	Ala	Ser	Glu	Glu	Glu	Val	Arg	Ser	Ala	Arg	Asn	Phe	Leu	Leu	
				85					90					95		
Lys	Gln	Tyr	Ala	Gly	Tyr	Glu	Glu	Ser	Glu	Glu	Ala	Ile	Glu	Gly	Ala	
			100					105					110			
Tyr	Asp	Lys	Ile	Ile	Met	Asn	Ser	Tyr	Thr	Asp	Arg	Lys	Lys	Ser	Lys	
		115				120					125					
Phe	Asn	Leu	Lys	Ser	Lys	Leu	Lys	Glu	Gln	Val	Glu	Gly	Ser	Pro	Ser	
	130					135					140					
Trp	Leu															
145																

(2) INFORMATION FOR SEQ ID NO:3669:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 790 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..790

(D) OTHER INFORMATION: / Ceres Seq. ID 1577737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3669:

tatttttcta	agcatggaag	ggtggttgg	tgccatgttg	ttcttgaacc	ccatacacgt	60
gtttcccgtg	gatttgcctt	tgtcagcatg	gacactgttg	aagaagcgga	sswtgcataa	120
agtatcttaa	tggttctgta	atggaaggtc	gaaacatcac	agttgaaaag	tcacgccgtg	180
gtcgcccaag	gacaccaact	cctggaagct	atcttggcca	tcggtacgag	cgtagggagc	240
gtgggaggtt	ccatagaggc	tatggtggtg	ggcgtgatga	gtattacggc	aatggcggcg	300
gcgggtatgg	ctaccgcagG	tctccgcctc	ccatgtactc	ttcctacagg	gagagtcggg	360
attattatcc	ctcctacaag	gacagccggg	actaccctcc	ctacagggac	ggcagggact	420
actctcctcc	ccacagggac	cctcgggact	actacgaaag	caggggtggc	cggggctact	480
cgccgcctcc	ttatggtggt	ggtaggtcaa	ggagggaccg	antcggtttc	accgtatcgg	540
atgccagaaa	ggggctacgg	tggaggccgc	cgggtgggtg	gcggcggata	tgacaggtaa	600
tgtagaggtt	ttctctccgc	cgggtggctgc	tgctgcgatg	gctgcgtatg	gctctcgcag	660
ctctggtgat	atggttagac	tgctgcctgt	agctgtgtac	ttggtgtact	gtcttcccgc	720
gtatgtggat	ttggtgaaaa	cttctgtatg	agcacctttt	atttgtagcc	tgcaatgatt	780
ccttcttaag						

(2) INFORMATION FOR SEQ ID NO:3670:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1577738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3670:

Met	Glu	Gly	Arg	Asn	Ile	Thr	Val	Glu	Lys	Ser	Arg	Arg	Gly	Arg	Pro
1				5					10					15	
Arg	Thr	Pro	Thr	Pro	Gly	Ser	Tyr	Leu	Gly	His	Arg	Tyr	Glu	Arg	Arg
				20				25					30		
Glu	Arg	Gly	Arg	Phe	His	Arg	Gly	Tyr	Gly	Gly	Gly	Arg	Asp	Glu	Tyr
				35				40					45		
Tyr	Gly	Asn	Gly	Gly	Gly	Gly	Tyr	Gly	Tyr	Arg	Arg	Ser	Pro	Pro	Pro
							55				60				
Met	Tyr	Ser	Ser	Tyr	Arg	Glu	Ser	Arg	Asp	Tyr	Tyr	Pro	Ser	Tyr	Lys
65					70				75					80	
Asp	Ser	Arg	Asp	Tyr	Pro	Pro	Tyr	Arg	Asp	Gly	Arg	Asp	Tyr	Ser	Pro
				85					90					95	
Pro	His	Arg	Asp	Pro	Arg	Asp	Tyr	Tyr	Glu	Ser	Arg	Gly	Gly	Arg	Gly
				100				105					110		
Tyr	Ser	Pro	Pro	Pro	Tyr	Gly	Gly	Arg	Ser	Arg	Arg	Arg	Asp	Arg	Xaa
				115			120				125				
Gly	Phe	Thr	Val	Ser	Asp	Ala	Arg	Lys	Gly	Leu	Arg	Trp	Arg	Pro	Pro
				130		135					140				
Gly	Gly	Trp	Arg	Arg	Ile										
145					150										

(2) INFORMATION FOR SEQ ID NO:3671:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1577739

005890004-104200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3671:
Met Val Val Gly Val Met Ser Ile Thr Ala Met Ala Ala Gly Met
1 5 10 15
Ala Thr Ala Gly Leu Arg Leu Pro Cys Thr Leu Pro Thr Gly Arg Val
20 25 30
Gly Ile Ile Ile Pro Pro Thr Arg Thr Ala Gly Thr Thr Leu Pro Thr
35 40 45
Gly Thr Ala Gly Thr Thr Leu Leu Pro Thr Gly Thr Leu Gly Thr Thr
50 55 60
Thr Lys Ala Gly Val Ala Gly Ala Thr Arg Arg Leu Leu Met Val Val
65 70 75 80
Val Gly Gln Gly Gly Thr Xaa Ser Val Ser Pro Tyr Arg Met Pro Glu
85 90 95
Arg Gly Tyr Gly Gly Gly Arg Arg Val Gly Gly Gly Gly Tyr Asp Arg
100 105 110

(2) INFORMATION FOR SEQ ID NO:3672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1577740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3672:

Met Ser Ile Thr Ala Met Ala Ala Ala Gly Met Ala Thr Ala Gly Leu
1 5 10 15
Arg Leu Pro Cys Thr Leu Pro Thr Gly Arg Val Gly Ile Ile Ile Pro
20 25 30
Pro Thr Arg Thr Ala Gly Thr Thr Leu Pro Thr Gly Thr Ala Gly Thr
35 40 45
Thr Leu Leu Pro Thr Gly Thr Leu Gly Thr Thr Thr Lys Ala Gly Val
50 55 60
Ala Gly Ala Thr Arg Arg Leu Leu Met Val Val Val Gly Gln Gly Gly
65 70 75 80
Thr Xaa Ser Val Ser Pro Tyr Arg Met Pro Glu Arg Gly Tyr Gly Gly
85 90 95
Gly Arg Arg Val Gly Gly Gly Gly Tyr Asp Arg
100 105

(2) INFORMATION FOR SEQ ID NO:3673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 926 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..926

(D) OTHER INFORMATION: / Ceres Seq. ID 1577749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3673:

aaaagatctc agccgccgctc gtctccgctcg ctccgccgca cctcccccca tcaccgcctc	60
actaaaaccc taatccctag ccgccatggc ggctgttgcg gcggccacct cgcacctcct	120
acgccaccac cgcaaccccc accttctcct cctccgcgca gantnctcat cctcccgctgc	180
tttaccgccag cagccggagc tgtccccga cccgaccgcc ggcacccccg acctcgccgg	240
cgcgccccca ctccctcaa accccagcac ggggagcccc ttctacacc agaactggcg	300
caaccagcc gcmgccaacc cgsmctctc gcttctgcmc amcgctcgtc cmggmagcmc	360

(2) INFORMATION FOR SEQ ID NO:3674:

(A) LENGTH: 202 amino acids

(C) STRANDEDNESS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1577750

Lys	Arg	Ser	Gln	Pro	Pro	Ser	Ser	Pro	Ser	Leu	Arg	Arg	Thr	Ser	Pro
1			5						10					15	
His	His	Arg	Leu	Thr	Lys	Thr	Leu	Ile	Pro	Ser	Arg	His	Gly	Gly	Cys
			20					25					30		
Cys	Gly	Gly	His	Leu	Ala	Pro	Pro	Thr	Pro	Pro	Pro	Gln	Pro	Pro	Pro
		35				40						45			
Ser	Pro	Pro	Pro	Arg	Arg	Xaa	Leu	Ile	Leu	Pro	Cys	Phe	Thr	Pro	Ala
	50					55					60				
Ala	Gly	Ala	Val	Pro	Arg	Pro	Asp	Arg	Arg	His	Pro	Arg	Pro	Arg	Arg
65				70						75					80
Arg	Gly	Pro	Thr	Pro	Ser	Lys	Pro	Gln	His	Gly	Glu	Pro	Leu	Leu	His
				85					90					95	
Pro	Glu	Leu	Ala	Gln	Pro	Ser	Arg	Xaa	Gln	Pro	Xaa	Leu	Leu	Ala	Ser
			100					105					110		
Xaa	Xaa	Arg	Arg	Arg	Xaa	Xaa	Xaa	Leu	Arg	Gly	Ala	Ala	Leu	His	Gly
		115				120						125			
Arg	Leu	Leu	Arg	Cys	Thr	Arg	Arg	His	Gly	Ala	Gln	Gly	Asp	Val	Arg
	130					135					140				
Gln	Val	Tyr	Gly	Gly	Ala	Ala	Val	Gly	Arg	His	Glu	Ala	Pro	Val	Arg
145					150					155					160
Pro	Leu	Gly	Ala	Leu	Pro	Arg	Arg	Arg	His	Gly	Glu	Ala	Gln	Pro	Pro
				165					170					175	
Arg	Arg	Arg	Pro	Leu	Gln	Ser	Leu	Pro	Pro	Arg	Gln	Pro	His	Asp	Gln
			180					185					190		
Gly	Pro	Ala	Ala	Arg	Asp	Ala	Arg	Ser	Arg						
		195					200								

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3675:

Met Ala Ala Val Ala Ala Ala Thr Ser His Leu Leu Arg His His Arg

1 5 10 15
Asn Pro His Leu Leu Leu Arg Ala Xaa Xaa Ser Ser Ser Arg Ala
20 25 30
Leu Pro Gln Gln Pro Glu Leu Ser Pro Asp Pro Thr Ala Gly Thr Pro
35 40 45
Asp Leu Ala Gly Ala Ala Pro Leu Pro Pro Asn Pro Ser Thr Gly Ser
50 55 60
Pro Phe Tyr Thr Gln Asn Trp Arg Asn Pro Ala Xaa Ala Asn Pro Xaa
65 70 75 80
Ser Ser Leu Leu Xaa Xaa Val Val Xaa Xaa Ser Xaa Phe Gly Ala Gln
85 90 95
His Phe Met Ala Ala Phe Tyr Asp Ala Pro Asp Val Thr Gly Leu Lys
100 105 110
Glu Thr Phe Ala Lys Tyr Met Ala Glu Gln Arg Trp Glu Asp Met Lys
115 120 125
His Leu Phe Asp His Trp Val Arg Ser Leu Asp Ala Ala Thr Gly Lys
130 135 140
Pro Asn His Pro Asp Val Asp Leu Phe Asn His Tyr Leu Arg Ala Asn
145 150 155 160
Leu Met Thr Arg Ala Leu Pro His Glu Met Leu Asp Leu Ala Asp His
165 170 175
Met Leu Glu Phe Glu Leu Gln Pro Asn Thr Ala Ser Tyr Asn Leu Val
180 185 190
Leu Lys Ser Met Val Ala Ser Gln Glu Thr Glu Gly Ala Glu Lys Leu
195 200 205
Ile Glu Arg
210

(2) INFORMATION FOR SEQ ID NO:3676:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1577752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3676:

Met Ala Ala Phe Tyr Asp Ala Pro Asp Val Thr Gly Leu Lys Glu Thr
1 5 10 15
Phe Ala Lys Tyr Met Ala Glu Gln Arg Trp Glu Asp Met Lys His Leu
20 25 30
Phe Asp His Trp Val Arg Ser Leu Asp Ala Ala Thr Gly Lys Pro Asn
35 40 45
His Pro Asp Val Asp Leu Phe Asn His Tyr Leu Arg Ala Asn Leu Met
50 55 60
Thr Arg Ala Leu Pro His Glu Met Leu Asp Leu Ala Asp His Met Leu
65 70 75 80
Glu Phe Glu Leu Gln Pro Asn Thr Ala Ser Tyr Asn Leu Val Leu Lys
85 90 95
Ser Met Val Ala Ser Gln Glu Thr Glu Gly Ala Glu Lys Leu Ile Glu
100 105 110
Arg

(2) INFORMATION FOR SEQ ID NO:3677:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1017 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..1017

(D) OTHER INFORMATION: / Ceres Seq. ID 1577771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3677:

(X1) SEQUENCE	DESCRIPTION	SEQ ID NO				
cccgcctaccc	aaatctctctc	gtcccagggcg	acgccagacg	gcattccgtca	gccagcaaca	60
tctccaccac	accctccccg	tcctccgacga	agaagcacag	cggagaggcg	gccgaagccg	120
acgcctcacc	aagtcaccag	tagctttctcc	gcgctcgtgc	gsccttcccg	cacttggtatg	180
ctcctgcgcg	cggcgccctag	agcggcgggcc	gtctagcggg	cgcccggagg	tgaaccacc	240
gatggccgac	gctctccttc	cacgcgcgtt	cctcgcgcgg	ttgtcagtcg	tatccggagc	300
ctcttcatca	gcctcttctgt	ccccgcctgt	tctttgggtg	ctctcgtcgc	cgggtccccc	360
gcgcmggccg	cgcctggcgg	cgggntcacc	cgcaaccccg	gcmtgcgcgn	ttcactcggc	420
acaagctctg	cgggacagct	ttggagaacc	ctgatataatt	gtttctaaaa	gtgaattttg	480
atgaaaacaa	acctatgtgc	aaacgactga	atgtcaaagt	cCttccctttc	ttccattttt	540
atcgtggagc	tgacgggcta	cttgaggctt	tctcctgttc	cttagctaag	tttcagaagc	600
tgaaggatgc	cattgcaatg	cacaacactg	ctcgtttgcag	cattggtcca	cctggtggag	660
ttggcgatgt	tgacttgctg	gataacgcga	gcctcgaaga	gaaacctcga	gaagctagcc	720
cacggtagat	tcatgagaat	gagctccacc	tcatccactt	ctacgtcctg	ctcattgttt	780
tcttccactat	agatctcaat	gtaatcagtt	gtggagaaca	taagtagcct	cgtttcatga	840
atcagatgta	tggattattg	taacgcattc	ttgaaaggga	aaaacatgta	ttatagcgtg	900
ataactgtac	cttttgtggt	tgttgtacag	aaccatagaa	ttgtacttca	ttttaggtga	960
agacgccttt	gaacatttaa	gtcccttgt	gggccgtttt	atagagtcag	tcagtc	

(2) INFORMATION FOR SEQ ID NO:3678:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1577772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3678:

	(X1)	SEQUENCE DESCRIPTION																	
Pro 1	Leu	Pro	Lys	Ser	Leu	Arg	Pro	Arg	Arg	Gln	Thr	Ala	Ser	Val					
				5						10									
Ser	Gln	Gln	His	Leu	His	His	Thr	Leu	Pro	Val	Pro	Asp	Glu	Glu	Ala				
				20						25									
Gln	Arg	Arg	Gly	Gly	Arg	Ser	Arg	Arg	Leu	Thr	Lys	Ser	Pro	Val	Ala				
				35						40									
Ser	Pro	Arg	Ser	Cys	Xaa	Leu	Pro	Ala	Leu	Gly	Cys	Ser	Leu	Arg	Arg				
				50						55									
Arg	Leu	Glu	Arg	Arg	Pro	Ser	Ser	Gly	Arg	Pro	Glu	Val	Asn	Pro	Pro				
				65						70									
Met	Ala	Asp	Ala	Leu	Leu	Pro	Arg	Arg	Phe	Leu	Ala	Pro	Leu	Ser	Val				
				85						90									
Val	Ser	Gly	Ala	Ser	Ser	Ser	Ala	Ser	Ser	Ser	Pro	Pro	Cys	Leu	Trp				
				100						105									
Val	Leu	Ser	Ser	Pro	Gly	Ser	Pro	Arg	Xaa	Pro	Arg	Leu	Ala	Ala	Xaa				
				115						120									
Ser	Pro	Ala	Thr	Pro	Xaa	Ser	Pro	Xaa	His	Ser	Ala	Gln	Ala	Leu	Pro				
				130						135									
Asp	Ser	Phe	Gly	Glu	Pro														
				145						150									

(2) INFORMATION FOR SEQ ID NO:3679:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..77
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3679:

```
Met Cys Lys Arg Leu Asn Val Lys Val Leu Pro Phe Phe His Phe Tyr
1           5           10           15
Arg Gly Ala Asp Gly Leu Leu Glu Ala Phe Ser Cys Ser Leu Ala Lys
          20          25          30
Phe Gln Lys Leu Lys Asp Ala Ile Ala Met His Asn Thr Ala Arg Cys
          35          40          45
Ser Ile Gly Pro Pro Val Gly Val Gly Asp Val Asp Leu Leu Asp Asn
          50          55          60
Ala Ser Pro Gln Glu Lys Pro Ala Glu Ala Ser Pro Arg
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:3680:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 792 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..792
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3680:

```
aagatttgcc ttggcttgcc gtgccctgcg ggagccaagc caaggacggc tagcgctcgc      60
cacgcgcgat gtccgggctt cctccggccg cgcgaccgct gctaccgtct ccctgcgcct      120
cttccctccgt tggttcggcg aaggcagcgt cggcatgctg ctccagccta aagcagtcgc      180
gcccaggccg aagtgtctgcc gccccttcca ccgtcgccgc gcgtcaggcc gcgcccgtct      240
tggtctggcg gctcgtcctt gtagcggcac cccctggcct gctgtctgct atctcaccag      300
catttgcaca gccagtttca gaaggcgag Cgctgttccg gaaggcttgt attggttgcc      360
atgacatggg aggaacatt ctacagccag gagccactct tttcctgaag gacctcgaga      420
gaaacggagt tgccacggag gaggaactgt ataacatcac atactatggg aaaggaagaa      480
tgcccgggtt tggagagaaa tgcaccccaa gaggacagt cacCttcggc ccccggtat      540
cggaagacga catcaagatc ctagtcttgt ttgtcaagtc gcaagcccag aacgggtggc      600
cgaagattga gggggatgga gattgatcaa actgaaaaaa cgatgagaag acggtgcttg      660
ttagtcagat gaaaatggtg acgggaagat agtgtttgta tagtttagga atctggtctt      720
tctgaacttg taacctttta gtctctgttt ctgaactgaa cttgtaacct tctggtccgt      780
gtttcagttt tc
```

(2) INFORMATION FOR SEQ ID NO:3681:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..120
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3681:

```
Arg Phe Ala Leu Ala Cys Arg Ala Leu Arg Glu Pro Ser Gln Gly Arg
1           5           10           15
Leu Ala Leu Ala Thr Arg Asp Val Arg Ala Ser Ser Gly Arg Ala Thr
          20          25          30
Ala Ala Thr Val Ser Leu Arg Leu Phe Leu Arg Cys Ser Gly Glu Gly
          35          40          45
Ser Val Gly Met Leu Leu Gln Pro Lys Ala Val Ala Pro Arg Pro Lys
```

00000000-00000000

50 55 60
Cys Cys Arg Pro Phe His Arg Arg Arg Ala Ser Gly Arg Ala Ala Leu
65 70 75 80
Gly Cys Gly Ala Arg Pro Cys Ser Gly Thr Pro Trp Pro Ala Cys Cys
85 90 95
Tyr Leu Thr Ser Ile Cys Thr Ala Ser Phe Arg Arg Arg Ser Ala Val
100 105 110
Pro Glu Gly Leu Tyr Trp Leu Pro
115 120

(2) INFORMATION FOR SEQ ID NO:3682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..185
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3682:

Met Ser Gly Leu Pro Pro Ala Ala Arg Pro Leu Leu Pro Ser Pro Cys
1 5 10 15
Ala Ser Ser Ser Val Val Arg Ala Lys Ala Ala Ser Ala Cys Cys Ser
20 25 30
Ser Leu Lys Gln Ser Arg Pro Gly Arg Ser Ala Ala Ala Pro Ser Thr
35 40 45
Val Ala Ala Arg Gln Ala Ala Pro Leu Leu Ala Ala Leu Val Leu
50 55 60
Val Ala Ala Pro Pro Gly Leu Pro Ala Ala Ile Ser Pro Ala Phe Ala
65 70 75 80
Gln Pro Val Ser Glu Gly Ala Ala Leu Phe Arg Lys Ala Cys Ile Gly
85 90 95
Cys His Asp Met Gly Gly Asn Ile Leu Gln Pro Gly Ala Thr Leu Phe
100 105 110
Leu Lys Asp Leu Glu Arg Asn Gly Val Ala Thr Glu Glu Leu Tyr
115 120 125
Asn Ile Thr Tyr Tyr Gly Lys Gly Arg Met Pro Gly Phe Gly Glu Lys
130 135 140
Cys Thr Pro Arg Gly Gln Cys Thr Phe Gly Pro Arg Leu Ser Glu Asp
145 150 155 160
Asp Ile Lys Ile Leu Ala Leu Phe Val Lys Ser Gln Ala Gln Asn Gly
165 170 175
Trp Pro Lys Ile Glu Gly Asp Gly Asp
180 185

(2) INFORMATION FOR SEQ ID NO:3683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..923
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3683:

atagccttt tctgcwgcg ctgcatttc cactgcgctc aagaaacgaa acccagctgc 60
accagcaact tctgccagca gacccaacga ccgaagcttt tttttccctt tcttttcac 120
gccgcgctc ggggttcaag gttcagcgcg tccccgaatg acgggcacgt acgargcctc 180
cgaccgtcct cctcctccca actccgcccg ccaccggacc gacaaagtcc ggcggaagcg 240

(2) INFORMATION FOR SEQ ID NO:3684:

(A) LENGTH: 263 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..263

(D) OTHER INFORMATION: / Ceres Seq. ID 1577788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3684:

(2) INFORMATION FOR SEQ ID NO:3685:

(A) LENGTH: 231 amino acids

[illegible]

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..231
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577789
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3685:

Tyr Ala Phe Ser Xaa Ala Ala Ala Ser Thr Arg Val Lys Lys Arg
1 5 10 15
Asn Pro Ala Ala Pro Ala Thr Ser Ala Ser Arg Pro Asn Asp Arg Ser
 20 25 30
Phe Phe Phe Pro Phe Phe Ser Ser Pro Pro Leu Gly Val Gln Gly Ser
 35 40 45
Ala Arg Pro Arg Met Thr Gly Thr Tyr Xaa Ala Ser Asp Arg Pro Pro
 50 55 60
Pro Pro Asn Ser Ala Gly His Arg Thr Asp Lys Val Arg Arg Lys Arg
65 70 75 80
Leu Thr Ala Gln Lys Arg Lys Glu Ile Lys Glu Ala Phe Asp Leu Phe
 85 90 95
Asp Ile Asp Gly Ser Gly Thr Ile Asp Ala Arg Glu Leu Asn Val Ala
 100 105 110
Met Arg Ala Leu Gly Phe Glu Met Thr Pro Glu Gln Ile Gly Gln Met
 115 120 125
Ile Ala Glu Val Asp Lys Asp Gly Ser Gly Thr Ile Asp Phe Asp Glu
 130 135 140
Phe Val His Met Met Thr Asp Lys Met Gly Glu Arg Asp Ala Arg Asp
145 150 155 160
Glu Leu His Lys Ala Phe Arg Ile Ile Asp Gln Asp Ala Asn Gly Lys
 165 170 175
Ile Ser Asp Met Asp Ile Gln Arg Leu Ala Ile Glu Thr Gly Glu His
 180 185 190
Phe Thr Leu Asp Glu Val Arg Glu Met Ile Glu Ala Ala Asp Glu Asp
 195 200 205
Gly Asp Gly Glu Ile Asp Leu Glu Glu Phe Met Lys Met Met Lys Arg
210 215 220
Thr Asp Phe Gly Ser Gly Phe
225 230

(2) INFORMATION FOR SEQ ID NO:3686:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 179 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..179
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577790
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3686:

Met Thr Gly Thr Tyr Xaa Ala Ser Asp Arg Pro Pro Pro Pro Asn Ser
1 5 10 15
Ala Gly His Arg Thr Asp Lys Val Arg Arg Lys Arg Leu Thr Ala Gln
 20 25 30
Lys Arg Lys Glu Ile Lys Glu Ala Phe Asp Leu Phe Asp Ile Asp Gly
 35 40 45
Ser Gly Thr Ile Asp Ala Arg Glu Leu Asn Val Ala Met Arg Ala Leu
50 55 60
Gly Phe Glu Met Thr Pro Glu Gln Ile Gly Gln Met Ile Ala Glu Val
65 70 75 80

Asp Lys Asp Gly Ser Gly Thr Ile Asp Phe Asp Glu Phe Val His Met
85 90 95
Met Thr Asp Lys Met Gly Glu Arg Asp Ala Arg Asp Glu Leu His Lys
100 105 110
Ala Phe Arg Ile Ile Asp Gln Asp Ala Asn Gly Lys Ile Ser Asp Met
115 120 125
Asp Ile Gln Arg Leu Ala Ile Glu Thr Gly Glu His Phe Thr Leu Asp
130 135 140
Glu Val Arg Glu Met Ile Glu Ala Ala Asp Glu Asp Gly Asp Gly Glu
145 150 155 160
Ile Asp Leu Glu Glu Phe Met Lys Met Met Lys Arg Thr Asp Phe Gly
165 170 175
Ser Gly Phe

(2) INFORMATION FOR SEQ ID NO:3687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..729
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3687:

accaggcacg	ccagcctcac	tccccagacc	acctcacacg	cacgaagcat	cagcagtgga	60
ctggactagc	tctaggtggg	caacatgaag	cttcagacca	ccgtcaccgt	tgctggcctc	120
ctcctcttcc	tctcctctct	ggcgctgcct	tccctccgsg	tctccatggc	tggatcaggg	180
ttctgcgamg	gctgcaagga	cgagttcgtc	gcgtgggaga	agtgcgtgga	ggagacggat	240
gcgcgggatg	ccagcattga	cgctcgtggag	cggtgccaag	acgtcacggc	Cgcgctgcgg	300
aagGtgGcat	ggacgcgGca	cgccgcctac	tacgagccta	tcctccgggc	cgagcgcgcc	360
atggctgcgg	acctcgnagc	tttcaggccc	aagaagccgc	ctccgactcc	gcggcgctcg	420
aggaaggcca	gaaggaggcg	gcagcggcgg	ccgaggcagc	gccgcgtccg	tcagacgaag	480
gccagaataa	gcaggtggct	gaggcggcag	ttgctggagga	gagcagagat	cctgcagcct	540
gattgggcga	aaaaaggcag	cggcgctcttc	aattttttgt	gagggatttg	aggatatgaa	600
ttccgtttgt	accttaggag	agcatcaatt	aacattttgt	gagggggata	gatttctgtc	660
cttttctctt	tacatgaaac	atgtgattct	attgattgaa	aaccaaaatt	gtccactttt	720

gccagatgc

(2) INFORMATION FOR SEQ ID NO:3688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3688:

Gln Ala Arg Gln Pro His Ser Pro Asp His Leu Thr Arg Thr Lys His	
1 5 10 15	
Gln Gln Trp Thr Gly Leu Ala Leu Gly Gly Gln His Glu Ala Ser Asp	
20 25 30	
His Arg His Arg Cys Trp Pro Pro Pro Leu Pro Pro Pro Pro Gly Ala	
35 40 45	
Ala Phe Pro Pro Xaa Leu His Gly Trp Ile Arg Val Leu Arg Xaa Leu	
50 55 60	
Gln Gly Arg Val Arg Arg Val Gly Glu Val Arg Gly Gly Asp Gly Cys	
65 70 75 80	

Arg Gly Cys Gln His
85

(2) INFORMATION FOR SEQ ID NO:3689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3689:

Met Lys Leu Gln Thr Thr Val Thr Val Ala Gly Leu Leu Leu Phe Leu
1 5 10 15
Leu Leu Leu Ala Leu Pro Ser Leu Xaa Val Ser Met Ala Gly Ser Gly
20 25 30
Phe Cys Xaa Gly Cys Lys Asp Glu Phe Val Ala Trp Glu Lys Cys Val
35 40 45
Glu Glu Thr Asp Ala Ala Asp Ala Ser Ile Asp Val Val Glu Arg Cys
50 55 60
Gln Asp Val Thr Ala Ala Leu Arg Lys Val Ala Trp Thr Arg His Ala
65 70 75 80
Xaa Tyr Tyr Glu Pro Ile Leu Arg Ala Glu Arg Ala Met Ala Ala Asp
85 90 95
Leu Xaa Ala Phe Arg Pro Lys Lys Pro Pro Pro Thr Pro Arg Arg Arg
100 105 110
Arg Lys Ala Arg Arg Arg Arg Gln Arg Arg Pro Arg Gln Arg Arg Val
115 120 125
Arg Gln Thr Lys Ala Arg Ile Ser Arg Trp Leu Arg Arg Gln Leu Arg
130 135 140
Arg Arg Ala Glu Ile Leu Gln Pro Asp Trp Ala Lys Lys Gly Ser Gly
145 150 155 160
Val Phe Asn Phe Leu
165

(2) INFORMATION FOR SEQ ID NO:3690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3690:

Met Ala Gly Ser Gly Phe Cys Xaa Gly Cys Lys Asp Glu Phe Val Ala
1 5 10 15
Trp Glu Lys Cys Val Glu Glu Thr Asp Ala Ala Asp Ala Ser Ile Asp
20 25 30
Val Val Glu Arg Cys Gln Asp Val Thr Ala Ala Leu Arg Lys Val Ala
35 40 45
Trp Thr Arg His Ala Xaa Tyr Glu Pro Ile Leu Arg Ala Glu Arg
50 55 60
Ala Met Ala Ala Asp Leu Xaa Ala Phe Arg Pro Lys Lys Pro Pro Pro
65 70 75 80
Thr Pro Arg Arg Arg Arg Lys Ala Arg Arg Arg Arg Gln Arg Arg Pro
85 90 95
Arg Gln Arg Arg Val Arg Gln Thr Lys Ala Arg Ile Ser Arg Trp Leu

100 105 110
Arg Arg Gln Leu Arg Arg Arg Ala Glu Ile Leu Gln Pro Asp Trp Ala
115 120 125
Lys Lys Gly Ser Gly Val Phe Asn Phe Leu
130 135

(2) INFORMATION FOR SEQ ID NO:3691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..440
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3691:

aactcgagcc aaacccctc aactcaactg ctgaacgcag agttcgatct agcacgcgca	60
gCGgcgNcc gctgccaca atggcgctccc ttttcaagga cccgagcaag ctctcagcgt	120
acagggaccg ccgattcaag ggcacacagg aggagtatga ggcaacgctg catgcgtcga	180
caacgctgta cattgggaat atgtccttct acaccacgga ggagcaggcc ttgcttgacg	240
cgaaatgctt caagtgaagt tgcttgctg gagacagaac tgtttagccc ttgaatttgc	300
ctatggaaga gtttgccctt ttactagtgt cgatgttgat ctggtatacc ttgctatgaa	360
ctggttaaag tttgtgctgg tttgggattt ttttgtgcat cttgtgatac ctcaagtctt	420
catcatttaa atgtttagcc	

(2) INFORMATION FOR SEQ ID NO:3692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3692:

Asn Ser Ser Gln Thr Pro Ser Thr Gln Leu Leu Asn Ala Glu Phe Asp	
1 5 10 15	
Leu Ala Arg Ala Ala Ala Xaa Arg Cys Pro Gln Trp Arg Pro Phe Ser	
20 25 30	
Arg Thr Arg Ala Ser Ser Gln Arg Thr Gly Thr Ala Asp Ser Arg Ala	
35 40 45	
His Arg Arg Ser Met Arg Gln Arg Cys Met Arg Arg Gln Arg Cys Thr	
50 55 60	
Leu Gly Ile Cys Pro Ser Thr Pro Arg Arg Ser Arg Pro Cys Leu Thr	
65 70 75 80	
Arg Asn Ala Ser Ser Glu Cys Ala Cys Leu Glu Thr Glu Leu Phe Ser	
85 90 95	
Pro	

(2) INFORMATION FOR SEQ ID NO:3693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1577815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3693:

Leu Glu Pro Asn Pro Leu Asn Ser Thr Ala Glu Arg Arg Val Arg Ser
1 5 10 15
Ser Thr Arg Ser Gly Xaa Pro Leu Pro Thr Met Ala Ser Leu Phe Lys
20 25 30
Asp Pro Ser Lys Leu Ser Ala Tyr Arg Asp Arg Arg Phe Lys Gly Thr
35 40 45
Gln Glu Glu Tyr Glu Ala Thr Leu His Ala Ser Thr Leu Tyr Ile
50 55 60
Gly Asn Met Ser Phe Tyr Thr Thr Glu Glu Gln Ala Leu Leu Asp Ala
65 70 75 80
Lys Cys Phe Lys

(2) INFORMATION FOR SEQ ID NO:3694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61

(D) OTHER INFORMATION: / Ceres Seq. ID 1577816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3694:

Met Leu Gln Val Ser Val Leu Ala Trp Arg Gln Asn Cys Leu Ala Leu
1 5 10 15
Glu Phe Ala Tyr Gly Arg Val Cys Pro Phe Thr Ser Val Asp Val Asp
20 25 30
Leu Val Tyr Leu Ala Met Asn Trp Leu Lys Phe Val Leu Val Trp Asp
35 40 45
Phe Phe Val His Leu Val Ile Pro Gln Val Phe Ile Ile
50 55 60

(2) INFORMATION FOR SEQ ID NO:3695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..843

(D) OTHER INFORMATION: / Ceres Seq. ID 1577817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3695:

agacactgac accgtttcgaa gcaaaaagag cgaacacgag cacgaacaca agcgcagagc 60
agccaagcgc cacacacacg ccgacgcgaa ccaaccaacc agctggtagt aggttcgccg 120
cgctgacgat gatgcctcgc cgcgcccttc tcttcgccgc ggtgctcctc gcggcctccg 180
ccgccgcggt ctccgggttc cacctgggag gggacgagag cggctctcgt aggggtgtgc 240
tcgcCGcgct ccgcgagcga gccgaggccg aggacgccgc tcgCttcgcc gtcgcccact 300
acaacaagaa ccagggcgcc gctttggagt ttactagggt gtcmaaacc aagcggcagg 360
tggtgaccgg gacctgcat gacctgatac tggaggcagc tgatgctgga aaaaagagtg 420
tgtacagagc aaaggtttgg gtgaagccgt ggaagattt caagtctgtc gttgagttc 480
gccttggttg agactctgaa tctgaaccgc agccttctgt tgcttctgat gttagctctg 540
ggcaagcaat tgccaaactc tctcttgaag cagatattgt acaagaagag gctcgccctgc 600
acaccattga gaatgatggg ctttccggcg atttcacatc atcatcttag gattccaggc 660
aaggatggaa agcgtaaagg tttaaaatga agatttaggt atttagagta tgtcaagctg 720
aaatgctttg ccttgtttat tggaatatgt atgtttcggt tcaaacgtgg gagcatagaa 780
ctgtatatatt cggtatttca cactgttcat ttccatgtct gtatataagg aggttcttct 840
ggc

(2) INFORMATION FOR SEQ ID NO:3696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..215
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3696:

Thr Leu Thr Pro Phe Glu Ala Lys Arg Ala Asn Thr Ser Thr Asn Thr
1 5 10 15
Ser Ala Glu Gln Pro Ser Ala Thr His Thr Pro Thr Arg Thr Asn Gln
20 25 30
Pro Ala Gly Ser Arg Phe Ala Ala Leu Thr Met Met Pro Arg Arg Ala
35 40 45
Leu Leu Phe Ala Ala Val Leu Leu Ala Ala Ser Ala Ala Val Ser
50 55 60
Gly Phe His Leu Gly Gly Asp Glu Ser Gly Leu Val Arg Gly Val Leu
65 70 75 80
Ala Ala Leu Arg Glu Arg Ala Glu Ala Glu Asp Ala Ala Arg Phe Ala
85 90 95
Val Ala His Tyr Asn Lys Asn Gln Gly Ala Ala Leu Glu Phe Thr Arg
100 105 110
Val Leu Lys Ser Lys Arg Gln Val Val Thr Gly Thr Leu His Asp Leu
115 120 125
Ile Leu Glu Ala Ala Asp Ala Gly Lys Lys Ser Val Tyr Arg Ala Lys
130 135 140
Val Trp Val Lys Pro Trp Glu Asp Phe Lys Ser Val Val Glu Phe Arg
145 150 155 160
Leu Val Gly Asp Ser Glu Ser Glu Pro Glu Pro Ser Val Ala Ser Asp
165 170 175
Val Ser Ser Gly Gln Ala Ile Ala Lys Leu Ser Leu Glu Ala Asp Ile
180 185 190
Val Gln Glu Ala Arg Leu His Thr Ile Glu Asn Asp Gly Leu Ser
195 200 205
Gly Asp Phe Thr Ser Ser Ser
210 215

(2) INFORMATION FOR SEQ ID NO:3697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..173
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3697:

Met Met Pro Arg Arg Ala Leu Leu Phe Ala Ala Val Leu Leu Ala Ala
1 5 10 15
Ser Ala Ala Ala Val Ser Gly Phe His Leu Gly Gly Asp Glu Ser Gly
20 25 30
Leu Val Arg Gly Val Leu Ala Ala Leu Arg Glu Arg Ala Glu Ala Glu
35 40 45
Asp Ala Ala Arg Phe Ala Val Ala His Tyr Asn Lys Asn Gln Gly Ala
50 55 60
Ala Leu Glu Phe Thr Arg Val Leu Lys Ser Lys Arg Gln Val Val Thr

(2) INFORMATION FOR SEQ ID NO:3698:

(A) LENGTH: 172 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1577820

(X1) SEQUENCE DESCRIPTION: 522 1000																
Met	Pro	Arg	Arg	Ala	Leu	Leu	Phe	Ala	Ala	Val	Leu	Leu	Ala	Ala	Ser	
1				5				10						15		
Ala	Ala	Ala	Val	Ser	Gly	Phe	His	Leu	Gly	Gly	Asp	Glu	Ser	Gly	Leu	
			20					25					30			
Val	Arg	Gly	Val	Leu	Ala	Ala	Leu	Arg	Glu	Arg	Ala	Glu	Ala	Glu	Asp	
		35					40					45				
Ala	Ala	Arg	Phe	Ala	Val	Ala	His	Tyr	Asn	Lys	Asn	Gln	Gly	Ala	Ala	
	50					55				60						
Leu	Glu	Phe	Thr	Arg	Val	Leu	Lys	Ser	Lys	Arg	Gln	Val	Val	Thr	Gly	
65				70					75					80		
Thr	Leu	His	Asp	Leu	Ile	Leu	Glu	Ala	Ala	Asp	Ala	Gly	Lys	Lys	Ser	
				85				90					95			
Val	Tyr	Arg	Ala	Lys	Val	Trp	Val	Lys	Pro	Trp	Glu	Asp	Phe	Lys	Ser	
			100					105					110			
Val	Val	Glu	Phe	Arg	Leu	Val	Gly	Asp	Ser	Glu	Ser	Glu	Pro	Glu	Pro	
		115					120					125				
Ser	Val	Ala	Ser	Asp	Val	Ser	Ser	Gly	Gln	Ala	Ile	Ala	Lys	Leu	Ser	
	130					135				140						
Leu	Glu	Ala	Asp	Ile	Val	Gln	Glu	Glu	Ala	Arg	Leu	His	Thr	Ile	Glu	
145				150					155					160		
Asn	Asp	Gly	Leu	Ser	Gly	Asp	Phe	Thr	Ser	Ser	Ser					
				165				170								

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 422 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..422

(D) OTHER INFORMATION: / Ceres Seq. ID 1577845

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:3059:

60
120

tg

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3700:

Lys	Glu	Arg	Glu	Arg	Gly	Arg	Gly	Arg	Asp	Trp	Arg	Glu	Ala	Pro	Ala
1				5					10					15	
Gln	Gly	Lys	Arg	Asn	Arg	Gly	Ala	Arg	Arg	Glu	Gly	Glu	Gly	Glu	Phe
			20					25					30		
Ser	Glu	Ala	Arg	Glu	Asp	Leu	Ala	Ala	Leu	Glu	Lys	Asp	Tyr	Glu	Glu
		35					40					45			
Val	Gly	Ala	Glu	Gly	Ala	Asp	Asp	Glu	Gly	Asp	Glu	Gly	Asp	Asp	Tyr
	50					55					60				

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3701:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..822

(D) OTHER INFORMATION: / Ceres Seq. ID 1577866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3702:

attccacggc	ctgtcgaccc	acaaaccacg	caaccgatat	attccccagc	acccccagtc	60
cagccgtcca	accgagacac	cgcgtgcgaa	ccaagcagac	cacagcaaga	agcgtagtcg	120
tcgccggaag	gaaaggcgcg	gasaagatgt	cgtggcaggc	gtacgtcgat	gagcacctra	180
tgtgcgarat	cgaaggacaa	catctcagcg	ccgccgscat	cgtcggtcac	gaggnacagcg	240
cttgggcgca	gtccgagagc	ttccccgart	taaagcctga	ggaggttgct	ggtatcataa	300
aggactttga	tgaacctggt	actcttgac	caactggtct	tttcgttgga	ggtacaaaagt	360
acatggtgat	ccaaggtgaa	cctggagttg	tcattccgagg	aaagaagggc	actgggggca	420
ttactatcaa	gaaaaccggc	atgtccttga	ttattggtGt	ctacgacgag	ccaatgactc	480
cagggcaatg	caacatggtg	gtggagagggc	tcggcgatta	cctgatcgag	cagggccttc	540
aaaagttcgt	catgyyctgt	tttgggtcatt	tgggcaccaa	agtttgcgcc	ycatttggtt	600
ctgtaatccg	tgagctcgtg	catgtacttg	gcgtattgca	tgcagtgaat	aatttagctt	660
gggtttgttt	gttgggggca	gtgttgggga	cggatttgga	ttgggggtta	tgcttggcat	720
cgcgtcgtat	cgaaactcag	ctgctgtttc	gctgagtaat	gtacatttcc	ctggtaatgg	780
tacttgtgga	ctctgatgct	tttaygggaa	cgagtgcatt	tt		

(2) INFORMATION FOR SEQ ID NO:3703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3703:

Ser	Thr	Ala	Cys	Arg	Pro	Thr	Asn	His	Ala	Thr	Asp	Ile	Phe	Pro	Ser
1			5					10					15		
Thr	Pro	Ser	Pro	Ala	Val	Gln	Pro	Arg	His	Arg	Val	Arg	Thr	Lys	Gln
			20					25					30		
Thr	Thr	Ala	Arg	Ser	Val	Val	Val	Ala	Gly	Arg	Lys	Gly	Ala	Xaa	Lys
			35					40					45		
Met	Ser	Trp	Gln	Ala	Tyr	Val	Asp	Glu	His	Xaa	Met	Cys	Xaa	Ile	Glu
			50					55				60			
Gly	Gln	His	Leu	Ser	Ala	Xaa	Ile	Val	Gly	His	Glu	Xaa	Ser	Ala	
			65					70					75		80
Trp	Ala	Gln	Ser	Glu	Ser	Phe	Pro	Xaa	Leu	Lys	Pro	Glu	Glu	Val	Ala
			85					90						95	
Gly	Ile	Ile	Lys	Asp	Phe	Asp	Glu	Pro	Gly	Thr	Leu	Ala	Pro	Thr	Gly
			100					105					110		
Leu	Phe	Val	Gly	Gly	Thr	Lys	Tyr	Met	Val	Ile	Gln	Gly	Glu	Pro	Gly
			115					120					125		
Val	Val	Ile	Arg	Gly	Lys	Lys	Gly	Thr	Gly	Gly	Ile	Thr	Ile	Lys	Lys
			130					135					140		
Thr	Gly	Met	Ser	Leu	Ile	Gly	Val	Tyr	Asp	Glu	Pro	Met	Thr	Pro	
			145					150					155		160
Gly	Gln	Cys	Asn	Met	Val	Val	Glu	Arg	Leu	Gly	Asp	Tyr	Leu	Ile	Glu
			165					170						175	
Gln	Gly	Phe													

(2) INFORMATION FOR SEQ ID NO:3704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131

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(D) OTHER INFORMATION: / Ceres Seq. ID 1577868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3704:

Met Ser Trp Gln Ala Tyr Val Asp Glu His Xaa Met Cys Xaa Ile Glu
1 5 10 15
Gly Gln His Leu Ser Ala Ala Xaa Ile Val Gly His Glu Xaa Ser Ala
20 25 30
Trp Ala Gln Ser Glu Ser Phe Pro Xaa Leu Lys Pro Glu Glu Val Ala
35 40 45
Gly Ile Ile Lys Asp Phe Asp Glu Pro Gly Thr Leu Ala Pro Thr Gly
50 55 60
Leu Phe Val Gly Gly Thr Lys Tyr Met Val Ile Gln Gly Glu Pro Gly
65 70 75 80
Val Val Ile Arg Gly Lys Lys Gly Thr Gly Gly Ile Thr Ile Lys Lys
85 90 95
Thr Gly Met Ser Leu Ile Ile Gly Val Tyr Asp Glu Pro Met Thr Pro
100 105 110
Gly Gln Cys Asn Met Val Val Glu Arg Leu Gly Asp Tyr Leu Ile Glu
115 120 125
Gln Gly Phe
130

(2) INFORMATION FOR SEQ ID NO:3705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1577869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3705:

Met Cys Xaa Ile Glu Gly Gln His Leu Ser Ala Ala Xaa Ile Val Gly
1 5 10 15
His Glu Xaa Ser Ala Trp Ala Gln Ser Glu Ser Phe Pro Xaa Leu Lys
20 25 30
Pro Glu Glu Val Ala Gly Ile Ile Lys Asp Phe Asp Glu Pro Gly Thr
35 40 45
Leu Ala Pro Thr Gly Leu Phe Val Gly Gly Thr Lys Tyr Met Val Ile
50 55 60
Gln Gly Glu Pro Gly Val Val Ile Arg Gly Lys Lys Gly Thr Gly Gly
65 70 75 80
Ile Thr Ile Lys Lys Thr Gly Met Ser Leu Ile Ile Gly Val Tyr Asp
85 90 95
Glu Pro Met Thr Pro Gly Gln Cys Asn Met Val Val Glu Arg Leu Gly
100 105 110
Asp Tyr Leu Ile Glu Gln Gly Phe
115 120

(2) INFORMATION FOR SEQ ID NO:3706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..371

(D) OTHER INFORMATION: / Ceres Seq. ID 1577881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3706:

atataaaagg atcgccctcc gcgcgcgcgc gctccttcgc aaaccctcct accccattcc

(2) INFORMATION FOR SEQ ID NO:3707:

(A) LENGTH: 95 amino acids

(C) STRANDEDNESS:

MOLECULE TYPE: peptid

(IX) FEATURE:

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1577882

(X1) SEQUENCE DESCRIPTION: SEQ INFORMATION																
Ile	Lys	Gly	Ser	Pro	Ser	Ala	Arg	Arg	Ser	Phe	Ala	Asn	Pro	Pro		
1				5				10				15				
Thr	Pro	Phe	Arg	Arg	Pro	Pro	Pro	Ala	Ala	Arg	Pro	Ala	Thr	Pro	Arg	
			20				25					30				
Arg	Arg	Gln	Asp	Glu	Asp	Asp	Pro	Gly	Val	Gly	Asp	Asp	Gly	His	Pro	
			35				40				45					
Gly	Gly	Arg	His	Gly	Asp	Gly	Gly	Gly	Gln	Ala	Gly	Asp	Gly	Gly	Gly	
			50			55					60					
Pro	Pro	Gly	Phe	Gly	Arg	Val	Ile	Leu	Ser	Ile	Tyr	Ser	Ile	Val	Leu	
65					70					75					80	
Pro	Phe	Ala	Ser	Val	Thr	Val	Leu	Val	Ser	Val	Leu	Pro	Leu	Asp		
				85					90					95		

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..52

(D) OTHER INFORMATION: / Ceres Seq. ID 1577883

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..800

(D) OTHER INFORMATION: / Ceres Seq. ID 1577905

(X1)	SEQUENCE	DESCRIPTION	SEQ ID NO			
ttttgatgaa	aacgtcgact	ctttttttgtc	gaatgatgat	gtagacggaa	gaggcatggt	60
tgacgacact	gaaaaagggt	cttcagagca	caatacacag	tccttaaagg	gtctctcttt	120
gagtgaagtt	ggtaacaacc	gtacaagtaa	caacaaagtt	gtttgctgtc	acttctcttc	180
agatgggaag	ttactcgcta	gtgcggcca	tgagaagaag	gtcttcctct	ggaatatgga	240
caatttttaag	atggatacca	aaatagaaga	ccatacaaac	tttatcacag	acataagatt	300
cagaactaat	tcaactcagt	tggctacatc	atcttctgac	ggaactgttc	gactttggaa	360
tgctgctgat	gaaagtggcg	ctttacaaac	ttttcatggg	cataggtctc	atgtaacatc	420
agtagatttt	cacccaagat	tgacagaggt	tctttgctct	tgcgacgaca	atggagAaaa	480
ttctcttctg	gacagttggt	cagactacat	ctactcatgt	tttgcggggtg	aagcaggggtg	540
gaactggaag	agtcaggttt	gaacctcgaa	gtgggcagct	cctcgctgtg	gcagctggaa	600
gcatggtgaa	cattttttgat	gttgaaaagc	aatccagctt	accctgtctc	gtgattcaga	660
tgctgctttc	tttcaagtga	tatgtcgatg	tagtgcgcga	gcaatgtatt	tggtttggct	720
acagctgttc	tgtcgctgtg	gcgtaaaaaca	ttagctatgt	atctatccat	atctgcatat	780
ttgaatgtat	ggtcgttttc					

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1577906

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1																
Phe 1	Asp 2	Glu 3	Asn 4	Val 5	Asp 6	Ser 7	Phe 8	Leu 9	Ser 10	Asn 11	Asp 12	Asp 13	Val 14	Asp 15	Gly 16	
Arg	Gly	Met	Phe 20	Ala	Ala	Leu	Glu	Lys 25	Gly	Ser	Ser	Glu	His 30	Asn	Thr	
Glu	Ser	Leu	Lys 35	Gly	Leu	Ser	Leu 40	Ser	Glu	Val	Gly	Asn 45	Asn	Arg	Thr	
Ser	Asn 50	Asn	Lys	Val	Val	Cys 55	Cys	His	Phe	Ser	Ser	Asp 60	Gly	Lys	Leu	
Leu 65	Ala	Ser	Ala	Gly	His 70	Glu	Lys	Lys	Val	Phe 75	Leu	Trp	Asn	Met	Asp 80	
Asn	Phe	Lys	Met	Asp 85	Thr	Lys	Ile	Glu	Asp 90	His	Thr	Asn	Phe	Ile 95	Thr	
Asp	Ile	Arg	Phe 100	Arg	Thr	Asn	Ser	Thr 105	Gln	Leu	Ala	Thr	Ser 110	Ser	Ser	
Asp	Gly	Thr 115	Val	Arg	Leu	Trp	Asn 120	Ala	Ala	Asp	Glu	Ser 125	Gly	Ala	Leu	
Gln	Thr 130	Phe	His	Gly	His	Arg 135	Ser	His	Val	Thr	Ser 140	Val	Asp	Phe	His	
Pro 145	Arg	Leu	Thr	Glu	Val 150	Leu	Cys	Ser	Cys	Asp 155	Asp	Asn	Gly	Glu	Asn 160	
Ser	Leu	Leu	Asp	Ser 165	Trp	Ser	Asp	Tyr	Ile 170	Tyr	Ser	Cys	Phe	Ala 175	Gly	
Glu	Ala	Gly	Trp 180	Asn	Trp	Lys	Ser	Gln 185	Val							

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3711:

(2) INFORMATION FOR SEQ ID NO:3712:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1577908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3712:

(2) INFORMATION FOR SEQ ID NO:3713:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 774 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..774

(D) OTHER INFORMATION: / Ceres Seq. ID 1577940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3713:

```
atatattcaa gcgcgcgcgc cagcgcgtgcc cccaaatagt acatctccct ccatgatgct      60
cgcaactcct cctagcatca ctccaccgcca ccttcacagc ggcatcatcc cgccaccggg      120
tccggggccac cgcaggagac tgcgtctccac tgcacgcgcc gccgtgaagc gagatggtgc      180
caccacggag gtagcaggcg atgaggggcg gtcgtcgtcg tgcgtcgtcg cgccgCccgc      240
cggaaagctc gaggggtgact aaggctgccg cgacggcgac cccggcgggcg ttttcgttgc      300
ccaaggacta cagccatacg ctgttccact ccgagttcct ggaggtgctg ggcctgatcg      360
acctcgagtc gctgcggaag cggccgaggc tcaccgtagg ggtgaagggtg aaggcgtccc      420
tgccgctccc ggtgctcgtg gtcctggcgg cctgtacct cgcggacgtg accagcGggt      480
cttgttgact ggacgcacatca tcacctggag ggcgacgcgc acgacgtagg ggactagtga      540
agaagggacg cctcactgc cbtgccctgc catgcccccg ctctccattg tagcggatgc      600
aggcatgcag cagcctcaac ttgcttggt aaacaatcag cttcaggaca taaactgact      660
tttagtttag tgggtgtgctt tgtaaaccct gcttttatct tactcgtctt atttctaact      720
attagatata atgtattcaa acacatcttt gaataagaaa cgatttttagt ctct
```

(2) INFORMATION FOR SEQ ID NO:3714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3714:

```
Tyr Ile Gln Ala Arg Ala Ser Ala Leu Pro Pro Asn Ser Thr Ser Pro
1      5      10      15
Ser Met Met Leu Ala Thr Pro Pro Ser Ile Thr His Arg His Leu His
      20      25      30
Ser Gly Ile Ile Pro Pro Pro Gly Pro Gly His Arg Arg Arg Leu Val
      35      40      45
Ser Thr Ala Arg Ala Ala Val Lys Arg Asp Gly Ala Thr Thr Glu Val
      50      55      60
Ala Gly Asp Glu Gly Ala Ser Ser Ser Ser Ser Ser Pro Pro Pro Ala
65      70      75      80
Gly Lys Leu Glu Gly Asp
      85
```

(2) INFORMATION FOR SEQ ID NO:3715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3715:

```
Met Met Leu Ala Thr Pro Pro Ser Ile Thr His Arg His Leu His Ser
1      5      10      15
Gly Ile Ile Pro Pro Pro Gly Pro Gly His Arg Arg Arg Leu Val Ser
      20      25      30
Thr Ala Arg Ala Ala Val Lys Arg Asp Gly Ala Thr Thr Glu Val Ala
      35      40      45
Gly Asp Glu Gly Ala Ser Ser Ser Ser Ser Ser Pro Pro Pro Ala Gly
50      55      60
Lys Leu Glu Gly Asp
65
```

(2) INFORMATION FOR SEQ ID NO:3716:

2025 RELEASE UNDER E.O. 14176

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..95
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3716:

Met Arg Ala Arg Arg Arg Arg Arg Arg Arg Arg Pro Pro Glu Ser
1 5 10 15
Ser Arg Val Thr Lys Ala Ala Ala Thr Ala Thr Pro Ala Ala Phe Ser
 20 25 30
Leu Pro Lys Asp Tyr Ser His Thr Leu Phe His Ser Glu Phe Leu Glu
 35 40 45
Val Leu Gly Leu Ile Asp Leu Glu Ser Leu Arg Lys Arg Pro Arg Leu
50 55 60
Thr Val Gly Val Thr Val Lys Ala Ser Leu Pro Leu Pro Val Leu Val
65 70 75 80
Val Leu Ala Ala Leu Tyr Leu Ala Asp Val Thr Ser Gly Ser Cys
 85 90 95

(2) INFORMATION FOR SEQ ID NO:3717:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 674 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..674
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3717:

ctcgctataa aacatgcccg cwccctgcact accactacta caaccagcgg tagtgccgg 60
catcatccgt ctcgtctcgt ctcgtctcgc ctctcctctc cttttccccc ctccctgcac 120
agcgccgctc accgtcaccg taccacagca gcgatcgatg gctgaggtag acaacgagcg 180
gcccgtgatg gtgggcgacg tccgggacgc gccggtgggc cgcgagaacg acctcgagggc 240
catcgagctC Gcgcgcttcg Cggctgcgca gcacaacagc aagaccaacg cgatgctgga 300
attcgagagg ctggtgaagg tgaggcacca ggtcgtggcc gggaccctgc accacttcac 360
cgctcagagg aaggaggccg gcggcggcga aaagaagctg tacgaggcca aggtGgtggg 420
agaaggcgtg ggagaacttc aagcagctgc agagcttcga gctcgtcgga gaNcgccgcg 480
gtcgccctgag gcgcacaggc ttttcgctgg aggctggagc acaacaatga aagaatttaa 540
ctgtcatccc actggaaaag tatgatataa tgaataaacc agcgtcttac ccacatgtat 600
tgtaccctaa tgagatatatt gaccactgta atagaatgag atgtgctaag gaatctgaaa 660
gccttcttgc tttt

(2) INFORMATION FOR SEQ ID NO:3718:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 183 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..183
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3718:

Met Pro Xaa Pro Ala Leu Pro Leu Leu Gln Pro Ala Val Val Ala Gly
1 5 10 15

Ile Ile Arg Leu Val Ser Ser Arg Leu Ala Ser Pro Leu Leu Phe Pro
20 25 30
Pro Pro Cys Thr Ala Pro Leu Thr Val Thr Val Pro Gln Gln Arg Ser
35 40 45
Met Ala Glu Val His Asn Glu Arg Pro Val Met Val Gly Asp Val Arg
50 55 60
Asp Ala Pro Val Gly Arg Glu Asn Asp Leu Glu Ala Ile Glu Leu Ala
65 70 75 80
Arg Phe Ala Val Ala Glu His Asn Ser Lys Thr Asn Ala Met Leu Glu
85 90 95
Phe Glu Arg Leu Val Lys Val Arg His Gln Val Val Ala Gly Thr Leu
100 105 110
His His Phe Thr Val Glu Val Lys Glu Ala Gly Gly Gly Glu Lys Lys
115 120 125
Leu Tyr Glu Ala Lys Val Val Gly Glu Gly Val Gly Glu Leu Gln Ala
130 135 140
Ala Ala Glu Leu Arg Ala Arg Arg Arg Xaa Pro Arg Ser Pro Glu Ala
145 150 155 160
His Arg Leu Phe Ala Gly Gly Trp Ser Thr Thr Met Lys Glu Phe Asn
165 170 175
Cys His Pro Thr Gly Lys Val
180

(2) INFORMATION FOR SEQ ID NO:3719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3719:

Met Ala Glu Val His Asn Glu Arg Pro Val Met Val Gly Asp Val Arg
1 5 10 15
Asp Ala Pro Val Gly Arg Glu Asn Asp Leu Glu Ala Ile Glu Leu Ala
20 25 30
Arg Phe Ala Val Ala Glu His Asn Ser Lys Thr Asn Ala Met Leu Glu
35 40 45
Phe Glu Arg Leu Val Lys Val Arg His Gln Val Val Ala Gly Thr Leu
50 55 60
His His Phe Thr Val Glu Val Lys Glu Ala Gly Gly Gly Glu Lys Lys
65 70 75 80
Leu Tyr Glu Ala Lys Val Val Gly Glu Gly Val Gly Glu Leu Gln Ala
85 90 95
Ala Ala Glu Leu Arg Ala Arg Arg Arg Xaa Pro Arg Ser Pro Glu Ala
100 105 110
His Arg Leu Phe Ala Gly Gly Trp Ser Thr Thr Met Lys Glu Phe Asn
115 120 125
Cys His Pro Thr Gly Lys Val
130 135

(2) INFORMATION FOR SEQ ID NO:3720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

000001-155555

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1577972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3720:

Met Val Gly Asp Val Arg Asp Ala Pro Val Gly Arg Glu Asn Asp Leu
1 5 10 15
Glu Ala Ile Glu Leu Ala Arg Phe Ala Val Ala Glu His Asn Ser Lys
20 25 30
Thr Asn Ala Met Leu Glu Phe Glu Arg Leu Val Lys Val Arg His Gln
35 40 45
Val Val Ala Gly Thr Leu His His Phe Thr Val Glu Val Lys Glu Ala
50 55 60
Gly Gly Gly Glu Lys Lys Leu Tyr Glu Ala Lys Val Val Gly Glu Gly
65 70 75 80
Val Gly Glu Leu Gln Ala Ala Ala Glu Leu Arg Ala Arg Arg Arg Xaa
85 90 95
Pro Arg Ser Pro Glu Ala His Arg Leu Phe Ala Gly Gly Trp Ser Thr
100 105 110
Thr Met Lys Glu Phe Asn Cys His Pro Thr Gly Lys Val
115 120 125

(2) INFORMATION FOR SEQ ID NO:3721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..800

(D) OTHER INFORMATION: / Ceres Seq. ID 1577981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3721:

aaaaaacctc ctgcagtcgt tttcacctcc tccctctctc acggcggcgtt ttctggcgac 60
ggcggcgcg ggcagcagca gcagccacct ggggaagagc aggtagcagg aaatggcggc 120
gttctctgagg tcaaaatggt caccagtttg acgtactttg atgggaagcc ttggaaatag 180
tttggttgagg gctgccaaact cttctgtttg ggcaataaca aggccttctc attgcatgac 240
tatcagtcag cAaaatcaga acattcatcc agatgaggac taacctgaag gtggtcgata 300
actccggggc caagcgggtg atgtgcatcc agtccctgag ggggaagaaa ggagcaaggc 360
tcggggacat gatcatcgga tccgtaaagg aggccagcc tcgtggcaag gtcaagaaaag 420
gagacgtagt ctacggcgtg gtcgtccgtg ccgccatgaa gaaaggacgc agcgatggca 480
gcgaggtcca gttcgacgac aacgcgggtg tcctcgtgaa caagaagggc gagctgatcg 540
gcacccgcgt ctttgggccc gtccccacg agctgaggaa gaagaagcac ctcaagatcc 600
tgccctggc tgaacacatt gtttgaggtg tgctgcatag ccaagtgtt gtgggaatgt 660
tttttttgt gtgttctctg tttgaataat gcattgtgaa acgatagcat ggaccgtttg 720
aactattttg atgacattgc tcgtccattt ggatggccaa tacgtgtcgt gatcgattct 780
ggagttccat tttttttgtt

(2) INFORMATION FOR SEQ ID NO:3722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1577982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3722:

Met Leu Ser Val Ser Lys Ile Arg Thr Phe Ile Gln Met Arg Thr Asn
1 5 10 15
Leu Lys Val Val Asp Asn Ser Gly Ala Lys Arg Val Met Cys Ile Gln
20 25 30

00000000-00000000

Ser Leu Arg Gly Lys Lys Gly Ala Arg Leu Gly Asp Met Ile Ile Gly
35 40 45
Ser Val Lys Glu Ala Gln Pro Arg Gly Lys Val Lys Lys Gly Asp Val
50 55 60
Val Tyr Gly Val Val Val Arg Ala Ala Met Lys Lys Gly Arg Ser Asp
65 70 75 80
Gly Ser Glu Val Gln Phe Asp Asp Asn Ala Val Val Leu Val Asn Lys
85 90 95
Lys Gly Glu Leu Ile Gly Thr Arg Val Phe Gly Pro Val Pro His Glu
100 105 110
Leu Arg Lys Lys Lys His Leu Lys Ile Leu Ala Leu Ala Glu His Ile
115 120 125
Val

(2) INFORMATION FOR SEQ ID NO:3723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3723:

Met Arg Thr Asn Leu Lys Val Val Asp Asn Ser Gly Ala Lys Arg Val
1 5 10 15
Met Cys Ile Gln Ser Leu Arg Gly Lys Lys Gly Ala Arg Leu Gly Asp
20 25 30
Met Ile Ile Gly Ser Val Lys Glu Ala Gln Pro Arg Gly Lys Val Lys
35 40 45
Lys Gly Asp Val Val Tyr Gly Val Val Val Arg Ala Ala Met Lys Lys
50 55 60
Gly Arg Ser Asp Gly Ser Glu Val Gln Phe Asp Asp Asn Ala Val Val
65 70 75 80
Leu Val Asn Lys Lys Gly Glu Leu Ile Gly Thr Arg Val Phe Gly Pro
85 90 95
Val Pro His Glu Leu Arg Lys Lys Lys His Leu Lys Ile Leu Ala Leu
100 105 110
Ala Glu His Ile Val
115

(2) INFORMATION FOR SEQ ID NO:3724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3724:

Met Cys Ile Gln Ser Leu Arg Gly Lys Lys Gly Ala Arg Leu Gly Asp
1 5 10 15
Met Ile Ile Gly Ser Val Lys Glu Ala Gln Pro Arg Gly Lys Val Lys
20 25 30
Lys Gly Asp Val Val Tyr Gly Val Val Val Arg Ala Ala Met Lys Lys
35 40 45
Gly Arg Ser Asp Gly Ser Glu Val Gln Phe Asp Asp Asn Ala Val Val

50 55 60
Leu Val Asn Lys Lys Gly Glu Leu Ile Gly Thr Arg Val Phe Gly Pro
65 70 75 80
Val Pro His Glu Leu Arg Lys Lys Lys His Leu Lys Ile Leu Ala Leu
85 90 95
Ala Glu His Ile Val
100

(2) INFORMATION FOR SEQ ID NO:3725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..747
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3725:

accaaccacc gtggccccgg caaattactc aaatttgccc ttctgtctc ggttccctct 60
tcccggcgca ccagcctacc tcgccgacgc caggccgcca cgccgccgga gacatgaacc 120
agcccgtgca gaagaacacc ctctacgtcg gtgggctggc ggaggagggtg gacgagaaga 180
tcctgcacgc cgcgttcgtg ccctttggtg aggtcaagga cgtcaagacg ccgctcgatc 240
agtccacgca gaagcaccgc tCcttcggct tcgtcacctt cctggagcgc gaggacgccg 300
ccgctgccat ggacaacatg gacggcgccg agctcttcgg ccgcgtgctt accgtcaact 360
acgccttccc cgagcgcacg aagggagggg agcagggatg ggctgcccag ccaatctggg 420
ccgatgcgga cacttggttc gagaggcagc agcaggaaga ggagatgcag cggctgcagg 480
cagagcaccg tgcagcgatg caggcagcag agaagctgca cagggagaaa ctggccgctg 540
aaaggggaagg cgagaaagaa gaagatccca tggctgccgc agaggcccag gctgtgaaac 600
aaagttctta agaaccgat atcaactcat aactcatgtg ctacgttgot gcctgtttgt 660
cagatatgac taaacgaatc ttgcgaatgc tgtttgtttt gctgaaagaa ccctatttct 720
cacctgacgt gggattctta ttggttt

(2) INFORMATION FOR SEQ ID NO:3726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..202
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3726:

Gln Pro Pro Trp Pro Arg Gln Ile Thr Gln Ile Cys Pro Ser Cys Leu
1 5 10 15
Gly Ser Leu Phe Pro Ala His Gln Pro Thr Ser Pro Thr Pro Gly Arg
20 25 30
His Ala Ala Gly Asp Met Asn Gln Pro Val Gln Lys Asn Thr Leu Tyr
35 40 45
Val Gly Gly Leu Ala Glu Glu Val Asp Glu Lys Ile Leu His Ala Ala
50 55 60
Phe Val Pro Phe Gly Glu Val Lys Asp Val Lys Thr Pro Leu Asp Gln
65 70 75 80
Ser Thr Gln Lys His Arg Ser Phe Gly Phe Val Thr Phe Leu Glu Arg
85 90 95
Glu Asp Ala Ala Ala Ala Met Asp Asn Met Asp Gly Ala Glu Leu Phe
100 105 110
Gly Arg Val Leu Thr Val Asn Tyr Ala Phe Pro Glu Arg Ile Lys Gly
115 120 125
Gly Glu Gln Gly Trp Ala Ala Gln Pro Ile Trp Ala Asp Ala Asp Thr

130 135 140
Trp Phe Glu Arg Gln Gln Glu Glu Glu Met Gln Arg Leu Gln Ala
145 150 155 160
Glu His Arg Ala Ala Met Gln Ala Ala Glu Lys Leu His Arg Glu Lys
165 170 175
Leu Ala Ala Glu Arg Glu Gly Glu Lys Glu Glu Asp Pro Met Ala Ala
180 185 190
Ala Glu Ala Gln Ala Val Lys Gln Ser Ser
195 200

(2) INFORMATION FOR SEQ ID NO:3727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3727:

Met Asn Gln Pro Val Gln Lys Asn Thr Leu Tyr Val Gly Gly Leu Ala
1 5 10 15
Glu Glu Val Asp Glu Lys Ile Leu His Ala Ala Phe Val Pro Phe Gly
20 25 30
Glu Val Lys Asp Val Lys Thr Pro Leu Asp Gln Ser Thr Gln Lys His
35 40 45
Arg Ser Phe Gly Phe Val Thr Phe Leu Glu Arg Glu Asp Ala Ala Ala
50 55 60
Ala Met Asp Asn Met Asp Gly Ala Glu Leu Phe Gly Arg Val Leu Thr
65 70 75 80
Val Asn Tyr Ala Phe Pro Glu Arg Ile Lys Gly Gly Glu Gln Gly Trp
85 90 95
Ala Ala Gln Pro Ile Trp Ala Asp Ala Asp Thr Trp Phe Glu Arg Gln
100 105 110
Gln Gln Glu Glu Met Gln Arg Leu Gln Ala Glu His Arg Ala Ala
115 120 125
Met Gln Ala Ala Glu Lys Leu His Arg Glu Lys Leu Ala Ala Glu Arg
130 135 140
Glu Gly Glu Lys Glu Glu Asp Pro Met Ala Ala Ala Glu Ala Gln Ala
145 150 155 160
Val Lys Gln Ser Ser
165

(2) INFORMATION FOR SEQ ID NO:3728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..967
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3728:

aaaactaacc ccaaacccca atccacccca tcccctctc atccactcgg ggcggccatg 60
gcctgctcct tctccgccc catcacccgtc tcttcgccc ctaccccggc cgccagaccc 120
ctcgtctgtg ccccgcatc cgtctgcac gctcgtccg cggtcgccac cactgccagg 180
ccgctccgcc tcgccgctc aaggtccgcg cgggctacca gactcgttg ccgcgccagg 240
tangtcgatg acttgccgt ggtcggaac aaggcgccag acttagaagc cgaggctgtg 300
ttcgaccagg agttcatcaa cgtgaagctc tctgattaca ttggaagaa gtacgtcatt 360

```
ctgtttcttct accccttgga tttcaccttc gtctgcmcga ccgagattAc tgcgttttagt 420
gacagatacg aggaatttga gaagttgaac actgaggttc ttggtgtttc cattgacagt 480
gtgtttctccc accttgcatg ggtgcagaca gacaggaagt cgggtgggct cggcgatctt 540
aaatacccac ttgtttctga tgtgacaaa tcaatttcaa aggccttttg tgttctgac 600
cctgaccagg gtattgcttt gagaggactg ttcattcattg acaaggaggg agtgattcag 660
cactctacca ttaacaacct tgccattggt cgtagtgtgg atgagaccat gaggaccctt 720
caggcattgc agtacgtcca ggagaacca gacgagggtg gcccggccg atggaaacca 780
ggggagaggt cgatgaagcc cgaccccaag ggaagcaaag agtacttcgc ggccatctag 840
attcgtcgtc attgagaagc aggtgcccg taagtgtcc agcagtaggt tctcgtgttc 900
agcggagctc gcgttttgac aagtgtattg tgctgatgtg catcccgatt tgagtgtctg 960
tctttgc
```

(2) INFORMATION FOR SEQ ID NO:3729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..279
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3729:

```
Lys Thr Asn Pro Lys Pro Gln Ser Thr Pro Ser Pro Pro His Pro Leu
1          5          10          15
Arg Ala Ala Met Ala Cys Ser Phe Ser Ala Ala Ile Thr Val Ser Ser
20          25          30
Ala Pro Thr Pro Ala Ala Arg Pro Leu Ala Ala Ala Pro Gln Ser Val
35          40          45
Cys Ile Ala Arg Ser Ala Val Ala Thr Thr Ala Arg Pro Leu Arg Leu
50          55          60
Ala Ala Ser Arg Ser Ala Arg Ala Thr Arg Leu Val Ala Arg Ala Arg
65          70          75          80
Xaa Val Asp Asp Leu Pro Leu Val Gly Asn Lys Ala Pro Asp Leu Glu
85          90          95
Ala Glu Ala Val Phe Asp Gln Glu Phe Ile Asn Val Lys Leu Ser Asp
100         105         110
Tyr Ile Gly Lys Lys Tyr Val Ile Leu Phe Phe Tyr Pro Leu Asp Phe
115         120         125
Thr Phe Val Cys Xaa Thr Glu Ile Thr Ala Phe Ser Asp Arg Tyr Glu
130         135         140
Glu Phe Glu Lys Leu Asn Thr Glu Val Leu Gly Val Ser Ile Asp Ser
145         150         155         160
Val Phe Ser His Leu Ala Trp Val Gln Thr Asp Arg Lys Ser Gly Gly
165         170         175
Leu Gly Asp Leu Lys Tyr Pro Leu Val Ser Asp Val Thr Lys Ser Ile
180         185         190
Ser Lys Ala Phe Gly Val Leu Ile Pro Asp Gln Gly Ile Ala Leu Arg
195         200         205
Gly Leu Phe Ile Ile Asp Lys Glu Gly Val Ile Gln His Ser Thr Ile
210         215         220
Asn Asn Leu Ala Ile Gly Arg Ser Val Asp Glu Thr Met Arg Thr Leu
225         230         235         240
Gln Ala Leu Gln Tyr Val Gln Glu Asn Pro Asp Glu Val Cys Pro Ala
245         250         255
Gly Trp Lys Pro Gly Glu Arg Ser Met Lys Pro Asp Pro Lys Gly Ser
260         265         270
Lys Glu Tyr Phe Ala Ala Ile
275
```

(2) INFORMATION FOR SEQ ID NO:3730:

(i) SEQUENCE CHARACTERISTICS:

2025 RELEASE UNDER E.O. 14176

- (A) LENGTH: 260 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..260
(D) OTHER INFORMATION: / Ceres Seq. ID 1578006
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3730:

Met Ala Cys Ser Phe Ser Ala Ala Ile Thr Val Ser Ser Ala Pro Thr
1 5 10 15
Pro Ala Ala Arg Pro Leu Ala Ala Ala Pro Gln Ser Val Cys Ile Ala
20 25 30
Arg Ser Ala Val Ala Thr Thr Ala Arg Pro Leu Arg Leu Ala Ala Ser
35 40 45
Arg Ser Ala Arg Ala Thr Arg Leu Val Ala Arg Ala Arg Xaa Val Asp
50 55 60
Asp Leu Pro Leu Val Gly Asn Lys Ala Pro Asp Leu Glu Ala Glu Ala
65 70 75 80
Val Phe Asp Gln Glu Phe Ile Asn Val Lys Leu Ser Asp Tyr Ile Gly
85 90 95
Lys Lys Tyr Val Ile Leu Phe Phe Tyr Pro Leu Asp Phe Thr Phe Val
100 105 110
Cys Xaa Thr Glu Ile Thr Ala Phe Ser Asp Arg Tyr Glu Glu Phe Glu
115 120 125
Lys Leu Asn Thr Glu Val Leu Gly Val Ser Ile Asp Ser Val Phe Ser
130 135 140
His Leu Ala Trp Val Gln Thr Asp Arg Lys Ser Gly Gly Leu Gly Asp
145 150 155 160
Leu Lys Tyr Pro Leu Val Ser Asp Val Thr Lys Ser Ile Ser Lys Ala
165 170 175
Phe Gly Val Leu Ile Pro Asp Gln Gly Ile Ala Leu Arg Gly Leu Phe
180 185 190
Ile Ile Asp Lys Glu Gly Val Ile Gln His Ser Thr Ile Asn Asn Leu
195 200 205
Ala Ile Gly Arg Ser Val Asp Glu Thr Met Arg Thr Leu Gln Ala Leu
210 215 220
Gln Tyr Val Gln Glu Asn Pro Asp Glu Val Cys Pro Ala Gly Trp Lys
225 230 235 240
Pro Gly Glu Arg Ser Met Lys Pro Asp Pro Lys Gly Ser Lys Glu Tyr
245 250 255
Phe Ala Ala Ile
260

(2) INFORMATION FOR SEQ ID NO:3731:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 828 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..828
(D) OTHER INFORMATION: / Ceres Seq. ID 1578007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3731:

agaaacagac	ctgcacggct	ccactccaac	tccctcccaa	gccccaaaggc	ggcaagcccc	60
caaccacctt	ccttttccac	atccacaccg	ccccgggttt	cctcacgcct	ccgccctccc	120
accgcgtcac	tcccgctcct	atccaccgcg	atggcctccc	gcctcgccgt	cgccgtcgcc	180
gtcgccgcgc	ccgcgtogtc	tccttccccg	gtcggcaccg	tcgccccgcm	ccgcgtcgcc	240
ctccgcccag	gcctccccgc	gacgtggcac	gctctccgcg	ccctccctcg	atcccggtggc	300

gcggccgctcg tgtgccaggc ccagggcggc caggacaccg ccatccaagt tcctgatgtg 360
agcaaatacca catggcaatc acttgtggtg gagagcgagc ttcccgCcc tcgttcagtt 420
ctgggcctca tgggtgtggac cgtgtaagat gatagacccc atcgttggca agctctcgaa 480
ggagtacgaa ggaaagctga agtggtacaa gctaaacacc gacgagaacc ctgacatcgc 540
gacccaattc ggcattccgga gcatccccac catgatgata ttcaagaatg gtgagaagaa 600
ggacgcggtg attggagccg tgccagagag caccctggtc acctgcatcg acaagtacgt 660
tgggtgggagg tgaaatctca atctgggcca ctagccttgg acttccatat gtagacggat 720
gggtatgtgt ataccgttca tatcgaactg ctgttgagta gttgtatgta gataataatg 780
tgatgctcac tccaataaat gcgattcaag gatgggcaag tcattctgg

(2) INFORMATION FOR SEQ ID NO:3732:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1578008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3732:

Arg Asn Arg Pro Ala Arg Leu His Ser Asn Ser Leu Pro Ser Pro Lys
1 5 10 15
Pro Ala Ser Pro Gln Pro Pro Ser Phe Ser Thr Ser Thr Pro Pro Arg
20 25 30
Val Ser Ser Arg Leu Arg Pro Pro Thr Arg Ser Leu Pro Ser Leu Ser
35 40 45
Thr Ala Met Ala Ser Arg Leu Ala Val Ala Val Ala Val Ala Pro
50 55 60
Ala Ser Ser Pro Ser Pro Val Gly Thr Val Ala Pro Xaa Arg Val Ala
65 70 75 80
Leu Arg Arg Gly Leu Pro Pro Thr Trp His Ala Leu Arg Ala Leu Pro
85 90 95
Arg Ser Arg Gly Ala Ala Val Val Cys Gln Ala Gln Gly Gly Gln Asp
100 105 110
Thr Ala Ile Gln Val Pro Asp Val Ser Lys Ser Thr Trp Gln Ser Leu
115 120 125
Val Val Glu Ser Glu Leu Pro Val Pro Arg Ser Val Leu Gly Leu Met
130 135 140
Val Trp Thr Val
145

(2) INFORMATION FOR SEQ ID NO:3733:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1578009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3733:

Glu Thr Asp Leu His Gly Ser Thr Pro Thr Pro Ser Gln Ala Pro Ser
1 5 10 15
Arg Gln Ala Pro Asn His Leu Pro Phe Pro His Pro His Arg Pro Gly
20 25 30
Phe Pro His Ala Ser Ala Leu Pro Pro Ala His Ser Arg Pro Tyr Pro
35 40 45
Pro Arg Trp Pro Pro Ala Ser Pro Ser Pro Ser Pro Arg Pro
50 55 60

Arg Arg Leu Leu Pro Arg Ser Ala Pro Ser Pro Arg Xaa Ala Ser Pro
65 70 75 80
Ser Ala Glu Ala Ser Arg Arg Arg Gly Thr Leu Ser Ala Pro Ser Leu
85 90 95
Asp Pro Val Ala Arg Pro Ser Cys Ala Arg Pro Arg Ala Ala Arg Thr
100 105 110
Pro Pro Ser Lys Phe Leu Met
115

(2) INFORMATION FOR SEQ ID NO:3734:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..117
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1578010
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3734:

Lys Gln Thr Cys Thr Ala Pro Leu Gln Leu Pro Pro Lys Pro Gln Ala
1 5 10 15
Gly Lys Pro Pro Thr Thr Phe Leu Phe His Ile His Thr Ala Pro Gly
20 25 30
Phe Leu Thr Pro Pro Pro Ser His Pro Leu Thr Pro Val Pro Ile His
35 40 45
Arg Asp Gly Leu Pro Pro Arg Arg Arg Arg Arg Arg Ala Arg
50 55 60
Val Val Ser Phe Pro Gly Arg His Arg Arg Pro Xaa Pro Arg Arg Pro
65 70 75 80
Pro Pro Arg Pro Pro Ala Asp Val Ala Arg Ser Pro Arg Pro Pro Ser
85 90 95
Ile Pro Trp Arg Gly Arg Arg Val Pro Gly Pro Gly Arg Pro Gly His
100 105 110
Arg His Pro Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:3735:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 628 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..628
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1578015
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3735:

atatatttga tttggaagga aaataactta agactcgtaa aggtcgtgga ggacgaggtg 60
tttcccgaag ggacggtgct gaagaagggc accaaggtgg tctacgccat gtactccatg 120
grgcgatgg agagcatctg gggcgacgac tgccgggagt acaggccgga gcggtggctc 180
cgggacggcc gcttcatgag cgagtcgcgc tacaagttca Cgccttcaa cggcgggccc 240
cgctgtgcc tcggcaagga cttcgcctac taccagatga agttcgccgc cgcctccatc 300
ctNccgCggy taccgcgtcg acgtcgtcga gggccacccc gtcgcgcccc agatggcgct 360
caccatgtac atgaagcacg gcctcaaggt cacgctgacc aagagagaca agaccaagct 420
ctgaactgtt ggtgccgagc cgagcttgcc aataagactc tgagactgaa gagagatata 480
cagtatgaaa gaagcagggc ttttcatgtt tttcatgtac atctagtata gaacttttat 540
atatatgtat agatacatat gtatatgtgt tggcaaaacg cttgaccttc aggtgatgta 600
accgtaata ttgtagcagt attatttc

(2) INFORMATION FOR SEQ ID NO:3736:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..176
 (D) OTHER INFORMATION: / Ceres Seq. ID 1578016
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3736:

Ile Tyr Leu Ile Trp Lys Glu Asn Asn Leu Arg Leu Val Lys Val Val
1 5 10 15
Glu Asp Glu Val Phe Pro Asp Gly Thr Val Leu Lys Lys Gly Thr Lys
 20 25 30
Val Val Tyr Ala Met Tyr Ser Met Xaa Arg Met Glu Ser Ile Trp Gly
 35 40 45
Asp Asp Cys Arg Glu Tyr Arg Pro Glu Arg Trp Leu Arg Asp Gly Arg
 50 55 60
Phe Met Ser Glu Ser Ala Tyr Lys Phe Thr Ala Phe Asn Gly Gly Pro
65 70 75 80
Arg Leu Cys Leu Gly Lys Asp Phe Ala Tyr Tyr Gln Met Lys Phe Ala
 85 90 95
Ala Ala Ser Ile Xaa Pro Pro Xaa Pro Arg Arg Arg Arg Arg Gly Pro
 100 105 110
Pro Arg Arg Ala Gln Asp Gly Ala His His Val His Glu Ala Arg Pro
 115 120 125
Gln Gly His Ala Asp Gln Glu Arg Gln Asp Gln Ala Leu Asn Cys Trp
 130 135 140
Cys Arg Ala Glu Leu Ala Asn Lys Thr Leu Arg Leu Lys Arg Asp Ile
145 150 155 160
Gln Tyr Glu Arg Ser Arg Ala Leu His Leu Phe His Leu His Leu Val
 165 170 175

(2) INFORMATION FOR SEQ ID NO:3737:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..140
 (D) OTHER INFORMATION: / Ceres Seq. ID 1578017
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3737:

Met Tyr Ser Met Xaa Arg Met Glu Ser Ile Trp Gly Asp Asp Cys Arg
1 5 10 15
Glu Tyr Arg Pro Glu Arg Trp Leu Arg Asp Gly Arg Phe Met Ser Glu
 20 25 30
Ser Ala Tyr Lys Phe Thr Ala Phe Asn Gly Gly Pro Arg Leu Cys Leu
 35 40 45
Gly Lys Asp Phe Ala Tyr Tyr Gln Met Lys Phe Ala Ala Ala Ser Ile
 50 55 60
Xaa Pro Pro Xaa Pro Arg Arg Arg Arg Gly Pro Pro Arg Arg Ala
65 70 75 80
Gln Asp Gly Ala His His Val His Glu Ala Arg Pro Gln Gly His Ala
 85 90 95
Asp Gln Glu Arg Gln Asp Gln Ala Leu Asn Cys Trp Cys Arg Ala Glu
 100 105 110
Leu Ala Asn Lys Thr Leu Arg Leu Lys Arg Asp Ile Gln Tyr Glu Arg

115 120 125
Ser Arg Ala Leu His Leu Phe His Leu His Leu Val
130 135 140

(2) INFORMATION FOR SEQ ID NO:3738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..137
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3738:

Met Xaa Arg Met Glu Ser Ile Trp Gly Asp Asp Cys Arg Glu Tyr Arg
1 5 10 15
Pro Glu Arg Trp Leu Arg Asp Gly Arg Phe Met Ser Glu Ser Ala Tyr
20 25 30
Lys Phe Thr Ala Phe Asn Gly Gly Pro Arg Leu Cys Leu Gly Lys Asp
35 40 45
Phe Ala Tyr Tyr Gln Met Lys Phe Ala Ala Ala Ser Ile Xaa Pro Pro
50 55 60
Xaa Pro Arg Arg Arg Arg Arg Gly Pro Pro Arg Arg Ala Gln Asp Gly
65 70 75 80
Ala His His Val His Glu Ala Arg Pro Gln Gly His Ala Asp Gln Glu
85 90 95
Arg Gln Asp Gln Ala Leu Asn Cys Trp Cys Arg Ala Glu Leu Ala Asn
100 105 110
Lys Thr Leu Arg Leu Lys Arg Asp Ile Gln Tyr Glu Arg Ser Arg Ala
115 120 125
Leu His Leu Phe His Leu His Leu Val
130 135

(2) INFORMATION FOR SEQ ID NO:3739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 922 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..922
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3739:

ctttccctcc ccattcccggtg aggcgtgagc gccacaccca cacgaaggat cccgaagccg 60
aagagaaccc taccgaggag gcagaaaatc cgtagcgcgc ctcatacgat tccgagatcc 120
gtgcctctta tcggcagcca tgatgctgcg cgcngcgggc aggcgactcc tcggcgtagg 180
aggcggcgat ccagcgcccc cggtcgtctg tgctgtggcg gcgagcagga gcagaggata 240
ccacgagcgg gtggtggacc actacaacaa cccgcgcaac gtggggtcct tggacaagga 300
cgacacggac gtcggaacgg ggatcgtcgg cgcgcggcgg tcgggggacg tcatgaagct 360
gcagatccgc gtcgacgagg ggtccggcag gatcgctgac gcgcgcttca agaCcttcgg 420
ctgcRgctcc gccatcgctt cctcctccgt cgcttccgaa tgggtcaagg gcaagcaagt 480
ggaggaagtg gtggccatca agaacaccga gattgcgaag cacctgtctc ttccaccagt 540
gaagctccac tgcagcatgc tcgctgagga agcaatcaag gccgcggtga aggattacga 600
ggcaaagaaa gggaagaaga tggccaaggc agaggagcag gacaccccat gcccgtaaga 660
gcgacagcta gtaaaactgaa gcgagcagag agtactgtat gtagtatgta acggctaacg 720
agcgaggtag tcgtgtcgtg tgtgccaaaa gaagcatgta tgtaatgtaa agctaggtaa 780
caacgatgtt tgggtttcat agaataagcg aacttgccgc agtggttttt ttatctgctc 840
tgcacatgaa taaggctctg ccattgctct ttatctgttt agtcggagca tgtatgctta 900
gtttgatcaa gcaatgctgt tg

(2) INFORMATION FOR SEQ ID NO:3740:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..172

(D) OTHER INFORMATION: / Ceres Seq. ID 1578032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3740:

Met Met Leu Arg Xaa Ala Gly Arg Arg Leu Leu Gly Val Gly Gly Gly
1 5 10 15
Asp Pro Ala Pro Ala Val Ala Ala Ala Val Ala Ala Ser Arg Ser Arg
20 25 30
Gly Tyr His Glu Arg Val Val Asp His Tyr Asn Asn Pro Arg Asn Val
35 40 45
Gly Ser Leu Asp Lys Asp Asp Thr Asp Val Gly Thr Gly Ile Val Gly
50 55 60
Ala Pro Ala Cys Gly Asp Val Met Lys Leu Gln Ile Arg Val Asp Glu
65 70 75 80
Gly Ser Gly Arg Ile Val Asp Ala Arg Phe Lys Thr Phe Gly Cys Xaa
85 90 95
Ser Ala Ile Ala Ser Ser Ser Val Ala Ser Glu Trp Val Lys Gly Lys
100 105 110
Gln Val Glu Glu Val Val Ala Ile Lys Asn Thr Glu Ile Ala Lys His
115 120 125
Leu Ser Leu Pro Pro Val Lys Leu His Cys Ser Met Leu Ala Glu Asp
130 135 140
Ala Ile Lys Ala Ala Val Lys Asp Tyr Glu Ala Lys Lys Gly Lys Lys
145 150 155 160
Met Ala Lys Ala Glu Glu Gln Asp Thr Pro Cys Pro
165 170

(2) INFORMATION FOR SEQ ID NO:3741:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1578033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3741:

Met Leu Arg Xaa Ala Gly Arg Arg Leu Leu Gly Val Gly Gly Gly Asp
1 5 10 15
Pro Ala Pro Ala Val Ala Ala Ala Val Ala Ala Ser Arg Ser Arg Gly
20 25 30
Tyr His Glu Arg Val Val Asp His Tyr Asn Asn Pro Arg Asn Val Gly
35 40 45
Ser Leu Asp Lys Asp Asp Thr Asp Val Gly Thr Gly Ile Val Gly Ala
50 55 60
Pro Ala Cys Gly Asp Val Met Lys Leu Gln Ile Arg Val Asp Glu Gly
65 70 75 80
Ser Gly Arg Ile Val Asp Ala Arg Phe Lys Thr Phe Gly Cys Xaa Ser
85 90 95
Ala Ile Ala Ser Ser Ser Val Ala Ser Glu Trp Val Lys Gly Lys Gln
100 105 110
Val Glu Glu Val Val Ala Ile Lys Asn Thr Glu Ile Ala Lys His Leu

115 120 125
Ser Leu Pro Pro Val Lys Leu His Cys Ser Met Leu Ala Glu Asp Ala
130 135 140
Ile Lys Ala Ala Val Lys Asp Tyr Glu Ala Lys Lys Gly Lys Lys Met
145 150 155 160
Ala Lys Ala Glu Glu Gln Asp Thr Pro Cys Pro
165 170

(2) INFORMATION FOR SEQ ID NO:3742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1578034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3742:

Met Lys Leu Gln Ile Arg Val Asp Glu Gly Ser Gly Arg Ile Val Asp
1 5 10 15
Ala Arg Phe Lys Thr Phe Gly Cys Xaa Ser Ala Ile Ala Ser Ser Ser
20 25 30
Val Ala Ser Glu Trp Val Lys Gly Lys Gln Val Glu Glu Val Val Ala
35 40 45
Ile Lys Asn Thr Glu Ile Ala Lys His Leu Ser Leu Pro Pro Val Lys
50 55 60
Leu His Cys Ser Met Leu Ala Glu Asp Ala Ile Lys Ala Ala Val Lys
65 70 75 80
Asp Tyr Glu Ala Lys Lys Gly Lys Lys Met Ala Lys Ala Glu Glu Gln
85 90 95
Asp Thr Pro Cys Pro
100

(2) INFORMATION FOR SEQ ID NO:3743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..753

(D) OTHER INFORMATION: / Ceres Seq. ID 1578035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3743:

aaatgacgcc atgccggcgc caccgagggc gaaagctgtc cagatcgtgt gattttgcat 60
cccattccgc agcgcgacac gsstgacctc ctgcacggcc tccacctccg tcttgaggcg 120
aacgtangtg cgaaggacca actctttcga agggaaatta tatctcaggt gcttaggagt 180
ctgccatggc cagcgagaat aaggtattta ggttcgagga agtcgccaag cacaacgtca 240
ccaaggactg ctggatcatc atcgccggca aggtgtatga tgtcactcct tttatggatg 300
agcatcctgg tggagatgag gttttgctag ctgtaactgg gaaagatgct acagctgatt 360
ttgaagatat tggccacagt gattccgcaa gggacatgat ggagaagtac cacatcgggc 420
agatagatgc ttcaacaatc ccagcaaagc gaacttatgt gcacccccag caagcgcca 480
gccactcaga caagaataat gatctcctca tcaagatcct gcagttcctt gtgCccatta 540
tgatcctggg ccttgcatct ggtatacgtc agtacagcaa atcagagtag tactgttctt 600
gaagacttgc ctttgagtc tgttttatgg taatggtttg gatgagaaca gttcagtaat 660
tgcttagtgt atttgtcagg tggatgttat ctcatgggtc atatactatg tattatggac 720
atccatgtgt tgccgaaatg tgctcttttc ccc

(2) INFORMATION FOR SEQ ID NO:3744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..134
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1578036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3744:

Met Ala Ser Glu Asn Lys Val Phe Arg Phe Glu Glu Val Ala Lys His
1 5 10 15
Asn Val Thr Lys Asp Cys Trp Ile Ile Ala Gly Lys Val Tyr Asp
20 25 30
Val Thr Pro Phe Met Asp Glu His Pro Gly Gly Asp Glu Val Leu Leu
35 40 45
Ala Val Thr Gly Lys Asp Ala Thr Ala Asp Phe Glu Asp Ile Gly His
50 55 60
Ser Asp Ser Ala Arg Asp Met Met Glu Lys Tyr His Ile Gly Gln Ile
65 70 75 80
Asp Ala Ser Thr Ile Pro Ala Lys Arg Thr Tyr Val His Pro Gln Gln
85 90 95
Ala Pro Ser His Ser Asp Lys Asn Asn Asp Leu Leu Ile Lys Ile Leu
100 105 110
Gln Phe Leu Val Pro Ile Met Ile Leu Gly Leu Ala Phe Gly Ile Arg
115 120 125
Gln Tyr Ser Lys Ser Glu
130

(2) INFORMATION FOR SEQ ID NO:3745:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..98
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1578037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3745:

Met Asp Glu His Pro Gly Gly Asp Glu Val Leu Leu Ala Val Thr Gly
1 5 10 15
Lys Asp Ala Thr Ala Asp Phe Glu Asp Ile Gly His Ser Asp Ser Ala
20 25 30
Arg Asp Met Met Glu Lys Tyr His Ile Gly Gln Ile Asp Ala Ser Thr
35 40 45
Ile Pro Ala Lys Arg Thr Tyr Val His Pro Gln Gln Ala Pro Ser His
50 55 60
Ser Asp Lys Asn Asn Asp Leu Leu Ile Lys Ile Leu Gln Phe Leu Val
65 70 75 80
Pro Ile Met Ile Leu Gly Leu Ala Phe Gly Ile Arg Gln Tyr Ser Lys
85 90 95
Ser Glu

(2) INFORMATION FOR SEQ ID NO:3746:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 803 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..803

(D) OTHER INFORMATION: / Ceres Seq. ID 1578042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3746:

aatccccaca	acaccagaat	cgcggaatca	cagacgcgtc	tatctcagct	tgctgcactg	60
cactaccctg	ccctgccatc	atatcgtaag	tgagcccggc	cgagcgagag	crngggagag	120
gcatggctgc	tccgaagctc	gcgacgctgg	cgctggccgt	gctcctggcg	gcgaccgtgg	180
tggctcccc	ggcgcggtg	cgcgcggcga	tgctgtgctc	caccgtgtac	agcacgctga	240
tgccgtgcct	gccgttcgtc	cagatgggcg	gggccatgcc	gccccagccg	tgctgcggcg	300
gcatccgcag	cctgctgcag	cagccaacaa	cacccccgac	cgccgcacta	tctgcggctg	360
cctcaagaac	gtcgccaacg	gCgccaacgg	gagcggcacc	tacatcagcc	scgcccgcgc	420
gctgcccagc	aagtgcggcg	tcgCcctgcc	gtacaagatc	agcaccaacg	ttaactgcaa	480
cacgattaat	taagtgatga	ggcgtcctgt	gcgcgtccgg	gcgaggaatg	catgcatggc	540
gctggcggag	agtaataaaa	taatgctact	ggtattttta	gctatatcga	ggtgtgcctg	600
tctctagtca	tttattatgg	tgtttaggaa	tggtctacac	agttcgtaac	ggtgtatcgt	660
ggatgcatgt	tgccgcgagc	agagtacgta	ggcatgaacc	gatgtgtgog	cttctgtctg	720
tttactctct	ctatgtagta	atgtgtgggt	gctttgatcc	agatgtattc	gctcgtgagt	780
cgtggaagta	gatcgtttca	gtg				

(2) INFORMATION FOR SEQ ID NO:3747:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1578043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3747:

Ile	Pro	Thr	Thr	Pro	Glu	Ser	Ala	Asn	His	Arg	Arg	Val	Tyr	Leu	Ser
1				5					10					15	
Leu	Leu	His	Cys	Thr	Thr	Leu	Pro	Cys	His	His	Ile	Val	Arg	Glu	Pro
				20				25					30		
Gly	Arg	Ala	Arg	Xaa	Xaa	Glu	Arg	His	Gly	Cys	Ser	Glu	Ala	Arg	Asp
				35				40				45			
Ala	Gly	Ala	Gly	Arg	Ala	Pro	Gly	Gly	Asp	Arg	Gly	Gly	Ser	Pro	Gly
				50			55				60				
Arg	Gly	Ala	Arg	Gly	Asp	Val	Val	Leu	His	Arg	Val	Gln	His	Ala	Asp
				65			70			75				80	
Ala	Val	Pro	Ala	Val	Arg	Pro	Asp	Gly	Arg	Gly	His	Ala	Ala	Pro	Ala
				85				90						95	
Val	Leu	Arg	Arg	His	Pro	Gln	Pro	Ala	Ala	Ala	Ala	Asn	Asn	Thr	Pro
				100				105						110	
Asp	Arg	Arg	Thr	Ile	Cys	Gly	Cys	Leu	Lys	Asn	Val	Ala	Asn	Gly	Ala
				115			120					125			
Asn	Gly	Ser	Gly	Thr	Tyr	Ile	Ser	Xaa	Ala	Ala	Ala	Leu	Pro	Ser	Lys
				130			135				140				
Cys	Gly	Val	Ala	Leu	Pro	Tyr	Lys	Ile	Ser	Thr	Asn	Val	Asn	Cys	Asn
				145			150			155				160	
Thr	Ile	Asn													

(2) INFORMATION FOR SEQ ID NO:3748:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

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(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1578044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3748:

Ser Pro Gln His Gln Asn Pro Arg Ile Thr Asp Ala Ser Ile Ser Ala
1 5 10 15
Cys Cys Thr Ala Leu Pro Cys Pro Ala Ile Ile Ser Tyr Val Ser Pro
20 25 30
Ala Glu Arg Glu Xaa Gly Arg Gly Met Ala Ala Pro Lys Leu Ala Thr
35 40 45
Leu Ala Leu Ala Val Leu Leu Ala Ala Thr Val Val Ala Pro Pro Ala
50 55 60
Ala Val Arg Ala Ala Met Ser Cys Ser Thr Val Tyr Ser Thr Leu Met
65 70 75 80
Pro Cys Leu Pro Phe Val Gln Met Gly Gly Ala Met Pro Pro Gln Pro
85 90 95
Cys Cys Gly Gly Ile Arg Ser Leu Leu Gln Gln Pro Thr Thr Pro Pro
100 105 110
Thr Ala Ala Leu Ser Ala Ala Ala Ser Arg Thr Ser Pro Thr Ala Pro
115 120 125
Thr Gly Ala Ala Pro Thr Ser Ala Xaa Pro Pro Arg Cys Pro Ala Ser
130 135 140
Ala Ala Ser Pro Cys Arg Thr Arg Ser Ala Pro Thr Leu Thr Ala Thr
145 150 155 160
Arg Leu Ile Lys

(2) INFORMATION FOR SEQ ID NO:3749:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1578045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3749:

Met Ala Ala Pro Lys Leu Ala Thr Leu Ala Leu Ala Val Leu Leu Ala
1 5 10 15
Ala Thr Val Val Ala Pro Pro Ala Ala Val Arg Ala Ala Met Ser Cys
20 25 30
Ser Thr Val Tyr Ser Thr Leu Met Pro Cys Leu Pro Phe Val Gln Met
35 40 45
Gly Gly Ala Met Pro Pro Gln Pro Cys Cys Gly Gly Ile Arg Ser Leu
50 55 60
Leu Gln Gln Pro Thr Thr Pro Pro Thr Ala Ala Leu Ser Ala Ala Ala
65 70 75 80
Ser Arg Thr Ser Pro Thr Ala Pro Thr Gly Ala Ala Pro Thr Ser Ala
85 90 95
Xaa Pro Pro Arg Cys Pro Ala Ser Ala Ala Ser Pro Cys Arg Thr Arg
100 105 110
Ser Ala Pro Thr Leu Thr Ala Thr Arg Leu Ile Lys
115 120

(2) INFORMATION FOR SEQ ID NO:3750:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 667 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3750:

(2) INFORMATION FOR SEQ ID NO:3751:

(A) LENGTH: 176 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(1X) FEATURE.

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1578057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3751:

(2) INFORMATION FOR SEQ ID NO:3752:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1578058

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1																
1	Val	His	Pro	Tyr	Phe	Arg	His	Asn	Ser	Gln	Pro	Glu	Pro	Pro	Lys	
				5				10						15		
Pro	Glu	Ala	Ala	Gly	Ala	Pro	Leu	Thr	Leu	Leu	Arg	Leu	Arg	Ser	Arg	
			20					25					30			
Lys	Arg	Lys	Met	Ser	Tyr	Tyr	Gly	Gln	Gln	Pro	Pro	Val	Gly	Val	Pro	
		35					40					45				
Pro	Gln	Gln	Gly	Tyr	Pro	Gly	Lys	Asp	Gly	Tyr	Pro	Pro	Ala	Gly	Tyr	
	50					55					60					
Pro	Ala	Gly	Arg	Leu	Pro	Pro	Ala	Gly	Ala	Gly	Leu	Pro	Ala	Ala	Gly	
65					70					75					80	
Leu	Pro	Thr	Ala	Gly	Leu	Pro	Ala	Ala	Val	Arg	Ala	Ala	Ala	Ser	Thr	
				85					90					95		
Ala	Ala	Ala	Glu	Gln	Arg	Ala	Phe	Leu	His	Gly	Arg	Met	Leu	Gly	Cys	
			100					105				110				
Pro	Leu	Leu	Leu	Xaa	Pro	Pro	Gly	Arg	Leu	Leu	Leu	Thr	Asp	Pro	Ser	
	115						120					125				
Cys	Arg	Val	Gln	His	Gly	Cys	Lys									
	130						135									

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid.

(ix) FEATURE:

(A) NAME

(B) LOCATION: 1..101

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:3753:

Ser Tyr Tyr Gly Gln Gln Pro Pro Val Gly Va

[illegible]

(2) INFORMATION FOR SEQ ID NO:3754:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 678 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..678

(D) OTHER INFORMATION: / Ceres Seq. ID 1578070

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3754:

(X1) SEQUENCE DESCRIPTION OF SEQ ID NO: 1

atgccacaac	aagaccgaca	accacaatc	tttctttgtg	cacagaaa	agaagaacc
tatggcacag	tctgtctcgc	cctccgtcaa	gctgctggtt	ctggttgtcc	tcctgtcgct

60
120

(2) INFORMATION FOR SEQ ID NO:3755:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3755:

(2) INFORMATION FOR SEQ ID NO:3756:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3756:

(x1) SEQUENCE DESCRIPTION: S22 18 NO. 10															
Cys	His	Asn	Lys	Thr	Gln	Asn	Pro	Gln	Ser	Phe	Phe	Val	His	Arg	Lys
1				5					10					15	
Lys	Lys	Glu	Pro	Met	Ala	Gln	Ser	Ser	Ser	Ala	Ser	Val	Lys	Leu	Leu
			20					25					30		
Val	Leu	Val	Val	Leu	Pro	Ala	Leu	Leu	Leu	Phe	Leu	Val	Gln	Ala	Gln

35 40 45
Xaa Ala Arg Pro Ala Ala Ala Asn Thr Thr Thr Pro Thr Pro Ala Thr
50 55 60
Thr Thr Gly Cys Ala Ala Ser Ser Val Thr Val Ser Gln Ser Asn Thr
65 70 75 80
Gly Asp Arg Ala Gly Tyr Asp Pro Val Phe Glu Val Thr Val Ser Asn
85 90 95
Ala Cys Arg Cys Ala Val Arg Ala Val Arg Leu Arg Ser Glu Gly Phe
100 105 110
Ala Ser Ser Val Pro Val Asp Pro Arg Leu Phe Arg Arg Ala Gly Arg
115 120 125
Asp Tyr Leu Val Ala Asp Gly Arg Arg Ile Glu Pro Gly Ala Asp Ala
130 135 140
Arg Phe Arg Tyr Ala Trp Asp Arg Ala Phe Arg Met Thr Ala Ala Ala
145 150 155 160
Val Arg Asp Asp Cys Ser
165

(2) INFORMATION FOR SEQ ID NO:3757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 878 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..878
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3757:

aaggcacgcg	ccgagcgagc	acgccatcaa	cgggcgcagg	tacgccctgg	agctgcagat	60
ggtgcaccag	agcgacacca	acaggtagcg	cgtggtctcg	cagctctaca	ggatctcgcg	120
gcggcgctct	gacaggacca	ttcacaggct	ggagcggtag	atccggagga	tcacgcgcag	180
gaggaagaac	cacgaggagc	tcacgcacga	ggaggtggac	ccgcggcggc	cggtagcgcg	240
gagcacggcc	tactacaagt	acacgggctc	cttcacgaca	ccgccctgca	cggagggcgt	300
gacgtgggta	gtggcgccac	agacacggcg	ggtgacgcgg	cgccagggtc	ggctgctgcg	360
gaacscgtcc	acgaaggcac	caggagcaac	aggaggccac	tccaggaagc	caacggCca	420
ggccatcacc	ttctactaca	cytcgccggc	gcacggccga	ggggcgaaac	gggactagca	480
cgcattgcaa	ggagacggcc	ggcggaatct	tggcgcccc	gtgctccttt	tctgtccagg	540
cgacacaggc	catggccaag	caaactcttg	catgtgatcg	atgtccgaca	gtgttaggtc	600
agagtgcaga	ccaatttttt	tttctctcca	gcgatcatca	attcgttgcg	gagtaatgct	660
gtagtgcgat	tgcataattg	cattggcaag	tgagtttggt	ccaaaaaaaa	ggacatcaaa	720
ttagtagaac	gtttgcgggt	tacactcctt	gttcctgtac	tgagtgcgcg	aattgcaatc	780
tcgaaaatca	tgtgattcta	aggatagcac	gtctgccaca	tgtaagggtg	aaaacgatcg	840
gtaacggtcg	gaaaaaatct	ctcaccgttt	ttactcgc			

(2) INFORMATION FOR SEQ ID NO:3758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578084

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3758:

Arg His Ala Pro Ser Glu His Ala Ile Asn Gly Arg Arg Tyr Ala Leu
1 5 10 15
Glu Leu Gln Met Val His Gln Ser Asp Thr Asn Arg Tyr Ala Val Val
20 25 30
Ser Gln Leu Tyr Arg Ile Ser Arg Arg Arg Pro Asp Arg Thr Ile His

00000000-00000000

35 40 45
Arg Leu Glu Arg Tyr Ile Arg Arg Ile Ile Ala Arg Arg Lys Asn His
50 55 60
Glu Glu Leu Ile Asp Glu Glu Val Asp Pro Arg Arg Pro Val Ser Arg
65 70 75 80
Ser Thr Ala Tyr Tyr Lys Tyr Thr Gly Ser Phe Thr Thr Pro Pro Cys
85 90 95
Thr Glu Gly Val Thr Trp Val Val Ala His Gln Thr Arg Arg Val Thr
100 105 110
Arg Arg Gln Val Arg Leu Leu Arg Asn Xaa Ser Thr Thr Ala Pro Gly
115 120 125
Ala Thr Gly Gly His Ser Arg Lys Pro Thr Ala Arg Ala Ile Thr Phe
130 135 140
Tyr Tyr Xaa Ser Pro Ala His Gly Arg Gly Ala Asn Gly Asp
145 150 155

(2) INFORMATION FOR SEQ ID NO:3759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1578085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3759:

Met Val His Gln Ser Asp Thr Asn Arg Tyr Ala Val Val Ser Gln Leu
1 5 10 15
Tyr Arg Ile Ser Arg Arg Arg Pro Asp Arg Thr Ile His Arg Leu Glu
20 25 30
Arg Tyr Ile Arg Arg Ile Ile Ala Arg Arg Lys Asn His Glu Glu Leu
35 40 45
Ile Asp Glu Glu Val Asp Pro Arg Arg Pro Val Ser Arg Ser Thr Ala
50 55 60
Tyr Tyr Lys Tyr Thr Gly Ser Phe Thr Thr Pro Cys Thr Glu Gly
65 70 75 80
Val Thr Trp Val Val Ala His Gln Thr Arg Arg Val Thr Arg Arg Gln
85 90 95
Val Arg Leu Leu Arg Asn Xaa Ser Thr Thr Ala Pro Gly Ala Thr Gly
100 105 110
Gly His Ser Arg Lys Pro Thr Ala Arg Ala Ile Thr Phe Tyr Tyr Xaa
115 120 125
Ser Pro Ala His Gly Arg Gly Ala Asn Gly Asp
130 135

(2) INFORMATION FOR SEQ ID NO:3760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..951

(D) OTHER INFORMATION: / Ceres Seq. ID 1578086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3760:

acccatgttc ctgttccac actcgactgt catcctgtga tatccgctcg ccagtcgccca 60
ctccgtttcg gcattccgcc tcttcccgac acacctcttt aactcgcttc cgtttccaaa 120
aaaatgctcc agttaattta atccagacga ggaatcgctt cgccgcggat ctctccgctc 180
gccgacaaga cccgctatcg gctccggcgg gaagactcgc actacggtgg ggcgcgctcg 240

cgccgctcgg cactgggctc gtcgggttcga cgttcgcttg tggagggtcgt cggggccagc 300
ggtgcccggg caatgcgggc agtttgtgga gccgtctgar gcgcttggt gggatctgag 360
ggtgtcaggt arggggcgcg asragctctg tcgggtggga rttggtggtg gttgtagcgt 420
agggcGcgtc gcgtgttttg ctgccgggat ggagcacgta gttgggggca agttcaagct 480
tgggaagaag atcgggagcg gatcatttgg ggagctctac ctccggcgtga acatgcagag 540
tgacgaggag gtggctgtca aactggtatt ccacgaacat cttccacgtg atttttgtgt 600
ccactatcca tgtcttggtg aacagttctg tgtttagacct tctccaaccg cccccccaa 660
acctcccctc acccttgcta ttgctaccga cctactgtgt actatggggg gaagtatctt 720
ttaggatgat gtagtaaaat ataatagaaa atacagatat gaggaaaaaa tatgggggaa 780
atggttggag atggtcttag gagttaactt tagtcggagt cactgaaatc tatagttagc 840
ctaattgctt gcaggagcta atgagcctgt agcactctga agtgagggtg tcaatgctga 900
aaagcaccca ctggaaactc atctcttgtt tgttctgatt ggattattct c

(2) INFORMATION FOR SEQ ID NO:3761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3761:

Pro Cys Ser Cys Ser His Thr Arg Leu Ser Ser Cys Asp Ile Arg Ser
1 5 10 15
Pro Val Ala Thr Pro Phe Arg His Ser Ala Ser Ser Arg His Thr Ser
20 25 30
Leu Thr Arg Phe Arg Phe Gln Lys Asn Ala Pro Val Asn Leu Ile Gln
35 40 45
Thr Arg Asn Arg Leu Ala Ala Asp Leu Ser Ala Arg Arg Gln Asp Pro
50 55 60
Leu Ser Ala Pro Ala Gly Arg Leu Ala Leu Arg Trp Gly Ala Ser Pro
65 70 75 80
Pro Leu Gly Thr Trp Leu Val Gly Ser Thr Phe Ala Cys Gly Gly Arg
85 90 95
Arg Gly Gln Arg Cys Arg Gly Asn Ala Val Ser Leu Trp Ser Arg Leu
100 105 110
Xaa Arg Leu Ala Gly Ile
115

(2) INFORMATION FOR SEQ ID NO:3762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3762:

Met Glu His Val Val Gly Gly Lys Phe Lys Leu Gly Lys Lys Ile Gly
1 5 10 15
Ser Gly Ser Phe Gly Glu Leu Tyr Leu Gly Val Asn Met Gln Ser Asp
20 25 30
Glu Glu Val Ala Val Lys Leu Val Phe His Glu His Leu Pro Arg Asp
35 40 45
Phe Cys Val His Tyr Pro Cys Leu Gly Glu Gln Phe Cys Val Arg Pro
50 55 60
Ser Pro Thr Ala Pro Pro Lys Pro Pro Leu Thr Leu Ala Ile Ala Thr

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3765:

Met Ala Arg Arg Asn Ile Gly Val Ala Val Asp Phe Ser Ser Cys Ser
1 5 10 15
Lys Ala Ala Leu Arg Trp Ala Ser Thr Asn Leu Ala Arg Asn Gly Asp
20 25 30
Arg Leu Ile Leu Ile His Val Asn Ser Ser Cys Gln Asn Glu Arg Gly
35 40 45
Ala Val His Leu Trp Glu Gln Ser Gly Ser Pro Leu Ile Pro Leu Ala
50 55 60
Glu Phe Ser Asp Val Ala Arg Thr Tyr Gly Val Ser Pro Asp Lys Glu
65 70 75 80
Thr Ile Glu Ile Leu Thr Gln Ala Ala Asn His Arg Gly Ile Glu Val
85 90 95
Phe Ala Lys Val Phe Tyr Gly Asp Pro Ala Lys Lys Leu Tyr Glu Ala
100 105 110
Ala Asp Met Val Pro Leu Ser Cys Met Val Val Gly Ser Arg Gly Leu
115 120 125
Ser Thr Leu Lys Arg Ala Leu Met Gly Ser Val Ser Thr Tyr Val Val
130 135 140
Asn His Ala Ala Cys Pro Val Thr Val Val Lys Glu Met Val
145 150 155

(2) INFORMATION FOR SEQ ID NO:3766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..630
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3766:

atgatggtgt	caagctttgg	gatcttcgga	aattaagaaa	ttttaggacc	ttctctccct	60
atgattcaga	tacgccaaca	aatactgtgg	aatttgattt	tagtggAaaa	ctatcttgcc	120
attggtggtt	cagatataag	ggtctaccaa	gtagctaattg	ttaaggccga	atggaatctc	180
atcaagacat	taccagattt	atctggaaca	gggaaagtaa	cttcggtaaa	gttcggagca	240
gatgctaagt	acatagccgt	aggttctatg	gaccgcaatc	tacggatatt	tggcctccct	300
ggagacgacc	aaatggagga	atcaaccaca	gcggcagagt	gaggaaaatc	catggttatc	360
agcattcatt	gtctatttgg	ccactgtcga	gaggtaatcc	acggagacac	accgctggcg	420
cccgtgacac	ttggcctggt	tggttacttg	ctaaaaattg	ctacacattt	ttgtgccaca	480
cttgtttaag	cacacttggt	taagggtgtt	aagggttatc	gctcaaattc	cgcgtcacag	540
cttgtttgtc	actcataaga	gaatattgcc	tgtaaaatga	gagtctgaac	gacttgcccc	600
taaaatgaga	tggaaaatca	gttagctgct				

(2) INFORMATION FOR SEQ ID NO:3767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3767:

Asp Gly Val Lys Leu Trp Asp Leu Arg Lys Leu Arg Asn Phe Arg Thr
1 5 10 15
Phe Ser Pro Tyr Asp Ser Asp Thr Pro Thr Asn Thr Val Glu Phe Asp
20 25 30
Phe Ser Gly Lys Leu Ser Cys His Trp Trp Phe Arg Tyr Lys Gly Leu
35 40 45

Pro Ser Ser
50

(2) INFORMATION FOR SEQ ID NO:3768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3768:

Met Ile Gln Ile Arg Gln Gln Ile Leu Trp Asn Leu Ile Leu Val Glu
1 5 10 15
Asn Tyr Leu Ala Ile Gly Gly Ser Asp Ile Arg Val Tyr Gln Val Ala
20 25 30
Asn Val Lys Ala Glu Trp Asn Leu Ile Lys Thr Leu Pro Asp Leu Ser
35 40 45
Gly Thr Gly Lys Val Thr Ser Val Lys Phe Gly Ala Asp Ala Lys Tyr
50 55 60
Ile Ala Val Gly Ser Met Asp Arg Asn Leu Arg Ile Phe Gly Leu Pro
65 70 75 80
Gly Asp Asp Gln Met Glu Glu Ser Thr Thr Ala Ala Glu
85 90

(2) INFORMATION FOR SEQ ID NO:3769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..876
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3769:

atcagccctc acgcatgttg cagcgatg gccggatctg aggttgagtg tgcgatcccg 60
ttggcatatc gacaaagttt ggtgggtccc accgcagatc ccggcccggt aggtactagt 120
tccgcggtcc cccctcccta gtctccgggg aggaccgtct cggccgcgag agtgcgctcg 180
tcgactccac tcagctctct cgctccctct cctcccccaa ggccccagag acaggcagcc 240
ggcgaggccc gccgcgcgca aGcaatggat ttcaaggggt tctgggagtc cagattcggg 300
ggcaagaagg aacccgagcc ggagcagaac gggcacgcca acgggggtcca gaaccagaag 360
aggacctccg atctggcggg ctacgagcag ttcgagcagc aggccaggca gaccaggtc 420
cgagccgcg cgattcgcga cggagacgct gatgtcataa gccccttcta ccttcatttg 480
agtcagctga aatgcgtaat ctgcgagaga cattgttgag ggatattatt cgcgggagcc 540
cagatgtgaa atgggagagc atcaaaggac tggaaaatgc aaaacgcctt ctaaaagagg 600
ctgttgatcat gcccataaag taccctaaat acttcactgg tctcctttct ccatggaaag 660
gcattcttact ttttggcccc ccagggacag gaaagacaat gctggcaaaa gcggtcgcta 720
ctgagtgcaa aaccaccttc ttcaacattt cagcatcatc aattgtcagc aaatggcggtg 780
gagattcaga gaagcttgtc aaagttctgt ttgagcttgc taggcatcat gcaccatcca 840
caatattcct tgatgaaata gatgctatca tcagcc

(2) INFORMATION FOR SEQ ID NO:3770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3770:

Met Asp Phe Lys Gly Phe Trp Glu Ser Arg Phe Gly Gly Lys Lys Glu
1 5 10 15
Pro Glu Pro Glu Gln Asn Gly His Ala Asn Gly Val Gln Asn Gln Lys
20 25 30
Arg Thr Ser Asp Leu Ala Val Tyr Glu Gln Phe Glu Gln Ala Arg
35 40 45
Gln Thr Gln Val Arg Ala Ala Ile Arg Asp Gly Asp Ala Asp Val
50 55 60
Ile Ser Pro Phe Tyr Leu His Leu Ser Gln Leu Lys Cys Val Ile Ser
65 70 75 80
Gln Arg His Cys

(2) INFORMATION FOR SEQ ID NO:3771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3771:

Met Arg Asn Leu Ala Glu Thr Leu Leu Arg Asp Ile Ile Arg Gly Ser
1 5 10 15
Pro Asp Val Lys Trp Glu Ser Ile Lys Gly Leu Glu Asn Ala Lys Arg
20 25 30
Leu Leu Lys Glu Ala Val Val Met Pro Ile Lys Tyr Pro Lys Tyr Phe
35 40 45
Thr Gly Leu Leu Ser Pro Trp Lys Gly Ile Leu Leu Phe Gly Pro Pro
50 55 60
Gly Thr Gly Lys Thr Met Leu Ala Lys Ala Val Ala Thr Glu Cys Lys
65 70 75 80
Thr Thr Phe Phe Asn Ile Ser Ala Ser Ser Ile Val Ser Lys Trp Arg
85 90 95
Gly Asp Ser Glu Lys Leu Val Lys Val Leu Phe Glu Leu Ala Arg His
100 105 110
His Ala Pro Ser Thr Ile Phe Leu Asp Glu Ile Asp Ala Ile Ile Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:3772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3772:

Met Pro Ile Lys Tyr Pro Lys Tyr Phe Thr Gly Leu Leu Ser Pro Trp
1 5 10 15
Lys Gly Ile Leu Leu Phe Gly Pro Pro Gly Thr Gly Lys Thr Met Leu

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20 25 30
Ala Lys Ala Val Ala Thr Glu Cys Lys Thr Thr Phe Phe Asn Ile Ser
35 40 45
Ala Ser Ser Ile Val Ser Lys Trp Arg Gly Asp Ser Glu Lys Leu Val
50 55 60
Lys Val Leu Phe Glu Leu Ala Arg His His Ala Pro Ser Thr Ile Phe
65 70 75 80
Leu Asp Glu Ile Asp Ala Ile Ile Ser
85

(2) INFORMATION FOR SEQ ID NO:3773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..776
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3773:

aaaagaatat ttagttgaag caaaattcaa gaaacttgaa gaagaggcct gcaatatttt 60
gtcctcgagt tctggtgaaa caatgaaaaa caacattgat gttttggttt gcaaagctga 120
atactaccac cagagtggag agtaccaaaa gtgttttAaa actcacatcc tcgttacttg 180
agagagaccc tttccatcta aagtgcacat tagttcattt ggcaactgca atggagcttg 240
gtcattccaa tgatctttat ctttttagcat gcaacttagt gaaggattat cctgaaaaag 300
ctctttcatg gtttgctgtc ggttgctatt actactgtat taagaagtat gatcaagcgc 360
gaagatactt cggcaaagct acaggttttag atgggacgtt tcctcctgct tggattggta 420
caggcattgc ctatgctgct caagaggaag gtgaccaagc aatggctgca tttcggacgg 480
cagctcggtt atttcctgga tGgtcatctg ccaactttat acatgggcat gcaatatgtg 540
cgaatgcama atttcaaacT ttgcagagca gttcttcaca caagcAaaat ccatctgccc 600
atctgatcca cttattttaca atgagttggg ggttggtgcg tataatatga aggagtaccg 660
aaaagcagtt cagttgtttg agttaacatt ggaccatact tcatcctctc tgaatgaaat 720
gtgggaacca acattggtga atcttgggca tgcacttcgg aaactcaagg aatata

(2) INFORMATION FOR SEQ ID NO:3774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3774:

Met Phe Trp Phe Ala Lys Leu Asn Thr Thr Thr Arg Val Glu Ser Thr
1 5 10 15
Lys Ser Val Leu Lys Leu Thr Ser Ser Leu Leu Glu Arg Asp Pro Phe
20 25 30
His Leu Lys Cys Thr Leu Val His Leu Ala Thr Ala Met Glu Leu Gly
35 40 45
His Ser Asn Asp Leu Tyr Leu Leu Ala Cys Asn Leu Val Lys Asp Tyr
50 55 60
Pro Glu Lys Ala Leu Ser Trp Phe Ala Val Gly Cys Tyr Tyr Tyr Cys
65 70 75 80
Ile Lys Lys Tyr Asp Gln Ala Arg Arg Tyr Phe Gly Lys Ala Thr Gly
85 90 95
Leu Asp Gly Thr Phe Pro Pro Ala Trp Ile Gly Thr Gly Ile Ala Tyr
100 105 110
Ala Ala Gln Glu Glu Gly Asp Gln Ala Met Ala Ala Phe Arg Thr Ala

115 120 125
Ala Arg Leu Phe Pro Gly Trp Ser Ser Ala Asn Phe Ile His Gly His
130 135 140
Ala Ile Cys Ala Asn Ala Xaa Phe Gln Thr Leu Gln Ser Ser Ser Ser
145 150 155 160
His Lys Gln Asn Pro Ser Ala His Leu Ile His Leu Phe Thr Met Ser
165 170 175
Trp Gly Leu Leu Arg Ile Ile
180

(2) INFORMATION FOR SEQ ID NO:3775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3775:

Met Glu Leu Gly His Ser Asn Asp Leu Tyr Leu Leu Ala Cys Asn Leu
1 5 10 15
Val Lys Asp Tyr Pro Glu Lys Ala Leu Ser Trp Phe Ala Val Gly Cys
20 25 30
Tyr Tyr Tyr Cys Ile Lys Lys Tyr Asp Gln Ala Arg Arg Tyr Phe Gly
35 40 45
Lys Ala Thr Gly Leu Asp Gly Thr Phe Pro Pro Ala Trp Ile Gly Thr
50 55 60
Gly Ile Ala Tyr Ala Ala Glu Glu Gly Asp Gln Ala Met Ala Ala
65 70 75 80
Phe Arg Thr Ala Ala Arg Leu Phe Pro Gly Trp Ser Ser Ala Asn Phe
85 90 95
Ile His Gly His Ala Ile Cys Ala Asn Ala Xaa Phe Gln Thr Leu Gln
100 105 110
Ser Ser Ser Ser His Lys Gln Asn Pro Ser Ala His Leu Ile His Leu
115 120 125
Phe Thr Met Ser Trp Gly Leu Leu Arg Ile Ile
130 135

(2) INFORMATION FOR SEQ ID NO:3776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3776:

Met Val Ile Cys Gln Leu Tyr Thr Trp Ala Cys Asn Met Cys Glu Cys
1 5 10 15
Xaa Ile Ser Asn Phe Ala Glu Gln Phe Thr Gln Ala Lys Ser Ile
20 25 30
Cys Pro Ser Asp Pro Leu Ile Tyr Asn Glu Leu Gly Val Val Ala Tyr
35 40 45
Asn Met Lys Glu Tyr Arg Lys Ala Val Gln Leu Phe Glu Leu Thr Leu
50 55 60
Asp His Thr Ser Ser Ser Leu Asn Glu Met Trp Glu Pro Thr Leu Val
65 70 75 80

Asn Leu Gly His Ala Leu Arg Lys Leu Lys Glu Tyr
85 90

(2) INFORMATION FOR SEQ ID NO:3777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..654
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3777:

tyatgctgat	acagttggag	acttgggata	tgcacagag	cttggaaact	atgcagagta	60
tagtggtgct	cctaagtgg	aggaggttct	gaattattct	agagttgttc	ttgattgtgc	120
aactgctgat	cctgatggc	gcaagagagc	ccttctcatt	ggaggtggca	tagctaactt	180
cactgatgtt	gctaccacat	tcaatggcat	catccgagcc	ttaagggaga	aggaatccaa	240
gttgaaggct	tcaagaatgc	acatttatgt	ccgccgaggt	ggtccaaatt	accaatctgg	300
actggctaaa	atgcgtaaGc	ttggtgcaga	actcggcggt	ccaattgagg	tgtatgggcc	360
agaagcgact	atgactggaa	tctgcaaaca	agcaattgaa	tgcacatgag	ctgcagcgta	420
atcagagcgt	aGcTctgNgg	tagtttggga	tctgcaaaca	cgcaattgaa	tgtgtcatgg	480
actcagcata	aatgagagat	ggatagtagt	tgcattatat	agttcacaca	tgggtgtttct	540
gttttttgtt	tcagatatgt	tgtagcgtgt	tgtttgaacg	aaaccttcac	agatcattac	600
tgcaaagaaa	ttgctgtgtg	ttaaaataaa	ttcaaagtct	agttttgtgc	cttt	

(2) INFORMATION FOR SEQ ID NO:3778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3778:

Xaa	Ala	Asp	Thr	Val	Gly	Asp	Leu	Gly	Tyr	Ala	Ser	Glu	Leu	Gly	Asn	
1				5				10						15		
Tyr	Ala	Glu	Tyr	Ser	Gly	Ala	Pro	Asn	Glu	Glu	Glu	Val	Leu	Asn	Tyr	
				20				25						30		
Ser	Arg	Val	Val	Leu	Asp	Cys	Ala	Thr	Ala	Asp	Pro	Asp	Gly	Arg	Lys	
				35				40						45		
Arg	Ala	Leu	Leu	Ile	Gly	Gly	Ile	Ala	Asn	Phe	Thr	Asp	Val	Ala		
				50				55						60		
Thr	Thr	Phe	Asn	Gly	Ile	Arg	Ala	Leu	Arg	Glu	Lys	Glu	Ser	Lys		
				65				70						75		
Leu	Lys	Ala	Ser	Arg	Met	His	Ile	Tyr	Val	Arg	Arg	Gly	Gly	Pro	Asn	
				85				90						95		
Tyr	Gln	Ser	Gly	Leu	Ala	Lys	Met	Arg	Lys	Leu	Gly	Ala	Glu	Leu	Gly	
				100				105						110		
Val	Pro	Ile	Glu	Val	Tyr	Gly	Pro	Glu	Ala	Thr	Met	Thr	Gly	Ile	Cys	
				115				120						125		
Lys	Gln	Ala	Ile	Glu	Cys	Ile	Met	Ala	Ala	Ala						
				130				135								

(2) INFORMATION FOR SEQ ID NO:3779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..722

(D) OTHER INFORMATION: / Ceres Seq. ID 1578190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3779:

(X1) SEQUENCE	DESCRIPTION	SEQ ID NO	LENGTH			
gaggacgaag	gttcgttcag	ttcaagacca	gacgargagg	aagagaggcg	cgcaaggntc	60
cggctcatcg	gcgcccttc	ccgccctccg	ctcatcgtcg	ccggtngccg	ccgcgcgggc	120
gccgtcgctc	ggtcgcgtgt	ccggccacgc	atctgcggcg	cccagcaaga	ggcgcgtcgt	180
ctcctgcagg	gccgtcagca	gcaggtcgct	gtccatcatc	aggtgcgagc	agagcgcgaa	240
gaagggcggc	gggcgggaca	catggctggg	ccgcgcggcc	atGGtbngcG	ttcgctccg	300
cgatcgccgt	cgaggtggcc	accggcaagg	gcttcctcca	ggtagggaac	gtcgtagagt	360
atgagtatac	acgtaacatc	gcagcagcgc	aggaacgcgc	aaacgcgtgc	gtaacaaaca	420
taccacgagt	ttgttgtgga	tggcgtgcag	aacttgggcg	tgggtactcc	ggcgcggaAS	480
STGGcgcctg	ccgtgtcggg	gctcgtcgtc	ggcctcgccg	tcttcttctc	gctccagtcg	540
ggaggaggca	cgcgagactg	acggctgatg	gaaccccatg	agctgagagc	acgcgcacgt	600
cgaacatcgt	ctccccactc	gacatcagtt	gctgtaatgg	ttggtgaagt	gaggatgaaa	660
accacgggca	tatatcatca	tcatcatgtc	atgtgtaaca	aagacgataa	ctctcatgtg	720
++						

(2) INFORMATION FOR SEQ ID NO:3780:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1578191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3780:

[illegible]

(2) INFORMATION FOR SEQ ID NO:3781:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1578192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3781:

Arg	Thr	Lys	Val	Arg	Ser	Val	Gln	Asp	Gln	Thr	Xaa	Arg	Lys	Arg	Gly
1				5					10					15	

(A) NAME/KEY: -

	1990-1991	1991-1992	1992-1993	1993-1994	1994-1995	1995-1996	1996-1997	1997-1998	1998-1999	1999-2000	2000-2001	2001-2002	2002-2003	2003-2004	2004-2005	2005-2006	2006-2007	2007-2008	2008-2009	2009-2010	2010-2011	2011-2012	2012-2013	2013-2014	2014-2015	2015-2016	2016-2017	2017-2018	2018-2019	2019-2020	2020-2021	2021-2022	2022-2023	2023-2024	2024-2025	2025-2026	2026-2027	2027-2028	2028-2029	2029-2030	2030-2031	2031-2032	2032-2033	2033-2034	2034-2035	2035-2036	2036-2037	2037-2038	2038-2039	2039-2040	2040-2041	2041-2042	2042-2043	2043-2044	2044-2045	2045-2046	2046-2047	2047-2048	2048-2049	2049-2050	2050-2051	2051-2052	2052-2053	2053-2054	2054-2055	2055-2056	2056-2057	2057-2058	2058-2059	2059-2060	2060-2061	2061-2062	2062-2063	2063-2064	2064-2065	2065-2066	2066-2067	2067-2068	2068-2069	2069-2070	2070-2071	2071-2072	2072-2073	2073-2074	2074-2075	2075-2076	2076-2077	2077-2078	2078-2079	2079-2080	2080-2081	2081-2082	2082-2083	2083-2084	2084-2085	2085-2086	2086-2087	2087-2088	2088-2089	2089-2090	2090-2091	2091-2092	2092-2093	2093-2094	2094-2095	2095-2096	2096-2097	2097-2098	2098-2099	2099-2100	2100-2101	2101-2102	2102-2103	2103-2104	2104-2105	2105-2106	2106-2107	2107-2108	2108-2109	2109-2110	2110-2111	2111-2112	2112-2113	2113-2114	2114-2115	2115-2116	2116-2117	2117-2118	2118-2119	2119-2120	2120-2121	2121-2122	2122-2123	2123-2124	2124-2125	2125-2126	2126-2127	2127-2128	2128-2129	2129-2130	2130-2131	2131-2132	2132-2133	2133-2134	2134-2135	2135-2136	2136-2137	2137-2138	2138-2139	2139-2140	2140-2141	2141-2142	2142-2143	2143-2144	2144-2145	2145-2146	2146-2147	2147-2148	2148-2149	2149-2150	2150-2151	2151-2152	2152-2153	2153-2154	2154-2155	2155-2156	2156-2157	2157-2158	2158-2159	2159-2160	2160-2161	2161-2162	2162-2163	2163-2164	2164-2165	2165-2166	2166-2167	2167-2168	2168-2169	2169-2170	2170-2171	2171-2172	2172-2173	2173-2174	2174-2175	2175-2176	2176-2177	2177-2178	2178-2179	2179-2180	2180-2181	2181-2182	2182-2183	2183-2184	2184-2185	2185-2186	2186-2187	2187-2188	2188-2189	2189-2190	2190-2191	2191-2192	2192-2193	2193-2194	2194-2195	2195-2196	2196-2197	2197-2198	2198-2199	2199-2200	2200-2201	2201-2202	2202-2203	2203-2204	2204-2205	2205-2206	2206-2207	2207-2208	2208-2209	2209-2210	2210-2211	2211-2212	2212-2213	2213-2214	2214-2215	2215-2216	2216-2217	2217-2218	2218-2219	2219-2220	2220-2221	2221-2222	2222-2223	2223-2224	2224-2225	2225-2226	2226-2227	2227-2228	2228-2229	2229-2230	2230-2231	2231-2232	2232-2233	2233-2234	2234-2235	2235-2236	2236-2237	2237-2238	2238-2239	2239-2240	2240-2241	2241-2242	2242-2243	2243-2244	2244-2245	2245-2246	2246-2247	2247-2248	2248-2249	2249-2250	2250-2251	2251-2252	2252-2253	2253-2254	2254-2255	2255-2256	2256-2257	2257-2258	2258-2259	2259-2260	2260-2261	2261-2262	2262-2263	2263-2264	2264-2265	2265-2266	2266-2267	2267-2268	2268-2269	2269-2270	2270-2271	2271-2272	2272-2273	2273-2274	2274-2275	2275-2276	2276-2277	2277-2278	2278-2279	2279-2280	2280-2281	2281
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(D) OTHER INFORMATION: / Ceres Seq. ID 1578201

(X1) SEQUENCE SUBSTITUTION						
atgagtctat	ttcagcggct	tgcggttctc	tgtattttca	tattatcgaa	acctcgtct	60
acatctccgt	ttcgacgaag	ccaaatctgt	cgtgttttat	aatcccaaaa	gtctccacct	120
aagtcaccga	ctcgatacgg	caagatcgac	agagagaccg	acgcgcgggc	agatcccaag	180
ctcaccggag	agggggaaga	gggcgaccga	agcggcgatg	ggtttcatca	tggacttcgc	240
ggagaatctg	atcctccgtc	tgatggagga	cccggacaag	cgcgaccCag	gttcggcggg	300
agcatgtcta	caagatgaag	gagcggtgcg	agcgcactaa	ggcggcgtgg	agcctccctc	360
tgcgcccCta	cggcttctgg	accttcgacc	gcttcaactc	gcagctctcc	tgggatcccc	420
agatcagcca	ggccgcgggc	Cgtcgggacc	cctacgacga	cctcatcgcc	cgccactctg	480
gctcgcggcc	gtcttcttga	acacccgttc	cgatctttgc	ccagaaggtc	tacttgggGc	540
atcaataaga	aactctttcc	cctcaaatcg	attgtggttc	catcctcttc	tgtctggaaa	600
atgtttgtac	caaactaacc	tatttctctg	tccagtttgg	catggaagta	taagtttgtt	660
acttctattc	tcaagttggt	gtctttgtat	tatgaaatgt	ttccaataat	cagcagtttt	720
tgatgtatgg	tctgtggatcc	g				

(i) SEQUENCE CHARACTERISTICS:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..40
```

- (D) OTHER INFORMATION: / Ceres Seq. ID 1578202

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Phe | Ile | Met | Asp | Phe | Ala | Glu | Asn | Leu | Ile | Leu | Arg | Leu | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Asp | Pro | Asp | Lys | Arg | Asp | Pro | Gly | Ser | Ala | Gly | Ala | Cys | Leu | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Glu | Gly | Ala | Val | Arg | Ala | His |     |     |     |     |     |     |     |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..61
```

- (D) OTHER INFORMATION: / Ceres Seq. ID 1578203

(X1) SEQUENCE DESCRIPTION															
Met	Lys	Glu	Arg	Cys	Glu	Arg	Thr	Lys	Ala	Ala	Trp	Ser	Leu	Pro	Leu
1				5					10					15	
Arg	Pro	Tyr	Gly	Phe	Trp	Thr	Phe	Asp	Arg	Phe	Asn	Ser	Gln	Leu	Ser
			20					25					30		
Trp	Asp	Pro	Gln	Ile	Ser	Gln	Ala	Ala	Gly	Arg	Arg	Asp	Pro	Tyr	Asp
			35				40					45			
Asp	Leu	Ile	Ala	Arg	His	Ser	Gly	Ser	Pro	Pro	Ser	Ser			
	50					55					60				

(i) SEQUENCE CHARACTERISTICS:

- ```
(i) CHAIN CHARACTERISTICS:
 (A) LENGTH: 40 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
```



(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..40  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3786:

Met Leu Ser Pro Asn Tyr Pro Ile Ser Cys Ser Ser Leu Ala Trp Lys  
1 5 10 15  
Tyr Lys Leu Cys Thr Ser Ile Leu Lys Leu Leu Ser Leu Tyr Tyr Glu  
20 25 30  
Met Phe Pro Ile Ile Ser Ser Phe  
35 40

(2) INFORMATION FOR SEQ ID NO:3787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..765  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3787:

gacaagcaag aacagctgtc gatccaattg tcacttgctc tccctccaac aagctaatta 60  
aggccggtca tccctcttct agctcgtttc attatccatg gcggaggaga agcaccacca 120  
ccaccacctg ttccaccaca agaaggacga ggagcaggag gagcagctcg ccggcgsgg 180  
tacgGcgagt ccgccgagta cacggaggcc acggtgacgg aggtcgtgtc cacgggcgag 240  
aacgagtacg acgagtacaa gaaggaggag aagcagcaca agcacaagca gcacctcggc 300  
gaggccggcg ccattGccgc cggcgccctc gcactctacg agaagcacga ggcaaagaag 360  
gacccgagc acgcgcaccg ccacaagatc gaggaggagg tcgcggcggc ggcgcccgctc 420  
ggctccggcg gCttcgCtt ccacgagcac cacgagaaga agaaggacca caaggacgcc 480  
gaggaggccg gcgccgagaa gaagcaccac ttcttcggct gattgatcct cccgtatcgt 540  
cgtcccCtcc ccgtgtgCta cgcgtgcCgt gtgtgagagt gatatcgagc gccCgccgtg 600  
ttgtgcgcgc gtacgtatgt atgcgctcgt gtgatgcacg aataagcgtg gctacgtaat 660  
ctatogtatg tatacgtgtg tgtatgcatg tgcttgtgta tgatcgtggt acgaggaccg 720  
aaaaaatgta tgcaactctg atttacttac atgtttagtt gtttc

(2) INFORMATION FOR SEQ ID NO:3788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..218  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3788:

Gln Ala Arg Thr Ala Val Asp Pro Ile Val Thr Cys Ser Pro Ser Asn  
1 5 10 15  
Lys Leu Ile Lys Ala Gly His Pro Ser Ser Ser Ser Phe His Tyr Pro  
20 25 30  
Trp Arg Arg Arg Ser Thr Thr Thr Thr Cys Ser Thr Thr Arg Arg  
35 40 45  
Thr Arg Ser Arg Arg Ser Ser Ser Pro Ala Xaa Val Arg Arg Val Arg  
50 55 60  
Arg Val His Gly Gly His Gly Asp Gly Gly Arg Val His Gly Arg Glu  
65 70 75 80  
Arg Val Arg Arg Val Gln Glu Gly Gly Glu Ala Ala Gln Ala Gln Ala  
85 90 95  
Ala Pro Arg Arg Gly Arg Arg His Arg Arg Arg Arg Leu Arg Thr Leu

100 105 110  
Arg Glu Ala Arg Gly Lys Glu Gly Pro Gly Ala Arg Ala Pro Pro Gln  
115 120 125  
Asp Arg Gly Gly Gly Arg Gly Gly Gly Gly Arg Arg Leu Arg Arg Leu  
130 135 140  
Arg Leu Pro Arg Ala Pro Arg Glu Glu Glu Gly Pro Gln Gly Arg Arg  
145 150 155 160  
Gly Gly Arg Arg Arg Glu Glu Ala Pro Leu Leu Arg Leu Ile Asp Pro  
165 170 175  
Pro Val Ser Ser Ser Pro Pro Arg Val Leu Arg Val Pro Cys Val Arg  
180 185 190  
Val Ile Ser Ser Ala Arg Arg Val Val Arg Ala Tyr Val Cys Met Arg  
195 200 205  
Ser Cys Asp Ala Arg Ile Ser Val Ala Thr  
210 215

(2) INFORMATION FOR SEQ ID NO:3789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..822
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3789:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| arggtccctg gctatcgaga gaactcgacg agttcatctc catcgtttgt gagagtttcg   | 60  |
| gttggggccag attgtcatatc tcagcgctct gcctcggtct caggcccagg gtgtactgaa | 120 |
| agccagctct tgcccgcac tacacggccc cattttcagc ttgcccctcc agaaccgggt    | 180 |
| cctatctgtg gtgtgccaga cttcaagatg aggggaaaga agagtgatga gctcgaacct   | 240 |
| gtcgaatgctk gcgatgaaga tgatgatggt ggtgacgatg gggacgagga tggtgacttt  | 300 |
| ggggaggagg gtgaagagga cgtctcagaa ggggagggat atgacaacc aaagggcaat    | 360 |
| gagaccaaga agcaaagagg tgatcctgag gaaaatggtg aggaagatga ggaagaacca   | 420 |
| gaagatcagg aggggtggcg cgacgacgat gatgacgacg atgacgatga tgagaacggg   | 480 |
| gatgacgagg acgacgacaa tDgggggatga cgatgaggag ggtgtagatg aagaagacga  | 540 |
| tgaccaggac gaggatgagg aggaagatga tgatgaagac tcgctccagc ccccaaagaa   | 600 |
| gaggaagaag tgaagatctt ctgccgcttt agttaccgtg cgctgagttc tgcttggtt    | 660 |
| ttcgtcatat cctcgcatct caactttccc atagagagtt aagaaggatc cacacgttca   | 720 |
| gcagcacgtg tgggcttgta ggagctttat gatttgaggc aattagggac aactcttatg   | 780 |
| tcattgttgc ttgcttctgt ggagtcgaac agatgtttcg ct                      |     |

(2) INFORMATION FOR SEQ ID NO:3790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..169
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3790:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Xaa Val Pro Gly Tyr Arg Glu Asn Ser Thr Ser Ser Ser Pro Ser Phe |  |
| 1 5 10 15                                                       |  |
| Val Arg Val Ser Val Gly Pro Asp Cys His Thr Gln Arg Pro Ala Ser |  |
| 20 25 30                                                        |  |
| Val Ser Gly Pro Gly Cys Thr Glu Ser Gln Leu Leu Pro Ala Ser Thr |  |
| 35 40 45                                                        |  |
| Arg Pro His Phe Gln Leu Ala Pro Pro Glu Pro Gly Pro Ile Cys Gly |  |
| 50 55 60                                                        |  |

Val Pro Asp Phe Lys Met Arg Gly Lys Lys Ser Asp Glu Leu Glu Pro  
65 70 75 80  
Val Asp Ala Xaa Asp Glu Asp Asp Asp Gly Gly Asp Asp Gly Asp Glu  
85 90 95  
Asp Gly Asp Phe Gly Glu Glu Gly Glu Glu Asp Val Ser Glu Gly Glu  
100 105 110  
Gly Tyr Asp Asn Pro Lys Gly Asn Glu Thr Lys Lys Gln Arg Gly Asp  
115 120 125  
Pro Glu Glu Asn Gly Glu Glu Asp Glu Glu Glu Pro Glu Asp Gln Glu  
130 135 140  
Gly Gly Gly Asp Asp Asp Asp Asp Asp Asp Asp Asp Glu Asn Gly  
145 150 155 160  
Asp Asp Glu Asp Asp Asp Asn Xaa Gly  
165

(2) INFORMATION FOR SEQ ID NO:3791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1578249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3791:

Met Ser Ser Asn Leu Ser Met Xaa Ala Met Lys Met Met Met Val Val  
1 5 10 15  
Thr Met Gly Thr Arg Met Val Thr Leu Gly Arg Arg Val Lys Arg Thr  
20 25 30  
Ser Gln Lys Gly Arg Asp Met Thr Thr Gln Arg Ala Met Arg Pro Arg  
35 40 45  
Ser Lys Glu Val Ile Leu Arg Lys Met Val Arg Lys Met Arg Lys Asn  
50 55 60  
Gln Lys Ile Arg Arg Val Ala Ala Thr Thr Met Met Thr Thr Met Thr  
65 70 75 80  
Met Met Arg Thr Gly Met Thr Arg Thr Thr Thr Xaa Gly Asp Asp Asp  
85 90 95  
Glu Glu Gly Val Asp Glu Glu Asp Asp Asp Gln Asp Glu Asp Glu Glu  
100 105 110  
Glu Asp Asp Asp Glu Asp Ser Leu Gln Pro Pro Lys Lys Arg Lys Lys  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1578250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3792:

Met Xaa Ala Met Lys Met Met Met Val Val Thr Met Gly Thr Arg Met  
1 5 10 15  
Val Thr Leu Gly Arg Arg Val Lys Arg Thr Ser Gln Lys Gly Arg Asp  
20 25 30  
Met Thr Thr Gln Arg Ala Met Arg Pro Arg Ser Lys Glu Val Ile Leu

35 40 45  
Arg Lys Met Val Arg Lys Met Arg Lys Asn Gln Lys Ile Arg Arg Val  
50 55 60  
Ala Ala Thr Thr Met Met Thr Thr Met Thr Met Met Arg Thr Gly Met  
65 70 75 80  
Thr Arg Thr Thr Thr Xaa Gly Asp Asp Asp Glu Glu Gly Val Asp Glu  
85 90 95  
Glu Asp Asp Asp Gln Asp Glu Asp Glu Glu Glu Asp Asp Asp Glu Asp  
100 105 110  
Ser Leu Gln Pro Pro Lys Lys Arg Lys Lys  
115 120

(2) INFORMATION FOR SEQ ID NO:3793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..928  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3793:

aagacagcaa ccacatgctc accagtgcac gccccgaag caaaagactt gctggatata 60  
accaaagatt aggttaagaa gcagctcgag ccgcccttcc ttccagtcac atggccgcgc 120  
ccgcttcttc gggtacctcc agaggttgag cactccgtag cagtacctcc gtgggttttc 180  
atcgccaccg cgggaataat ccggtgatca gccccgcgctc ttctgtgtgc cgacgaagcc 240  
ttactggtgg atcaacgatg aactcctcgg gcacgaacgg tgccttccct cctatcaaag 300  
gaagtacacg aatccccgca gttggtcctg gccctgccag tccgtcagga ggaaacctgc 360  
cgatacccaa catgcctcca tgggccaagt ggctgggtcgG cgccgccata gtcgcgatac 420  
caatctacag gaggttcaga acactagaag ataagataga gaagacggcg gaggtggcga 480  
tcgaggtggt ggacacgggt gcgggggtcgg cggagaagggt ggccggcgagg tcgccggcgc 540  
gttccccggc aacgagagcc tcagggaggg ggctgcgagg atcaaggcgg tcacggatga 600  
gatcgaggag gacgccgaga gagccgaggg cctgatcgag aaggttgacg agataaagga 660  
acaagttgat tcaatcgctg atcccttaat cgacaagggt gtcaaggata aagaaacct 720  
gagagaagga accaaggagg aggcaatgac atgatgtaga ttattgaagg tataaagatt 780  
ggttaggcgg tgccgcgggt gtaaccggaa gaaaatacct accgcatgta aaaaaaatca 840  
ctaaatataa atataagaag cttttcagaa aaaaaactct tctctaacag ttatgtaaga 900  
caagttctta aatttacaaa cttcttct

(2) INFORMATION FOR SEQ ID NO:3794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..174  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3794:

Met Ala Ala Pro Ala Ser Ser Val Thr Ser Arg Gly Leu Ala Leu Arg  
1 5 10 15  
Ser Ser Thr Ser Val Gly Phe His Arg His Arg Gly Asn Asn Pro Val  
20 25 30  
Ile Ser Pro Ala Ser Ser Arg Arg Arg Arg Ser Leu Thr Gly Gly Ser  
35 40 45  
Thr Met Asn Ser Ser Gly Met Asn Gly Ala Phe Pro Pro Ile Lys Gly  
50 55 60  
Ser Thr Arg Ile Pro Ala Val Gly Pro Gly Pro Ala Ser Pro Ser Gly  
65 70 75 80

Gly Asn Leu Pro Ile Pro Asn Met Pro Pro Trp Ala Lys Trp Leu Val  
85 90 95  
Gly Ala Ala Ile Val Ala Ile Pro Ile Tyr Arg Arg Phe Arg Thr Leu  
100 105 110  
Glu Asp Lys Ile Glu Lys Thr Ala Glu Val Ala Ile Glu Val Val Asp  
115 120 125  
Thr Val Ala Gly Ser Ala Glu Lys Val Ala Ala Arg Ser Pro Ala Arg  
130 135 140  
Ser Pro Ala Thr Arg Ala Ser Gly Arg Arg Arg Arg Gly Ser Arg Arg  
145 150 155 160  
Ser Arg Met Arg Ser Arg Arg Thr Pro Arg Glu Pro Arg Pro  
165 170

(2) INFORMATION FOR SEQ ID NO:3795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3795:

Met Asn Ser Ser Gly Met Asn Gly Ala Phe Pro Pro Ile Lys Gly Ser  
1 5 10 15  
Thr Arg Ile Pro Ala Val Gly Pro Gly Pro Ala Ser Pro Ser Gly Gly  
20 25 30  
Asn Leu Pro Ile Pro Asn Met Pro Pro Trp Ala Lys Trp Leu Val Gly  
35 40 45  
Ala Ala Ile Val Ala Ile Pro Ile Tyr Arg Arg Phe Arg Thr Leu Glu  
50 55 60  
Asp Lys Ile Glu Lys Thr Ala Glu Val Ala Ile Glu Val Val Asp Thr  
65 70 75 80  
Val Ala Gly Ser Ala Glu Lys Val Ala Ala Arg Ser Pro Ala Arg Ser  
85 90 95  
Pro Ala Thr Arg Ala Ser Gly Arg Arg Arg Gly Ser Arg Arg Ser  
100 105 110  
Arg Met Arg Ser Arg Arg Thr Pro Arg Glu Pro Arg Pro  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3796:

Met Asn Gly Ala Phe Pro Pro Ile Lys Gly Ser Thr Arg Ile Pro Ala  
1 5 10 15  
Val Gly Pro Gly Pro Ala Ser Pro Ser Gly Gly Asn Leu Pro Ile Pro  
20 25 30  
Asn Met Pro Pro Trp Ala Lys Trp Leu Val Gly Ala Ala Ile Val Ala  
35 40 45  
Ile Pro Ile Tyr Arg Arg Phe Arg Thr Leu Glu Asp Lys Ile Glu Lys  
50 55 60  
Thr Ala Glu Val Ala Ile Glu Val Val Asp Thr Val Ala Gly Ser Ala

(D) OTHER INFORMATION: / Ceres Seq. ID 1578319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3799:

Met Ser Arg Ser Gly Gln Pro Pro Asp Leu Lys Lys Tyr Met Asp Lys  
1 5 10 15  
Lys Leu Gln Ile Lys Leu Asn Ala Asn Arg Val Val Ile Gly Thr Leu  
20 25 30  
Arg Gly Phe Asp Gln Phe Met Asn Leu Val Ile Asp Asn Thr Val Glu  
35 40 45  
Val Asn Gly Asn Asp Lys Thr Asp Ile Gly Met Val Val Ile Arg Gly  
50 55 60  
Asn Ser Val Val Met Ile Glu Ala Leu Glu Pro Val Ala Lys Ser Gln  
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:3800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..67  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3800:

Met Asp Lys Lys Leu Gln Ile Lys Leu Asn Ala Asn Arg Val Val Ile  
1 5 10 15  
Gly Thr Leu Arg Gly Phe Asp Gln Phe Met Asn Leu Val Ile Asp Asn  
20 25 30  
Thr Val Glu Val Asn Gly Asn Asp Lys Thr Asp Ile Gly Met Val Val  
35 40 45  
Ile Arg Gly Asn Ser Val Val Met Ile Glu Ala Leu Glu Pro Val Ala  
50 55 60  
Lys Ser Gln  
65

(2) INFORMATION FOR SEQ ID NO:3801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..826  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3801:

cccatcgatt ttctcttgga atcgtaacct cagaaagcca aatctcattc tccggcgctc 60  
aggcccaccc aagcgtcgac tctcccgatc caatcggtac ctctagtctc ctgcgccggc 120  
gtagcggcgt cgggcgaaca gcggtgactt ggcgagggcg cttggccggc gacaatcatc 180  
cactaggatg gaaggtgagg cagagaccgt ggttggttct tgttctaaac catgtgggcc 240  
tctggaggac tactacattc cagattacat tctgaagcca gGtgcccaac aagtacttgt 300  
tgatcatgcg gcaccctgcc ccgttgtagt gttcatcaac tcaagatctg gaggccaaact 360  
tggaagtagt ttaatcaaaa catatcgtga gcttctcaat gaagcacagg tttttgatct 420  
ctcaaaagag gctccagata aggtattgca tcggtttatat gccaaccttg aaaggctgaa 480  
gatggaagga gacattcttg cagttcaaat ttKggaggac actgaggcta attgttgacg 540  
gcggtgatgg tacagctagc tggctgcttg gggtagtcag tgaccttaag ctttcccacc 600  
cacctccagt ggcaactgtg cctctgggaa cgggaaataa cctccccttt tcatttggat 660  
ggggaaagaa gaatccttct actgaccaag aggctgtaaa atcattcctc gggctagtaa 720  
agcatgcaaa agaaattaag attgatagtt ggcacatcat tttgagaatg cgagttccag 780  
aggaaggctc atgtgatect attgctccac tagatttgcc tcattc

(2) INFORMATION FOR SEQ ID NO:3802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3802:

```
Met Glu Gly Glu Ala Glu Thr Val Val Gly Ser Cys Ser Lys Pro Cys
1 5 10 15
Gly Pro Leu Glu Asp Tyr Tyr Ile Pro Asp Tyr Ile Leu Lys Pro Gly
 20 25 30
Ala Gln Gln Val Leu Val Asp His Ala Ala Pro Cys Pro Val Val Val
 35 40 45
Phe Ile Asn Ser Arg Ser Gly Gly Gln Leu Gly Ser Ser Leu Ile Lys
50 55 60
Thr Tyr Arg Glu Leu Leu Asn Glu Ala Gln Val Phe Asp Leu Ser Lys
65 70 75 80
Glu Ala Pro Asp Lys Val Leu His Arg Leu Tyr Ala Asn Leu Glu Arg
 85 90 95
Leu Lys Met Glu Gly Asp Ile Leu Ala Val Gln Ile Xaa Glu Asp Thr
 100 105 110
Glu Ala Asn Cys Cys Arg Arg
 115
```

(2) INFORMATION FOR SEQ ID NO:3803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..648
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3803:

```
aagcagcagc agcacagtca tccacactaa cgaacgaact cttgctccga tcacgagcta 60
gctgaggtcg acgatggcgg ctgtgctgaa cagcaggaag acggcgcagg cggtggtggc 120
cgtgctggtg gcggcggcgc tgctggcttc gtccacttcg gcggcgatca cCtgcgggca 180
ggtgggggtcg tcgCtggcgc cgtgcatccc gtacgcgacg gggagggccca gcgcgctccc 240
cgcgctcgtc tgcagcggcg tcaagagcct caacagcgcg gcgcggacca gcgcggaccg 300
ccaggcggCg tgccgctgcc tcaagagcct cgccaacagc gtcaagagcg tcaacatggg 360
caccgtcgcc accatccccg gcaagtgcgg cgtctccgtc ggattcccca tcagcatgtc 420
caccgactgc aacaagatca gctaagttac gacgaccaag ctaataagcc taccgaacgt 480
acacgaacgt cccgcgcgct gcacgagtga tgaagccagg ggagaaataa aataaagccg 540
ctgtattgcc aggagcagca tgcattatatt atcgatctat atatatactg tactgtagta 600
ctctattata tatgtatata tgtgtggcct gcagtgcgag ttgcttcg
```

(2) INFORMATION FOR SEQ ID NO:3804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3804:

(2) INFORMATION FOR SEQ ID NO:3805:

(A) LENGTH: 676 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..676

(D) OTHER INFORMATION: / Ceres Seq. ID 1578352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3805:

| (X1) SEQUENCE DESTRUCTION: SEQ ID NO: 1 |            |             |            |             |            |     |
|-----------------------------------------|------------|-------------|------------|-------------|------------|-----|
| gacacacctc                              | ccaacacctc | cactcccggc  | ggcgggcgcg | gcgggcgasa  | gcggcagcag | 60  |
| catccgaaga                              | tggtgaagtt | cctcaagccc  | ggcaaggccg | ttatcctcct  | ccagggcCGc | 120 |
| ttcgccggca                              | ggaaggcagt | tatcgggcgc  | gtggccctgg | tgaactacgg  | ggaggactat | 180 |
| ggccgtctcg                              | ttgtcatcgt | cgatgttggtc | gaccagaaca | gggcacttgt  | ggatgccct  | 240 |
| gatatggtca                              | ggtgccaggt | gaactttcaag | cggctctcac | ttactgacat  | caagattgac | 300 |
| atcaaacgtg                              | tccccaagaa | gacagccctg  | atcaaggcga | tggaggaaagc | tgatgtgaag | 360 |
| accaagtggg                              | agaacagctc | atggggcaag  | aagctgattg | tccagaagag  | gagagcatcg | 420 |
| ctcaatgact                              | ttgataggtt | caaagtcatg  | ctggcgaaga | ttaagagggg  | cgggtctatc | 480 |
| aggcaagagc                              | tgcccaagct | gaagaaggcg  | tccacggctt | aaggagtctc  | tttccgtgaa | 540 |
| tgtcatgtta                              | gagtttttgg | ttatgagttg  | gatcagcaat | tcgattgagc  | gttgtcaaag | 600 |
| ccagaattac                              | caatatgttc | cctgtaaacc  | catttcaaac | tttatcaagc  | acgggcgtgc | 660 |
| tcaggatact                              | tttgcc     |             |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:3806:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1578353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3806:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Thr | Pro | Pro | Lys | Pro | Tyr | Thr | Pro | Gly | Gly | Gly | Gly | Gly | Gly | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Xaa | Arg | Gln | Gln | His | Pro | Lys | Met | Val | Lys | Phe | Leu | Lys | Pro | Gly | Lys |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Val | Ile | Leu | Leu | Gln | Gly | Arg | Phe | Ala | Gly | Arg | Lys | Ala | Val | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Arg | Val | Ala | Leu | Val | Asn | Tyr | Gly | Glu | Asp | Tyr | Gly | Arg | Leu | Val |

50 55 60  
Val Ile Val Asp Val Val Asp Gln Asn Arg Ala Leu Val Asp Ala Pro  
65 70 75 80  
Asp Met Val Arg Cys Gln Val Asn Phe Lys Arg Leu Ser Leu Thr Asp  
85 90 95  
Ile Lys Ile Asp Ile Lys Arg Val Pro Lys Lys Thr Ala Leu Ile Lys  
100 105 110  
Ala Met Glu Glu Ala Asp Val Lys Thr Lys Trp Glu Asn Ser Ser Trp  
115 120 125  
Gly Lys Lys Leu Ile Val Gln Lys Arg Arg Ala Ser Leu Asn Asp Phe  
130 135 140  
Asp Arg Phe Lys Val Met Leu Ala Lys Ile Lys Arg Gly Gly Ala Ile  
145 150 155 160  
Arg Gln Glu Leu Ala Lys Leu Lys Lys Ala Ser Thr Ala  
165 170

(2) INFORMATION FOR SEQ ID NO:3807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3807:

Met Val Lys Phe Leu Lys Pro Gly Lys Ala Val Ile Leu Leu Gln Gly  
1 5 10 15  
Arg Phe Ala Gly Arg Lys Ala Val Ile Gly Arg Val Ala Leu Val Asn  
20 25 30  
Tyr Gly Glu Asp Tyr Gly Arg Leu Val Val Ile Val Asp Val Val Asp  
35 40 45  
Gln Asn Arg Ala Leu Val Asp Ala Pro Asp Met Val Arg Cys Gln Val  
50 55 60  
Asn Phe Lys Arg Leu Ser Leu Thr Asp Ile Lys Ile Asp Ile Lys Arg  
65 70 75 80  
Val Pro Lys Lys Thr Ala Leu Ile Lys Ala Met Glu Glu Ala Asp Val  
85 90 95  
Lys Thr Lys Trp Glu Asn Ser Ser Trp Gly Lys Lys Leu Ile Val Gln  
100 105 110  
Lys Arg Arg Ala Ser Leu Asn Asp Phe Asp Arg Phe Lys Val Met Leu  
115 120 125  
Ala Lys Ile Lys Arg Gly Gly Ala Ile Arg Gln Glu Leu Ala Lys Leu  
130 135 140  
Lys Lys Ala Ser Thr Ala  
145 150

(2) INFORMATION FOR SEQ ID NO:3808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3808:

Met Val Arg Cys Gln Val Asn Phe Lys Arg Leu Ser Leu Thr Asp Ile  
1 5 10 15

Lys Ile Asp Ile Lys Arg Val Pro Lys Lys Thr Ala Leu Ile Lys Ala  
20 25 30  
Met Glu Glu Ala Asp Val Lys Thr Lys Trp Glu Asn Ser Ser Trp Gly  
35 40 45  
Lys Lys Leu Ile Val Gln Lys Arg Arg Ala Ser Leu Asn Asp Phe Asp  
50 55 60  
Arg Phe Lys Val Met Leu Ala Lys Ile Lys Arg Gly Gly Ala Ile Arg  
65 70 75 80  
Gln Glu Leu Ala Lys Leu Lys Lys Ala Ser Thr Ala  
85 90

(2) INFORMATION FOR SEQ ID NO:3809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..730
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3809:

|            |             |            |             |            |             |     |
|------------|-------------|------------|-------------|------------|-------------|-----|
| tagtcgctgg | agatagagcc  | gagaacaagg | gcaactgacg  | cggtcaccct | cgcccccaac  | 60  |
| acagagagaa | ggctctgctct | ccaccggatg | gactcccacg  | gcaagcccaa | gcccgcgggt  | 120 |
| tcgacgccgc | cgacgccgcc  | gaagccgccg | aagccgccga  | cgccgccgaa | gccgcgcgacg | 180 |
| ccgcgcgacg | cgacgccgcc  | gacgcccgag | gcgaggaagg  | ggttcatgcg | ccgcatcttc  | 240 |
| cctttcctcc | tagccgccaa  | cctctttgtc | gtagcttatg  | tcctcgtagc | ggccaaccaa  | 300 |
| aaggactcag | caaagaagga  | cccaacgact | gatcctgcta  | ctgcaactgc | tgggaagcct  | 360 |
| gctgagccag | tctctatccc  | cagaaaggag | ctcccaccaa  | tccctgaaga | tgaccagcgc  | 420 |
| aagCtctaca | aatggatgct  | ggaagagaag | cggaagatca  | agccacgcaa | tgtgtgccgag | 480 |
| aagaagaaac | tcgatgagga  | gaaggccctt | ctaaaagagt  | tcatccgagc | aggatccCtc  | 540 |
| ccaagcttct | aaaagagatc  | aagccatttg | ggctctctgt  | gtctgatgtt | cagccaagaa  | 600 |
| gatgattggg | cctgattgga  | ttgtgtacaa | acacagtact  | gtgctatctt | gtaaactgat  | 660 |
| gtctccatga | tgtagcctcc  | tcgagttcaa | aggttggtgtg | gatgcaaact | agtgtgtgtg  | 720 |
| gcattggttc |             |            |             |            |             |     |

(2) INFORMATION FOR SEQ ID NO:3810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3810:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Asp Ser His Gly Lys Pro Lys Pro Ala Gly Ser Thr Pro Pro Thr |  |
| 1 5 10 15                                                       |  |
| Pro Pro Lys Pro Pro Lys Pro Pro Thr Pro Pro Lys Pro Pro Thr Pro |  |
| 20 25 30                                                        |  |
| Pro Thr Pro Thr Pro Pro Thr Pro Glu Ala Arg Lys Gly Phe Met Arg |  |
| 35 40 45                                                        |  |
| Arg Ile Phe Pro Phe Leu Leu Ala Ala Asn Leu Phe Val Val Ala Tyr |  |
| 50 55 60                                                        |  |
| Val Leu Val Arg Ala Asn Gln Lys Asp Ser Ala Lys Lys Asp Pro Thr |  |
| 65 70 75 80                                                     |  |
| Thr Asp Pro Ala Thr Ala Thr Ala Gly Lys Pro Ala Glu Pro Val Ser |  |
| 85 90 95                                                        |  |
| Ile Pro Arg Lys Glu Leu Pro Pro Ile Pro Glu Asp Asp Gln Arg Lys |  |
| 100 105 110                                                     |  |

(2) INFORMATION FOR SEQ ID NO:3811:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3811:

(2) INFORMATION FOR SEQ ID NO:3812:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3812:

(2) INFORMATION FOR SEQ ID NO:3813:

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..831

(D) OTHER INFORMATION: / Ceres Seq. ID 1578386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3813:

|            |             |            |             |            |             |     |
|------------|-------------|------------|-------------|------------|-------------|-----|
| aaacttgtca | agctttttcca | agaaacctag | ctagctagct  | agtaagaggc | acaggccggc  | 60  |
| accatgtcgc | accaccattc  | ccaccacaaa | tctcattctc  | acaaccgtac | ccaccaccac  | 120 |
| tctcactctc | actccggang  | agntggaggc | ggcggcgggc  | gtggcggtgc | cgggtggaggc | 180 |
| ggaggcggag | tggctaaatg  | ccactgtgat | tgtcacacc   | atgatcattc | accgccaagg  | 240 |
| caaccgttct | tcccgccacc  | gcagcttcca | ccaccacaaa  | tctttcttcc | tgcaggacca  | 300 |
| ccgctccctc | cgcttgggcc  | gctcccattt | ccgccaccga  | tattcttcgg | acctccggcg  | 360 |
| ccgccacccc | cgccccggcc  | accgttcatg | tgcccacgac  | cgccaccatg | catgtaccgg  | 420 |
| agGtggtaat | ggagataaaa  | gttgatatac | acgggtgtgca | tgtgtttgtg | ccaaagcttc  | 480 |
| tcgtacgtgg | tgttcgagtt  | tctgtcacc  | caaataagaa  | cagagctctt | ctccggatag  | 540 |
| aactatcttc | acagggttcc  | ctgttcaagt | taggatggca  | cgcacatca  | tatctcggaa  | 600 |
| ggaagccctc | ggggagtctt  | ctccatgtat | gggtggagtt  | ttgaaagaag | tcattatatt  | 660 |
| attgctagtt | cttgttccct  | actagatgtt | ctcgttgatg  | cgtggatttt | atacgtgtac  | 720 |
| ttgttctctt | gtgctttcca  | ccggccctga | tgtcgtcccg  | ttgtaaccga | tgttcggttg  | 780 |
| tgtttcaatg | tgtcttttgt  | ttaatgatat | gttggtgtgc  | tgttttctt  | c           |     |

(2) INFORMATION FOR SEQ ID NO:3814:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1578387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3814:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | His | His | His | Ser | His | His | Lys | Ser | His | Ser | His | Asn | Arg | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | His | His | Ser | His | Ser | His | Ser | Gly | Xaa | Xaa | Gly | Gly | Gly | Gly | Gly |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Gly | Gly | Ala | Gly | Gly | Gly | Gly | Gly | Val | Ala | Lys | Cys | His | Cys |     |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Asp | Cys | Ser | His | His | Asp | His | Ser | Pro | Pro | Arg | Gln | Pro | Phe | Phe | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Pro | Gln | Leu | Pro | Pro | Pro | Gln | Ile | Phe | Leu | Pro | Ala | Gly | Pro | Pro |
|     |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Pro | Pro | Pro | Gly | Pro | Leu | Pro | Phe | Pro | Pro | Pro | Ile | Phe | Phe | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Pro | Pro | Pro | Pro | Pro | Pro | Pro | Pro | Pro | Phe | Met | Cys | Pro | Arg |     |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Pro | Pro | Pro | Cys | Met | Tyr | Arg | Arg | Trp |     |     |     |     |     |     |     |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3815:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1578388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3815:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Ile | His | Arg | Gln | Gly | Asn | Arg | Ser | Ser | Arg | His | Arg | Ser | Phe |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |

His His His Lys Ser Phe Phe Leu Gln Asp His Arg Ser Leu Arg Leu  
20 25 30  
Gly Arg Ser His Phe Arg His Arg Tyr Ser Ser Asp Leu Arg Arg Arg  
35 40 45  
His Pro Arg Pro Arg His Arg Ser Cys Ala His Asp Arg His His Ala  
50 55 60  
Cys Thr Gly Gly Gly Asn Gly Asp Lys Ser  
65 70

(2) INFORMATION FOR SEQ ID NO:3816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3816:

Met His Val Pro Glu Val Val Met Glu Ile Lys Val Asp Ile His Gly  
1 5 10 15  
Val His Val Phe Val Pro Lys Leu Leu Val Arg Gly Val Arg Val Ser  
20 25 30  
Val Thr Pro Asn Lys Asn Arg Ala Leu Leu Arg Ile Glu Leu Ser Ser  
35 40 45  
Gln Gly Ser Leu Phe Lys Leu Gly Trp His Ala Ser Ser Tyr Leu Gly  
50 55 60  
Arg Lys Pro Ser Gly Ser Leu Leu His Val Trp Val Glu Phe  
65 70 75

(2) INFORMATION FOR SEQ ID NO:3817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..750
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3817:

atctcttctt tccccctctcc ctccccctcgc cgtcgctgtc gtgcgcgtcc gtgctagcca 60  
tggatctagg cgctcccgcgt cgacggcgct taccgatccg cctcttgAct ggtgtcgctc 120  
gccgtcctca tggctctcac cgcgcgttcc agtgccgaag tcatcaccct caccgaagag 180  
accttctccg acaagataaa ggagaaggac acggtgtggt ttgtgcagtt ctgcgtcccc 240  
tgggtgtaaac actgcaagaa ccttggaaca ctatgggagg acctgggaaa ggttatggaa 300  
ggtgcggatg aaattgagat tgggcaagtt gactgtggtg tcagcaaacc agtatgtcga 360  
aaggtcgata tacactccta cccaacattc aaggtgtttt atgaaggcga agaagtagta 420  
aaatataaag gacctaggaa tgtggaatcg ctgaagaact tcgtgttgaa tgaagctgag 480  
aaagcaggtg aggcaaagct tcaagctgat tgaggcaggg gagtttcagc aagcatgtgg 540  
cgtagacaag gaacaatgct gtgcAacatt gtcttctatc ctgtcattta caaagccaat 600  
ttacaggaaa gaaatgatct tatgaccccg tatcagagta ttcctcttcg aaagtaactc 660  
cgaatcagtt catagaagct gtactccatt ccatagtttt tatcacattg acaaactccg 720  
aatcagttaa tagaagctgt actccattcg

(2) INFORMATION FOR SEQ ID NO:3818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3818:

(2) INFORMATION FOR SEQ ID NO:3819:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1578396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3819:

(2) INFORMATION FOR SEQ ID NO:3820:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1578397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3820:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gly | Ala | Asp | Glu | Ile | Glu | Ile | Gly | Gln | Val | Asp | Cys | Gly | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Lys | Pro | Val | Cys | Ser | Lys | Val | Asp | Ile | His | Ser | Tyr | Pro | Thr | Phe |





(2) INFORMATION FOR SEQ ID NO:3823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3823:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | Ser | Val | Pro | Gly | Ser | Ser | Ala | Pro | Ser | Val | Arg | Pro | Pro | Pro | Arg |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Met | Ser | Asp | Glu | Ala | Arg | Arg | Gly | Pro | Ala | Gly | Ala | Ala | Gln | Val | Val |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu | Arg | Ala | Ser | Ser | Glu | Asp | Arg | Lys | Pro | Val | Gly | Ser | Gly | Ser | Pro |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Pro | Pro | Ala | Ala | Thr | Ala | Thr | Ala | Val | Ala | His | Lys | Ile | Gln | Leu | Lys |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Ser | Ala | Asp | Met | Lys | Glu | Glu | Met | Arg | Gln | Glu | Ala | Phe | Glu | Ile | Ala |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Arg | Ile | Ala | Phe | Glu | Lys | His | Ser | Met | Glu | Lys | Asp | Ile | Ala | Glu | Tyr |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ile | Lys | Lys | Glu | Phe | Asp | Lys | Asn | His | Gly | Pro | Thr | Trp | His | Cys | Ile |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Val | Gly | Arg | Asn | Phe | Gly | Ser | Tyr | Val | Thr | His | Glu | Thr | Asn | Tyr | Phe |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Val | Tyr | Phe | Tyr | Ile | Asp | Ser | Lys | Ala | Val | Leu | Leu | Phe | Lys | Ser | Gly |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:3824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3824:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Asp | Glu | Ala | Arg | Arg | Gly | Pro | Ala | Gly | Ala | Ala | Gln | Val | Val |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Leu | Arg | Ala | Ser | Ser | Glu | Asp | Arg | Lys | Pro | Val | Gly | Ser | Gly | Ser | Pro |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Pro | Pro | Ala | Ala | Thr | Ala | Thr | Ala | Val | Ala | His | Lys | Ile | Gln | Leu | Lys |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Ala | Asp | Met | Lys | Glu | Glu | Met | Arg | Gln | Glu | Ala | Phe | Glu | Ile | Ala |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Arg | Ile | Ala | Phe | Glu | Lys | His | Ser | Met | Glu | Lys | Asp | Ile | Ala | Glu | Tyr |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Ile | Lys | Lys | Glu | Phe | Asp | Lys | Asn | His | Gly | Pro | Thr | Trp | His | Cys | Ile |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Val | Gly | Arg | Asn | Phe | Gly | Ser | Tyr | Val | Thr | His | Glu | Thr | Asn | Tyr | Phe |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Val | Tyr | Phe | Tyr | Ile | Asp | Ser | Lys | Ala | Val | Leu | Leu | Phe | Lys | Ser | Gly |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:3825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..855
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3825:

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| aactcactcg  | tcccccttcca | gttccgcttc | cgatctgcgc | ttcgatctcc | ctcttcgcag | 60  |
| aggtgcttgt  | gagcatgtat  | ctgctaggca | acaaaagtgg | aaagaagaaa | gtgtatgtcg | 120 |
| attatatgaa  | tgtccctcta  | ccgatgccca | tcgaagagaa | ttacggtggg | cgcttctttg | 180 |
| acgacgacga  | cgatcttgcc  | caagttcttc | aagatcagga | aatattgtat | catttaattc | 240 |
| aaggaagtaa  | tgggtgggga  | ggtttctacc | tcaaagactg | gtaagcatgg | ccatgccaaa | 300 |
| tgccactttg  | ttgccataga  | catattcaac | gggaaaaagc | ttgaagatat | tgttccttca | 360 |
| tcacacaact  | gtgatattcc  | gcagtgaac  | cgtactgagt | accagctgat | tgatatatca | 420 |
| gaggatggat  | ttgtgagcct  | tcttacttca | gatggcaaca | ctaaggatga | tcttagactc | 480 |
| ccaactgatg  | agactcttgt  | ggcccagatc | aaggaagggg | ttgaaagcgg | caaggatcct | 540 |
| Ggttgtgact  | gtccagtcctg | ctatggggga | ggagcagatc | tgcgcgctga | aggatgtttg | 600 |
| ccccaaagtaa | cttacctgcc  | ttggaatact | gtatctcaaa | acctaaatcg | aaaaaagaag | 660 |
| tgtatcaagg  | attgctacag  | agacatccat | ctggcttgag | ctggcttttg | ctatggcaaa | 720 |
| cacaagtgca  | gggatcgctg  | ggtgtgtcac | cgtgtctgca | ttatctgtgg | ttacattctg | 780 |
| gacctgtat   | tttctatggg  | tttatgcccc | ctactgttta | gtattaatta | tcaataaatt | 840 |
| tgtttgggac  | ggttg       |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:3826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3826:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Thr | Arg | Pro | Leu | Pro | Val | Pro | Leu | Pro | Ile | Cys | Ala | Ser | Ile | Ser |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Leu | Phe | Ala | Glu | Val | Leu | Val | Ser | Met | Tyr | Leu | Leu | Gly | Asn | Lys | Ser |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Gly | Lys | Lys | Lys | Val | Tyr | Val | Asp | Tyr | Met | Asn | Val | Pro | Leu | Pro | Tyr |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |  |
| Ala | Ile | Glu | Glu | Asn | Tyr | Gly | Gly | Arg | Phe | Phe | Asp | Asp | Asp | Asp | Asp |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Leu | Ala | Gln | Val | Leu | Gln | Asp | Gln | Glu | Ile | Leu | Tyr | His | Leu | Ile | Gln |  |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |  |
| Gly | Ser | Asn | Gly | Gly | Gly | Gly | Phe | Tyr | Leu | Lys | Asp | Trp |     |     |     |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:3827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1578424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3827:

Met Val Val Glu Val Ser Thr Ser Lys Thr Gly Lys His Gly His Ala  
1 5 10 15  
Lys Cys His Phe Val Ala Ile Asp Ile Phe Asn Gly Lys Lys Leu Glu  
20 25 30  
Asp Ile Val Pro Ser Ser His Asn Cys Asp Ile Pro His Val Asn Arg  
35 40 45  
Thr Glu Tyr Gln Leu Ile Asp Ile Ser Glu Asp Gly Phe Val Ser Leu  
50 55 60  
Leu Thr Ser Asp Gly Asn Thr Lys Asp Asp Leu Arg Leu Pro Thr Asp  
65 70 75 80  
Glu Thr Leu Val Ala Gln Ile Lys Glu Gly Phe Glu Ser Gly Lys Asp  
85 90 95  
Leu Gly Cys Asp Cys Pro Val Cys Tyr Gly Gly Gly Ala Asp Leu Arg  
100 105 110  
Ala Glu Gly Cys Trp Pro Gln Val Thr Tyr Leu Pro Trp Asn Thr Val  
115 120 125  
Ser Gln Asn Leu Asn Arg Lys Lys Lys Cys Ile Lys Asp Cys Tyr Arg  
130 135 140  
Asp Ile His Leu Ala  
145

(2) INFORMATION FOR SEQ ID NO:3828:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1578425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3828:

Met Leu Ala Pro Ser Asn Leu Pro Ala Leu Glu Tyr Cys Ile Ser Lys  
1 5 10 15  
Pro Lys Ser Lys Lys Glu Val Tyr Gln Gly Leu Leu Gln Arg His Pro  
20 25 30  
Ser Gly Leu Ser Trp Leu Leu Leu Trp Gln Thr Gln Val Gln Gly Ser  
35 40 45  
Leu Gly Val Ala Pro Cys Leu His Tyr Leu Trp Leu His Ser Gly Pro  
50 55 60  
Cys Ile Phe Tyr Gly Phe Met Pro Pro Thr Val  
65 70 75

(2) INFORMATION FOR SEQ ID NO:3829:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 670 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..670

(D) OTHER INFORMATION: / Ceres Seq. ID 1578443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3829:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aaccggagaa caacgcactt gtgttgcgta cgtcggtcac atgcattgca tctgcatccg | 60  |
| gagtagcgag ttctagacac agcaggcaac agactgargt agcccagcga gcgagcgagc | 120 |
| aatggcaacc ctacgcgccg cccccctcgt cgGcgcgggc gccgtcgcca ggccgtgtca | 180 |
| ggctcaaggt ttgccgcagc tgagggtgag agccgagaag gcgaggtgcg gcgccgccca | 240 |

(2) INFORMATION FOR SEQ ID NO:3830:

(A) LENGTH: 66 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1578444

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1578445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3831:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Thr | Leu | Ser | Ala | Ala | Pro | Leu | Val | Gly | Ala | Ala | Ala | Val | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Pro | Cys | Gln | Ala | Gln | Gly | Leu | Pro | Gln | Leu | Arg | Val | Arg | Ala | Glu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Lys | Ala | Arg | Cys | Gly | Ala | Ala | His | Ser | Arg | Arg | Pro | Ser | Gln | Arg | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Gly | Asn | Asn | Gly | Ala | Ser | Ser | Ser | Leu | Leu | Ala | Xaa | Ala | Thr | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Val | Thr | Thr | Ser | Pro | Xaa | Leu | Ala | Leu | Val | Asp | Glu | Arg | Met | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Glu | Gly | Thr | Gly | Leu | Ser | Leu | Gly | Leu | Ser | Asn | Asn | Leu | Leu | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Trp | Ile | Leu | Leu | Gly | Val | Phe | Gly | Leu | Ile | Trp | Ser | Leu | Tyr | Thr | Val |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Tyr | Thr | Ser | Thr | Leu | Asp | Glu | Asp | Asp | Asp | Ser | Gly | Leu | Ser | Leu |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3832:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1027 base pairs

[illegible]

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..1027
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1578448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3832:

|             |            |            |             |            |             |      |
|-------------|------------|------------|-------------|------------|-------------|------|
| ctcaataaaaa | tatgtactcg | gaatcggaag | aagctgcctt  | ccttttccat | ccgcggaacg  | 60   |
| acgcacgcgg  | acgcctcctt | gttcgggtc  | ctactccgc   | cgcctagagg | cctcgccctc  | 120  |
| ccccctccgg  | cgaaaaccga | ttctctccgg | cgtttctctg  | tcccttagtg | caagcaagga  | 180  |
| caccgctcct  | ctagcgagct | ccgttctgaa | gcggcaagaa  | agatgattaa | tcttttcaaa  | 240  |
| ataaagggtc  | aaaagaaaga | ggaggcagca | agtctgctgg  | aaaggccct  | gttaagaaac  | 300  |
| agtctgctgg  | ggagctccgt | cttcataaag | atattagtga  | gctcaacctg | ccgaagacca  | 360  |
| cgtcaatttc  | ttttcccaat | ggcaaggatg | atctgatgaa  | ttttgagacc | accatccgac  | 420  |
| ctgatgaagg  | atattacatg | ggaggcactt | tcgttttcac  | ctttcaagtg | tccccatctt  | 480  |
| atcctcatga  | tcctccgaag | Gtcaaagca  | agaccaagGt  | gtaccatcca | aattattgatc | 540  |
| tggaaggcaa  | tgtatgtctg | aacattctgc | gcgaagattg  | gaagcctggt | ctcaacatca  | 600  |
| acactgttat  | ttatggcctg | aatcttcttt | ttacgcaacc  | aaacgcagag | gatoctctga  | 660  |
| accacgaagc  | tgcagttgtc | cttcgtgaca | atccaaagat  | gtttgaggca | aatgtgagaa  | 720  |
| gagccatggc  | tggaggctac | gtcggccaac | actattttcca | aagatgtgct | tgacttgatg  | 780  |
| tgggtggtggc | ttgaaaacga | tcaacagagc | ccctccccct  | gtatcagcac | cagcgcgccc  | 840  |
| agctttgtgt  | gcggaaagta | cttctggaag | caaaatccaa  | accgttcatg | gtgtgatact  | 900  |
| gtgatgcata  | tgtttgcccg | cctttgtgat | gtgtggtata  | gtggtggtgc | ataatgacat  | 960  |
| ggaaatgctt  | ctctaactgt | atcattcatt | ccataaatcc  | taaacgagga | atgggaagtg  | 1020 |

gattgtt

(2) INFORMATION FOR SEQ ID NO:3833:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 74 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..74
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1578449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3833:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ile | Lys | Tyr | Val | Leu | Gly | Ile | Gly | Arg | Ser | Cys | Leu | Pro | Phe | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Ala | Glu | Arg | Arg | Thr | Arg | Thr | Pro | Pro | Cys | Ser | Gly | Ser | Tyr | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Arg | Leu | Glu | Ala | Ser | Pro | Ser | Pro | Leu | Arg | Arg | Lys | Pro | Ile | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Gly | Val | Ser | Trp | Ser | Leu | Ser | Ala | Ser | Lys | Asp | Thr | Ala | Pro | Leu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Ser | Ser | Val | Leu | Lys | Arg | Gln | Glu | Arg |     |     |     |     |     |     |
| 65  |     |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3834:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 125 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..125
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1578450
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3834:

Met Asn Phe Glu Thr Thr Ile Arg Pro Asp Glu Gly Tyr Tyr Met Gly  
1 5 10 15  
Gly Thr Phe Val Phe Thr Phe Gln Val Ser Pro Ser Tyr Pro His Asp  
20 25 30  
Pro Pro Lys Val Lys Cys Lys Thr Lys Val Tyr His Pro Asn Ile Asp  
35 40 45  
Leu Glu Gly Asn Val Cys Leu Asn Ile Leu Arg Glu Asp Trp Lys Pro  
50 55 60  
Val Leu Asn Ile Asn Thr Val Ile Tyr Gly Leu Asn Leu Leu Phe Thr  
65 70 75 80  
Gln Pro Asn Asp Glu Asp Pro Leu Asn His Glu Ala Ala Val Val Leu  
85 90 95  
Arg Asp Asn Pro Lys Met Phe Glu Ala Asn Val Arg Arg Ala Met Ala  
100 105 110  
Gly Gly Tyr Val Gly Gln His Tyr Phe Gln Arg Cys Ala  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1578451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3835:

Met Gly Gly Thr Phe Val Phe Thr Phe Gln Val Ser Pro Ser Tyr Pro  
1 5 10 15  
His Asp Pro Pro Lys Val Lys Cys Lys Thr Lys Val Tyr His Pro Asn  
20 25 30  
Ile Asp Leu Glu Gly Asn Val Cys Leu Asn Ile Leu Arg Glu Asp Trp  
35 40 45  
Lys Pro Val Leu Asn Ile Asn Thr Val Ile Tyr Gly Leu Asn Leu Leu  
50 55 60  
Phe Thr Gln Pro Asn Asp Glu Asp Pro Leu Asn His Glu Ala Ala Val  
65 70 75 80  
Val Leu Arg Asp Asn Pro Lys Met Phe Glu Ala Asn Val Arg Arg Ala  
85 90 95  
Met Ala Gly Gly Tyr Val Gly Gln His Tyr Phe Gln Arg Cys Ala  
100 105 110

(2) INFORMATION FOR SEQ ID NO:3836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..847

(D) OTHER INFORMATION: / Ceres Seq. ID 1578452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3836:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| argccatggc tgcagccgc ccttgagtc tgccccaag atgacgatga tccccctcgc     | 60  |
| cggttcacc gccctatctg ccgccgccct cctgtctatc ttctctctct tctgtctgca   | 120 |
| aactcaagga ggagccagaa gcagcgagga ggagcggtag gtgccggtgc gcaggggtgt  | 180 |
| gtaccggtcc atgacaccgg crgcggcgag tgcrgcgacg acggcagagg cagcggcagc  | 240 |
| gncggcatcg tacgagccgt tcgaggtgtg cgaggggtgc cgggtgCtgcg cgccgtcgtc | 300 |
| gtcgtcgtcc aacggcagca gcagctgcgt ggacacgagc tgctgCtacg ccatcgactg  | 360 |
| cgacctcccc ggcaagccCt tcggcacctg cgccttcacc ccgcaaacct gcggctgcgg  | 420 |

cgggcgccagc agcaactgca cccccctcgt cctgatgatg actcctcttt cctgcaactt 480  
ggctacttct tctggatcat ccacgtcttt acgttacgtt acgattagat cgcagattag 540  
atgactcacg tcacgtactc catcatgatg gatagattat ccagttaatt cccagctagc 600  
gttctgogtg aagttaataa tacaatgaat aataatgtgt gttcgtttca gagattgtga 660  
ctgcagttgg ttccatgcat ttccagagtc ggcggttctt gttggcttga caacttgtac 720  
tgtcagggtc ggcggcctaa cctgttgcgc tcgtatacct actgtatgtt aggtatagat 780  
tgaacacatta ttttatactg tatgactatt acaaaactat aaagcaatac actcatttat 840  
tattgcc

(2) INFORMATION FOR SEQ ID NO:3837:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1578453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3837:

Xaa Pro Trp Leu Asp Ala Ala Leu Glu Ser Cys Pro Gln Asp Asp Asp  
1 5 10 15  
Asp Pro Pro Arg Arg Leu His Arg Pro Ile Cys Arg Arg Pro Pro Ala  
20 25 30  
His Leu Leu Leu Leu Pro Ala Ala Asn Ser Arg Arg Ser Gln Lys Gln  
35 40 45  
Arg Gly Gly Ala Val Arg Ala Gly Ala Gln Gly Gly Val Pro Val His  
50 55 60  
Asp Thr Gly Xaa Gly Glu Cys Xaa Asp Asp Gly Arg Gly Ser Gly Ser  
65 70 75 80  
Xaa Gly Ile Val Arg Ala Val Arg Gly Val Arg Gly Val Pro Val Leu  
85 90 95  
Arg Ala Val Val Val Val Val Gln Arg Gln Gln Gln Leu Arg Gly His  
100 105 110  
Glu Leu Leu Leu Arg His Arg Leu Arg Pro Pro Arg Gln Ala Leu Arg  
115 120 125  
His Leu Arg Leu His Pro Ala Asn Leu Arg Leu Arg Arg Gln Gln  
130 135 140  
Gln Leu His Pro Pro Arg Pro Asp Asp Asp Ser Ser Phe Leu Gln Leu  
145 150 155 160  
Gly Tyr Phe Phe Trp Ile Ile His Arg Leu Thr Leu Arg Tyr Asp  
165 170 175

(2) INFORMATION FOR SEQ ID NO:3838:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1578454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3838:

Xaa His Gly Ser Thr Pro Pro Leu Ser Pro Ala Pro Lys Met Thr Met  
1 5 10 15  
Ile Pro Leu Ala Gly Phe Thr Ala Leu Ser Ala Ala Gly Leu Leu Leu  
20 25 30  
Ile Phe Ser Ser Phe Leu Leu Gln Thr Gln Gly Gly Ala Arg Ser Ser  
35 40 45  
Glu Glu Glu Arg Tyr Val Pro Val Arg Arg Val Val Tyr Arg Ser Met

50 55 60  
Thr Pro Xaa Ala Ala Ser Xaa Ala Thr Thr Ala Glu Ala Ala Ala Ala  
65 70 75 80  
Xaa Ala Ser Tyr Glu Pro Phe Glu Val Cys Glu Gly Cys Arg Cys Cys  
85 90 95  
Ala Pro Ser Ser Ser Ser Ser Asn Gly Ser Ser Ser Cys Val Asp Thr  
100 105 110  
Ser Cys Cys Tyr Ala Ile Asp Cys Asp Leu Pro Gly Lys Pro Phe Gly  
115 120 125  
Thr Cys Ala Phe Thr Pro Gln Thr Cys Gly Cys Gly Gly Ala Ser Ser  
130 135 140  
Asn Cys Thr Pro Leu Val Leu Met Met Thr Pro Leu Ser Cys Asn Leu  
145 150 155 160  
Ala Thr Ser Ser Gly Ser Ser Ile Val Leu Arg Tyr Val Thr Ile Arg  
165 170 175  
Ser Gln Ile Arg  
180

(2) INFORMATION FOR SEQ ID NO:3839:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1578455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3839:

Met Thr Met Ile Pro Leu Ala Gly Phe Thr Ala Leu Ser Ala Ala Gly  
1 5 10 15  
Leu Leu Leu Ile Phe Ser Ser Phe Leu Leu Gln Thr Gln Gly Gly Ala  
20 25 30  
Arg Ser Ser Glu Glu Glu Arg Tyr Val Pro Val Arg Arg Val Val Tyr  
35 40 45  
Arg Ser Met Thr Pro Xaa Ala Ala Ser Xaa Ala Thr Thr Ala Glu Ala  
50 55 60  
Ala Ala Ala Xaa Ala Ser Tyr Glu Pro Phe Glu Val Cys Glu Gly Cys  
65 70 75 80  
Arg Cys Cys Ala Pro Ser Ser Ser Ser Ser Asn Gly Ser Ser Ser Cys  
85 90 95  
Val Asp Thr Ser Cys Cys Tyr Ala Ile Asp Cys Asp Leu Pro Gly Lys  
100 105 110  
Pro Phe Gly Thr Cys Ala Phe Thr Pro Gln Thr Cys Gly Cys Gly Gly  
115 120 125  
Ala Ser Ser Asn Cys Thr Pro Leu Val Leu Met Met Thr Pro Leu Ser  
130 135 140  
Cys Asn Leu Ala Thr Ser Ser Gly Ser Ser Ile Val Leu Arg Tyr Val  
145 150 155 160  
Thr Ile Arg Ser Gln Ile Arg  
165

(2) INFORMATION FOR SEQ ID NO:3840:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 954 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..954



(D) OTHER INFORMATION: / Ceres Seq. ID 1578464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3840:

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| aaacatactc  | cgtttccgaa | tccgttccac | cattgcctat  | tgccccatcc | tccccgctag | 60  |
| gtttttgccag | catggccgcc | gccgccgcc  | ggaggctcct  | ctccccgccg | gcctcctcgt | 120 |
| cctccctctc  | cgcgctcctc | cgtcgcggcg | ctgtcccggga | gcagtcgctg | gtgttgcgcc | 180 |
| cggctgttgt  | cgcggcgggc | tcccgcctcg | gcttccagcg  | cgggatggcg | cggcggcctg | 240 |
| gcggggacgg  | ctacgtctcg | acgcggtctg | gcgcggggcg  | ggaccgcgog | cmcatggcca | 300 |
| cggagatggc  | gccgctgttc | cccgggtgcg | actacgagca  | ttggctcatc | gtgatggaca | 360 |
| agccccggcg  | ggagggcgcc | agCaagcagc | agatgattga  | ctgctacatc | cagaccctcg | 420 |
| ccaaggtcct  | tggaagcgag | gaggaggcga | agaagaagat  | ctacaacgtc | tcgtgcgagc | 480 |
| gctacttcgg  | gtttgggtgc | gagatcgatg | aggagacatc  | taacaagctc | gaggggctcc | 540 |
| ctggGtgttc  | tctttgtgct | cccggattcg | tatgttgatg  | ctgaatacaa | ggactacgga | 600 |
| gctgaactct  | tcgtcaacgg | tgagattggt | cagaggaccc  | ccgagaggca | gaggagggtg | 660 |
| gagcccgtgc  | cacagagggc | agcagacagg | ccgagggtaca | atgacagaac | ccgtacgcac | 720 |
| gcaggaggga  | gaaccagcga | tgaactttgc | gataaaatca  | taaaaaatac | cacagcaaca | 780 |
| agtcccaggt  | ggtttcagct | ctggaattca | aggatcaccc  | agtatcgctc | gtattaaatt | 840 |
| ggcaatctca  | ctttacgtgc | agtctagagt | atcgtttcta  | tgtgctcagc | ttggacgtat | 900 |
| tgtattctgt  | aattacagct | acttggagat | ttggaaggac  | ctggcttgca | acgt       |     |

(2) INFORMATION FOR SEQ ID NO:3841:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1578465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3841:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ile | Leu | Arg | Phe | Arg | Ile | Arg | Ser | Thr | Ile | Ala | Tyr | Cys | Pro | Ile |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Pro | Ala | Arg | Phe | Cys | Gln | His | Gly | Arg | Arg | Arg | Arg | Pro | Glu | Ala |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Pro | Leu | Pro | Pro | Arg | Leu | Leu | Val | Leu | Pro | Leu | Arg | Ala | Pro | Pro | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Arg | Cys | Pro | Gly | Ala | Val | Ala | Gly | Val | Ala | Pro | Gly | Cys | Cys | Arg |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Gly | Leu | Pro | Pro | Arg | Leu | Pro | Ala | Arg | Asp | Gly | Ala | Ala | Ala | Trp |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Arg | Gly | Arg | Leu | Arg | Leu | Asp | Ala | Val | Trp | Arg | Gly | Arg | Gly | Pro | Arg |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Xaa | His | Gly | His | Gly | Asp | Gly | Ala | Ala | Val | Pro | Arg | Val | Arg | Leu | Arg |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ala | Leu | Ala | His | Arg | Asp | Gly | Gln | Ala | Arg | Arg | Gly | Gly | Arg | Gln | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Ala | Ala | Asp | Asp |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3842:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1578466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3842:

Thr Tyr Ser Val Ser Glu Ser Val Pro Pro Leu Pro Ile Ala Pro Ser

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(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..714
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1578468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3844:

```
acatcccgat ccttctctcg gcggcccgtt ggtcacgtga ctcaccccc tgtgctctcc 60
tctcgtggcc ttgtttcctg gcggcgacgg ctggctcgagc ggcgcgcgcc ttggctaggt 120
cttcgctggg tccttccccg gcgacgagcg tccatctggg gtcgactgaa ctgagcaggc 180
agtaggaaga gacactatgt tgttcttctc ctacttcCaa ggagctggtg gggaaggagg 240
tgacagtgga gctcaagaat gacttggcga tccgcgggac gctccactcg gttgaccagt 300
acctcaacat caagctcgag aacacccgcg tagtcgacca ggacaagtat ccccatatgc 360
tttcagtgcg gaactgcttc atcaggggct cggtggtgct gtacgtgctg ctcccgagG 420
acggcgtgga catcgacatc ctccacgacg ccaccaggag ggaggcgcgc ggaggctgat 480
cctgatgcgc acccgctccc tcacctgctg gctgctgctt catccccgat tgtacgaagc 540
atgcatgtac ggtgtgtggt agacagatgc cccagtttag ttctttggtg cttgacctgac 600
atagatatcc caggttggtat gatgacctga atcacctgat atattattgt catatcatat 660
gcaatggtct tgcattgggt tgctatatta ttaccatatt gtattatcac atcg
```

(2) INFORMATION FOR SEQ ID NO:3845:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 57 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..57
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1578469
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3845:

```
Thr Ser Arg Ser Phe Ser Arg Arg Pro Val Gly His Val Thr His Pro
1 5 10 15
Pro Val Leu Ser Ser Arg Gly Leu Val Ser Trp Arg Arg Arg Leu Val
20 25 30
Glu Arg Arg Arg Pro Trp Leu Gly Leu Arg Trp Val Leu Pro Arg Arg
35 40 45
Arg Ala Ser Ile Trp Gly Arg Leu Asn
50 55
```

(2) INFORMATION FOR SEQ ID NO:3846:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 60 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..60
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1578470
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3846:

```
Ile Pro Ile Leu Ser Ala Ala Arg Trp Ser Arg Asp Ser Ser Pro
1 5 10 15
Cys Ala Leu Leu Ser Trp Pro Cys Phe Leu Ala Ala Thr Ala Gly Arg
20 25 30
Ala Ala Pro Pro Leu Ala Arg Ser Ser Leu Gly Pro Ser Pro Ala Thr
35 40 45
Ser Val His Leu Gly Ser Thr Glu Leu Ser Arg Gln
50 55 60
```

(2) INFORMATION FOR SEQ ID NO:3847:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 40 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..40  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1578471  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3847:  
Met Leu Ser Val Arg Asn Cys Phe Ile Arg Gly Ser Val Val Arg Tyr  
1                  5                  10                  15  
Val Leu Leu Pro Gln Asp Gly Val Asp Ile Asp Ile Leu His Asp Ala  
                  20                  25                  30  
Thr Arg Arg Glu Ala Arg Gly Gly  
                  35                  40

(2) INFORMATION FOR SEQ ID NO:3848:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 905 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..905  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1578472  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3848:  
aaacagatac acacacactc gggtaaagct atctcgagct agctagctgc tgtaascggt 60  
gccatggcca aaatggtggt gctctgcgtg ctctgtctct tcctcctgat gcccttggcc 120  
tccttagccc tgacgcagga cttctgcgtc gccgacctga cctgcagcga cacgccggcg 180  
gggtaccctg gcaagtccag cgtcaccgcc aacgacttct acttccacgg cctggccggc 240  
cagggcaaaa taaaccact catcaaggcc gccgtgacct cggccttctg gggccagttc 300  
ccgggcgtca acgccttggc atctctgcgg ccaggctcga catcgagggtg ggcggcgctg 360  
tgccgctgca caccaccccg gcgggctcag agtcctctct cgtgacctcag ggcaccgNtc 420  
gccgcgggct tcatcagctc cggctccaac accgtctaca ccaagacgct gtacgccggc 480  
gacatcatgg tggtccccc gggcctgctc cactaccagt acaacgccgg canccggcgc 540  
tgccgtgggc ctctgcgcct tcagcagccc caaccccgcc ctgcagatca ccgactttgc 600  
gctctttgcc aacaacctcc cgtccgccgt cgtggagaag gtcaccttct tggacgacgc 660  
gcagggtgaag aagctcaaga gtgtgctcgg cggcagcggg taacttggtt ttcgagacaa 720  
tacagtgcag gctgggtatg catcgctgcc gtcgtcgtct tgggtccgtg tcatogaatg 780  
gaacgcgtgt gcttgctgct gcatgcgtgc gtgcacctgt cgtcgcgtgt caaagtactc 840  
gtgggtctatt tcattctacc cttatttatt catctacttt tcattcaggg atgtattcag 900  
tttcc

(2) INFORMATION FOR SEQ ID NO:3849:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 113 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..113  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1578473  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3849:  
Met Ala Lys Met Val Leu Leu Cys Val Leu Val Ser Phe Leu Leu Met  
1                  5                  10                  15  
Pro Leu Ala Ser Leu Ala Leu Thr Gln Asp Phe Cys Val Ala Asp Leu  
                  20                  25                  30

Thr Cys Ser Asp Thr Pro Ala Gly Tyr Pro Cys Lys Ser Ser Val Thr  
35 40 45  
Ala Asn Asp Phe Tyr Phe His Gly Leu Ala Gly Gln Gly Lys Ile Asn  
50 55 60  
Pro Leu Ile Lys Ala Ala Val Thr Pro Ala Phe Val Gly Gln Phe Pro  
65 70 75 80  
Gly Val Asn Ala Leu Ala Ser Leu Arg Pro Gly Ser Thr Ser Arg Trp  
85 90 95  
Ala Ala Ser Cys Arg Cys Thr Pro Thr Arg Arg Ala Gln Ser Ser Ser  
100 105 110  
Ser

(2) INFORMATION FOR SEQ ID NO:3850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3850:

Met Val Leu Leu Cys Val Leu Val Ser Phe Leu Leu Met Pro Leu Ala  
1 5 10 15  
Ser Leu Ala Leu Thr Gln Asp Phe Cys Val Ala Asp Leu Thr Cys Ser  
20 25 30  
Asp Thr Pro Ala Gly Tyr Pro Cys Lys Ser Ser Val Thr Ala Asn Asp  
35 40 45  
Phe Tyr Phe His Gly Leu Ala Gly Gln Gly Lys Ile Asn Pro Leu Ile  
50 55 60  
Lys Ala Ala Val Thr Pro Ala Phe Val Gly Gln Phe Pro Gly Val Asn  
65 70 75 80  
Ala Leu Ala Ser Leu Arg Pro Gly Ser Thr Ser Arg Trp Ala Ala Ser  
85 90 95  
Cys Arg Cys Thr Pro Thr Arg Arg Ala Gln Ser Ser Ser Ser  
100 105 110

(2) INFORMATION FOR SEQ ID NO:3851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3851:

Met Val Phe Pro Gln Gly Leu Leu His Tyr Gln Tyr Asn Ala Gly Xaa  
1 5 10 15  
Arg Arg Cys Arg Gly Pro Arg Arg Leu Gln Gln Pro Gln Pro Arg Pro  
20 25 30  
Ala Asp His Arg Leu Cys Ala Leu Cys Gln Gln Pro Pro Val Arg Arg  
35 40 45  
Arg Gly Glu Gly His Leu Leu Gly Arg Arg Ala Gly Glu Glu Ala Gln  
50 55 60  
Glu Cys Ala Arg Arg Gln Arg Leu Thr Cys Phe Ser Arg Gln Tyr Ser  
65 70 75 80  
Ala Gly Trp Val Cys Ile Val Ala Val Val Val Leu Val Arg Arg His

85 90 95  
Arg Met Glu Arg Val Cys Leu Leu Leu His Ala Cys Val His Leu Ser  
100 105 110  
Ser Arg Val Lys Val Leu Val Val Tyr Phe Ile Leu Pro Leu Phe Ile  
115 120 125  
His Leu Leu Phe Ile Gln Gly Cys Ile Gln Phe  
130 135

(2) INFORMATION FOR SEQ ID NO:3852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..590
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3852:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aaatcgaatc gagcccatcc atctccattt cmrcmgchgc mgccgccgag agaccccaac | 60  |
| cccacccatc caccaccatg tndmgcmgcc tccacaccct arcmcccgcc ttgcgcaggg | 120 |
| ctaccgcgcg cgcgcgcggg gccctgcGg cgctccgctc ctctgcagcc cgcgcgcgcc  | 180 |
| cgctctcctc ggccggtacg gcggtggcgg cgccggctac ggtggcggcg gcggtacgg  | 240 |
| tggtggtggc ggccggtacg gcggtggcaa ccgtggcggc ggctacggca actccgacgg | 300 |
| gaactggagg aactgagcgg tggggcccgc gcggccaagt tatcctgttc gctaccgtgt | 360 |
| tgtttaccct agtcagagg gtttatcttc gttcgtctca tgttgtgtgt tgcccatctg  | 420 |
| tgtttttgat tgcaaggctg ctttgtgtca gttgttagtg ctgtgttcat cctcggtccc | 480 |
| agcagaccca tgcataacc agcatggact gcggatcgat ggatgctgtt acccccgtca  | 540 |
| ggctttatcc taagttaatc ttcaaggaaa aaatggtgct tcttggtgct            |     |

(2) INFORMATION FOR SEQ ID NO:3853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3853:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Lys Ser Asn Arg Ala His Pro Ser Pro Phe Xaa Xaa Xaa Xaa Pro Pro |  |
| 1 5 10 15                                                       |  |
| Arg Asp Pro Asn Pro Thr His Pro Pro Cys Xaa Xaa Ala Ser Thr     |  |
| 20 25 30                                                        |  |
| Pro Xaa Xaa Pro Pro Cys Ala Gly Leu Pro Pro Pro Pro Gly Pro     |  |
| 35 40 45                                                        |  |
| Leu Arg Arg Pro Pro Pro Leu Gln Pro Ala Pro Pro Arg Ser Pro Arg |  |
| 50 55 60                                                        |  |
| Arg Leu Arg Arg Trp Arg Arg Arg Leu Arg Trp Arg Arg Arg Leu Arg |  |
| 65 70 75 80                                                     |  |
| Trp Trp Trp Arg Arg Leu Arg Arg Trp Gln Pro Trp Arg Arg Leu Arg |  |
| 85 90 95                                                        |  |
| Gln Leu Arg Arg Glu Leu Glu Glu Leu Ser Gly Gly Ala Arg Ala Ala |  |
| 100 105 110                                                     |  |
| Lys Leu Ser Cys Ser Leu Pro Cys Cys Leu Pro                     |  |
| 115 120                                                         |  |

(2) INFORMATION FOR SEQ ID NO:3854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid

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- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..151  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578481  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3854:

Ile Glu Ser Ser Pro Ser Ile Ser Ile Xaa Xaa Xaa Xaa Ala Ala Glu  
1 5 10 15  
Arg Pro Gln Pro His Pro Ser Thr Thr Met Xaa Xaa Xaa Leu His Thr  
20 25 30  
Leu Xaa Pro Ala Leu Arg Arg Ala Thr Ala Ala Ala Ala Gly Ala Pro  
35 40 45  
Ala Ala Ser Ala Ser Ser Ala Ala Arg Ala Ala Pro Leu Ser Ser Ala  
50 55 60  
Ala Thr Ala Val Ala Ala Ala Ala Thr Val Ala Ala Ala Ala Thr Val  
65 70 75 80  
Val Val Ala Ala Ala Thr Ala Val Ala Thr Val Ala Ala Ala Thr Ala  
85 90 95  
Thr Pro Thr Gly Thr Gly Gly Thr Glu Arg Trp Gly Pro Arg Gly Gln  
100 105 110  
Val Ile Leu Phe Ala Thr Val Leu Phe Thr Leu Val Gln Arg Val Tyr  
115 120 125  
Leu Arg Ser Ser His Val Cys Cys Cys Pro Ser Val Phe Leu Ile Ala  
130 135 140  
Arg Ser Leu Cys Val Ser Cys  
145 150

(2) INFORMATION FOR SEQ ID NO:3855:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 126 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..126  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3855:

Met Xaa Xaa Xaa Leu His Thr Leu Xaa Pro Ala Leu Arg Arg Ala Thr  
1 5 10 15  
Ala Ala Ala Ala Gly Ala Pro Ala Ala Ser Ala Ser Ser Ala Ala Arg  
20 25 30  
Ala Ala Pro Leu Ser Ser Ala Ala Thr Ala Val Ala Ala Ala Thr  
35 40 45  
Val Ala Ala Ala Ala Thr Val Val Val Ala Ala Ala Thr Ala Val Ala  
50 55 60  
Thr Val Ala Ala Ala Thr Ala Thr Pro Thr Gly Thr Gly Gly Thr Glu  
65 70 75 80  
Arg Trp Gly Pro Arg Gly Gln Val Ile Leu Phe Ala Thr Val Leu Phe  
85 90 95  
Thr Leu Val Gln Arg Val Tyr Leu Arg Ser Ser His Val Cys Cys Cys  
100 105 110  
Pro Ser Val Phe Leu Ile Ala Arg Ser Leu Cys Val Ser Cys  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3856:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 747 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3856:

(2) INFORMATION FOR SEQ ID NO:3857:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1578487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3857:

(2) INFORMATION FOR SEO ID NO:3858:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1578488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3858:

Met Arg Lys His Arg Ile Val Ser Leu Val Ala Ala Leu Leu Val Leu  
1 5 10 15  
Leu Ala Leu Ala Ala Val Ser Ser Thr Arg Ser Xaa Gln Lys Glu Ser  
20 25 30  
Ala Ala Asp Asn Ala Gly Met Leu Ala Gly Gly Ile Lys Asp Val Pro  
35 40 45  
Ala Asn Glu Asn Asp Leu Gln Leu Gln Glu Leu Ala Arg Phe Ala Val  
50 55 60  
Asn Glu His Asn Gln Lys Ala Asn Ala Leu Leu Gly Phe Glu Lys Leu  
65 70 75 80  
Val Lys Ala Lys Thr Gln Val Val Ala Gly Thr Met Tyr Tyr Leu Thr  
85 90 95  
Ile Glu Val Lys Asp Gly Glu Val Asn Lys Leu Tyr Glu Ala Lys Val  
100 105 110  
Trp Glu Lys Pro Trp Glu Asn Phe Lys Gln Leu Gln Glu Phe Lys Pro  
115 120 125  
Val Glu Glu Gly Ala Ser Ala  
130 135

(2) INFORMATION FOR SEQ ID NO:3859:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1578489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3859:

Met Leu Ala Gly Gly Ile Lys Asp Val Pro Ala Asn Glu Asn Asp Leu  
1 5 10 15  
Gln Leu Gln Glu Leu Ala Arg Phe Ala Val Asn Glu His Asn Gln Lys  
20 25 30  
Ala Asn Ala Leu Leu Gly Phe Glu Lys Leu Val Lys Ala Lys Thr Gln  
35 40 45  
Val Val Ala Gly Thr Met Tyr Tyr Leu Thr Ile Glu Val Lys Asp Gly  
50 55 60  
Glu Val Asn Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Glu  
65 70 75 80  
Asn Phe Lys Gln Leu Glu Phe Lys Pro Val Glu Glu Gly Ala Ser  
85 90 95  
Ala

(2) INFORMATION FOR SEQ ID NO:3860:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 781 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..781

(D) OTHER INFORMATION: / Ceres Seq. ID 1578490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3860:

```
agacagcctc cccattcatc agattcagat cagatcgtag cagccaagga ttccgcgctc 60
cggggggtgcc atgaagctga agctcctctc tccctgcctt ctctcctcgc ccttctttgc 120
caccgcggcg tacgcggcgt cggcgtcggc gtcgcgcgcg gcggccgctc tcaggggcgc 180
gggcgccccg tcgcagtcgg agttggagtc ggacccggag aaccagtgcg tgtacacggt 240
gtacgtgcgg acggggtcca tctggaaggg cggcacggac tcgaccatcg gcgtgacgct 300
gctgggcgCc cgacggcacg ggcattccga tccgggacct ggcggggtgg ggcggcctca 360
tgggcgccgg ccacgactac tacgagcgcg gcaacctgga catcttcagc ggccggggcc 420
cctgcatgag ccaGGgcgcg ctgcGvcag aacctcacct ccgacggcac cggcgcgcac 480
cacggctggt actgcaacta cctcgaggcc acggtcacgg ggccccacct cgggtgcgcg 540
cagcagctct tcaccgtcga gcagtggctc gccaccgacg cgtcgcctta ccgcctgtac 600
gcggtcgtcg acaagtgcaa gacgaagsgg caggagncgc gacgctcgcc ggccggcgag 660
gccgaggcca ccgtgaccgc gctctaggta cgaccagtag taaatcatcg acagaggcta 720
gctcctgcct ctgctgtgtg taattactgt atgtgagtga ccgatcccat cggattgcgt 780
t
```

(2) INFORMATION FOR SEQ ID NO:3861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3861:

```
Arg Gln Pro Pro His Ser Ser Asp Ser Asp Gln Ile Val Ala Ala Lys
1 5 10 15
Asp Ser Ala Leu Arg Gly Cys His Glu Ala Glu Ala Pro Leu Ser Leu
 20 25 30
Pro Ser Pro Pro Arg Leu Leu Cys His Arg Gly Val Arg Gly Val Gly
 35 40 45
Val Gly Val Ala Arg Gly Gly Arg Arg Gln Gly Arg Gly Arg Pro Val
 50 55 60
Ala Val Gly Val Gly Val Gly Pro Gly Glu Pro Val Arg Val His Gly
65 70 75 80
Val Arg Ala Asp Gly Val His Leu Glu Gly Arg His Gly Leu Asp His
 85 90 95
Arg Arg Asp Ala Ala Gly Arg Pro Thr Ala Arg Ala Ser Gly Ser Gly
 100 105 110
Thr Trp Arg Gly Gly Ala Ala Ser Trp Ala Pro Ala Thr Thr Thr Thr
 115 120 125
Ser Ala Ala Thr Trp Thr Ser Ser Ala Ala Gly Ala Pro Ala
130 135 140
```

(2) INFORMATION FOR SEQ ID NO:3862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3862:

```
Met Lys Leu Lys Leu Leu Ser Pro Cys Leu Leu Leu Leu Ala Phe Phe
1 5 10 15
Ala Thr Ala Ala Tyr Ala Ala Ser Ala Ser Ala Ser Arg Ala Ala Ala
 20 25 30
Val Val Arg Gly Ala Gly Ala Pro Ser Gln Ser Glu Leu Glu Ser Asp
```

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35 40 45  
Pro Glu Asn Gln Cys Val Tyr Thr Val Tyr Val Arg Thr Gly Ser Ile  
50 55 60  
Trp Lys Gly Gly Thr Asp Ser Thr Ile Gly Val Thr Leu Leu Gly Ala  
65 70 75 80  
Arg Arg His Gly His Pro Asp Pro Gly Pro Gly Gly Val Gly Arg Pro  
85 90 95  
His Gly Arg Arg Pro Arg Leu Leu Arg Ala Arg Gln Pro Gly His Leu  
100 105 110  
Gln Arg Pro Gly Pro Leu His Glu Pro Gly Arg Pro Ala Xaa  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: ~
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3863:

Met Gly Ala Gly His Asp Tyr Tyr Glu Arg Gly Asn Leu Asp Ile Phe  
1 5 10 15  
Ser Gly Arg Gly Pro Cys Met Ser Gln Gly Ala Leu Xaa His Glu Pro  
20 25 30  
His Leu Arg Arg His Arg Arg Ala Pro Arg Leu Val Leu Gln Leu Pro  
35 40 45  
Arg Gly His Gly His Gly Ala Pro Pro Arg Val Arg Ala Ala Ala Leu  
50 55 60  
His Arg Arg Ala Val Ala Arg His Arg Arg Val Ala Leu Pro Pro Val  
65 70 75 80  
Arg Gly Arg Arg Gln Val Gln Asp Glu Xaa Ala Gly Xaa Ala Thr Leu  
85 90 95  
Ala Gly Arg Arg Gly Arg Gly His Arg Asp Arg Ala Leu Gly Thr Thr  
100 105 110  
Ser Ser Lys Ser Ser Thr Glu Ala Ser Ser Cys Leu Cys Cys Val  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..714
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3864:

atcagcctcg attgattcgt ctccctttc cctcgatctc cattctccag tgtgggtcgtg 60  
cagtgtttctc ttctctgctt gagatacgat acgaagatca gcccctgarc cgatcccatg 120  
gctgcwgcct cccctctccg tccagcaacg ccggcmgcgc tccGgcacgg ggcgtgccac 180  
gggctGgggc tggcgctacc gaggaNgttt kycGccgtcg gCGgcaaNcg cgatgcgccg 240  
cgCtaacgccc ggacgcgcgc ggccggccggg accagtagcg aggcgcgctg gtggacgagg 300  
gcatgcccgt gctgcggcgg cggtatccggg aggcgtggat ggtggagacc aactacgagg 360  
cgcccgcga gtgggcgcgc tgggagaagc ggtactacc cgcctaCgtc tccgacgtgt 420  
ctagcctcgt cggcgcgctg cagctgctgc tcatgggcac caggcccggc gtcgccatcg 480  
ccgtgcgccg cctgggtgctg gccagcgtcc ccgtgtccac cgtcgccgcg ctacacatct 540  
ggcgatgggtg gccgaggccg tctgcagtc cgtccatcac atttcttgat ccagtcggac 600

catcttttggg tctccttttt tcttttcatt tgtaaccttg aggcagtctg ccgcgtgaat 660  
agtattggag gcttgtagtt gcagctggat tgatctaaag attcttttagc cttg

(2) INFORMATION FOR SEQ ID NO:3865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..210
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3865:

Gln Pro Arg Leu Ile Arg Leu Pro Phe Pro Ser Ile Ser Ile Leu Gln  
1 5 10 15  
Cys Gly Arg Ala Val Phe Ser Phe Leu Pro Glu Ile Arg Tyr Glu Asp  
20 25 30  
Gln Pro Leu Xaa Arg Ser His Gly Cys Xaa Phe Pro Leu Pro Ser Ser  
35 40 45  
Asn Ala Gly Xaa Ala Pro Ala Arg Gly Val Pro Arg Ala Gly Ala Gly  
50 55 60  
Ala Thr Glu Xaa Val Xaa Arg Arg Arg Arg Gln Xaa Arg Cys Ala Ala  
65 70 75 80  
Leu Arg Arg Asp Ala Ser Gly Gly Arg Asp Gln Tyr Gly Gly Ala Leu  
85 90 95  
Val Asp Glu Gly Met Pro Val Leu Arg Arg Arg Ile Arg Glu Ala Trp  
100 105 110  
Met Val Glu Thr Asn Tyr Glu Ala Pro Ala Glu Trp Ala Pro Trp Glu  
115 120 125  
Lys Arg Tyr Tyr Pro Ala Tyr Val Ser Asp Val Ser Ser Leu Val Gly  
130 135 140  
Ala Leu Gln Leu Leu Leu Met Gly Thr Arg Pro Gly Val Ala Ile Ala  
145 150 155 160  
Val Ala Ala Leu Val Leu Ala Ser Val Pro Val Ser Thr Val Ala Ala  
165 170 175  
Leu His Ile Trp Arg Trp Trp Pro Arg Pro Ser Cys Ser Pro Ser Ile  
180 185 190  
Thr Phe Leu Asp Pro Val Gly Pro Ser Phe Gly Leu Leu Phe Ser Phe  
195 200 205  
His Leu  
210

(2) INFORMATION FOR SEQ ID NO:3866:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3866:

Met Ala Xaa Ala Ser Leu Ser Arg Pro Ala Thr Pro Xaa Ala Leu Arg  
1 5 10 15  
His Gly Ala Cys His Gly Leu Gly Leu Ala Leu Pro Arg Xaa Phe Xaa  
20 25 30  
Ala Val Gly Gly Xaa Arg Asp Ala Pro Arg Tyr Ala Gly Thr Arg Ala  
35 40 45  
Ala Ala Gly Thr Ser Thr Glu Ala Arg Trp Trp Thr Arg Ala Cys Pro

50 55 60  
Cys Cys Gly Gly Gly Ser Gly Arg Arg Gly Trp Trp Arg Pro Thr Thr  
65 70 75 80  
Arg Arg Pro Pro Ser Gly Arg Arg Gly Arg Ser Gly Thr Thr Pro Pro  
85 90 95  
Thr Ser Pro Thr Cys Leu Ala Ser Ser Ala Arg Cys Ser Cys Cys Ser  
100 105 110  
Trp Ala Pro Gly Pro Ala Ser Pro Ser Pro Ser Pro Pro Trp Cys Trp  
115 120 125  
Pro Ala Ser Pro Cys Pro Pro Ser Pro Arg Tyr Thr Ser Gly Asp Gly  
130 135 140  
Gly Arg Gly Arg Pro Ala Val Arg Pro Ser His Phe Leu Ile Gln Ser  
145 150 155 160  
Asp His Leu Leu Val Ser Phe Phe Leu Phe Ile Cys Asn Leu Glu Ala  
165 170 175  
Val Cys Arg Val Asn Ser Ile Gly Gly Leu  
180 185

(2) INFORMATION FOR SEQ ID NO:3867:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3867:

Met Pro Val Leu Arg Arg Arg Ile Arg Glu Ala Trp Met Val Glu Thr  
1 5 10 15  
Asn Tyr Glu Ala Pro Ala Glu Trp Ala Pro Trp Glu Lys Arg Tyr Tyr  
20 25 30  
Pro Ala Tyr Val Ser Asp Val Ser Ser Leu Val Gly Ala Leu Gln Leu  
35 40 45  
Leu Leu Met Gly Thr Arg Pro Gly Val Ala Ile Ala Val Ala Ala Leu  
50 55 60  
Val Leu Ala Ser Val Pro Val Ser Thr Val Ala Leu His Ile Trp  
65 70 75 80  
Arg Trp Trp Pro Arg Pro Ser Cys Ser Pro Ser Ile Thr Phe Leu Asp  
85 90 95  
Pro Val Gly Pro Ser Phe Gly Leu Leu Phe Ser Phe His Leu  
100 105 110

(2) INFORMATION FOR SEQ ID NO:3868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 683 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..683
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3868:

aagcagacccc gggcgggccc tggcaattca cgcacctsgc gtgcacacag acacaggcag 60  
gcacacagcg caatcacctg ctgcctcgc agtcgtactc acggtcttgc acacaccctg 120  
ccccatcttc ttccggtgtc gccatcccct ccgtcgaccg ccgcgtccgg ccgcggcaac 180  
ccgacctgtg tcaatcgcca tgactacctc aaggcgttct gctgatagga agatatcacg 240  
at ttgagaag aatatcaca agaggggtc tgttcctgag acagccaaga aggcaaacga 300  
ttatcctgtt gggcctattc ttcttgggtt ctttgtcttc gtggttggtg gatcatctct 360

```
ctttcagatc atcaagacag catcaaacgc tgggtctattc tgagggtgaat cggttgacac 420
atgcagtttg tcactagaaa ctatacaagt gtagggcgtg gcttaatgtc gcctttttaa 480
tggtgtaccg tggagagttt taagttatat atgtaatgga agtgctaatt taagtcacct 540
gtctgacagg aaagatggtg gagtagtCca taatacatat cgagtatagt tatagttcgt 600
gttaaattatt tctatgctca aattggtcgc atcattgggc tattgtactc ttcgatttat 660
cgagtaattt ggtaattctt cgc
```

(2) INFORMATION FOR SEQ ID NO:3869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1578525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3869:

```
Lys Gln Thr Arg Ala Gly Pro Gly Asn Ser Arg Thr Xaa Arg Ala His
1 5 10 15
Arg His Arg Gln Ala His Ser Ala Ile Thr Val Ser Pro Arg Ser Arg
20 25 30
Thr His Gly Leu Ala His Thr Arg Pro His Pro Leu Pro Val Ser Pro
35 40 45
Ser Pro Pro Ser Thr Ala Ala Ser Gly Arg Gly Asn Pro Thr Cys Val
50 55 60
Asn Arg His Asp Tyr Leu Lys Ala Ser Cys
65 70
```

(2) INFORMATION FOR SEQ ID NO:3870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1578526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3870:

```
Ser Arg Pro Gly Arg Ala Leu Ala Ile His Ala Pro Xaa Val His Thr
1 5 10 15
Asp Thr Gly Arg His Thr Ala Gln Ser Pro Ser Arg Leu Ala Val Val
20 25 30
Leu Thr Val Leu His Thr Pro Val Pro Ile Leu Phe Arg Cys Arg His
35 40 45
Pro Leu Arg Arg Pro Pro Arg Pro Ala Ala Ala Thr Arg Pro Val Ser
50 55 60
Ile Ala Met Thr Thr Ser Arg Arg Leu Ala Asp Arg Lys Ile Ser Arg
65 70 75 80
Phe Glu Lys Asn Ile Thr Lys Arg Gly Ser Val Pro Glu Thr Ala Lys
85 90 95
Lys Ala Asn Asp Tyr Pro Val Gly Pro Ile Leu Leu Gly Phe Phe Val
100 105 110
Phe Val Val Val Gly Ser Ser Leu Phe Gln Ile Ile Lys Thr Ala Ser
115 120 125
Asn Ala Gly Leu Phe
130
```

(2) INFORMATION FOR SEQ ID NO:3871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..67  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578527  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3871:  
Met Thr Thr Ser Arg Arg Leu Ala Asp Arg Lys Ile Ser Arg Phe Glu  
1 5 10 15  
Lys Asn Ile Thr Lys Arg Gly Ser Val Pro Glu Thr Ala Lys Lys Ala  
20 25 30  
Asn Asp Tyr Pro Val Gly Pro Ile Leu Leu Gly Phe Phe Val Phe Val  
35 40 45  
Val Val Gly Ser Ser Leu Phe Gln Ile Ile Lys Thr Ala Ser Asn Ala  
50 55 60  
Gly Leu Phe  
65

(2) INFORMATION FOR SEQ ID NO:3872:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 707 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..707  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3872:

atccatatgc actagcagta tcacctcatt taatatgcgg ccggcatcgt cgccagagct 60  
ctcgataagg ctgccagag tctcatctca tacgccggag gtgctccaga gagcagggct 120  
gaagaggtgc ggcaagagct gcaggctgag gtacaccaac tatcgcgcg tgatctgggc 180  
gacgaactgc gtgcgcgTtt tgcagggtgg cctgatcgcg gaaGcagctg ccggggcgga 240  
cgggcaacga cgtgaggaac cgttggaaca cgaaactgag agcaagcagc tgcggcagcg 300  
cgggatcgac cccaccgccc ccatcgccgg cctcatgcac atcttcgtcg gcgccctctc 360  
cttacggcga cgacggcacg ggaacgacga cggcacggga gagatcatcg acgccaccct 420  
ggactgRcga caagaagaca cgggtggacc agtcacgcg ctagtctgtg gccgaccggg 480  
cctactacgc tggctcctcc tccgagatgg gctggatcat gggcttgatg aatgctgatt 540  
aattagcggg tatacaatgg atccatgagg cttaaagcaaa ctgactgaaa tagtcacttt 600  
agaggctaaa gtttcaaaca taaagaacta aaagggacta aaatgtttta gctcctttag 660  
cttgtaagga cgagttaaac tcgactaaaa cagctgggtcc cacaccc

(2) INFORMATION FOR SEQ ID NO:3873:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 178 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..178  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3873:

Ser Ile Cys Thr Ser Ser Ile Thr Ser Phe Asn Met Arg Pro Ala Ser  
1 5 10 15  
Ser Pro Glu Leu Ser Ile Arg Leu Ala Arg Xaa Ser Ser His Thr Pro  
20 25 30  
Glu Val Leu Gln Arg Ala Gly Leu Lys Arg Cys Gly Lys Ser Cys Arg  
35 40 45

```
(2) INFORMATION FOR SEQ ID NO:3874:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 167 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..167
 (D) OTHER INFORMATION: / Ceres Seq. ID 1578542
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3874:
```

```
(2) INFORMATION FOR SEQ ID NO:3875:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 697 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
```



(B) LOCATION: 1..697

(D) OTHER INFORMATION: / Ceres Seq. ID 1578543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3875:

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| aaacagtctc | ggcctctcct  | cccggttcc   | tcacacggca | ctccagccgc | tagccctcac | 60  |
| tcaaccagac | aaccagtaca  | ccaccgccac  | caagcccggg | ccgaataact | ctgccgggca | 120 |
| accgccgccc | ttcgccggca  | aagaacgccc  | accagatcca | ccccggcctg | ctatggagtc | 180 |
| cgcggtgaac | ccgaaGgcgt  | acccgctggc  | tgatgcgcaG | ctgacgatgg | gtatcctcga | 240 |
| tatcatccag | caggccgcca  | actacaagca  | gtcaagaag  | ggagcgaacg | aagcgacgaa | 300 |
| aaccctgaat | agggggatat  | cggagttcgt  | tgtgatggcg | gcggaacacg | agcctctcga | 360 |
| gatcctgctc | cacctccctt  | tgttagccga  | ggataagaac | gtcccatatg | tatttgttcc | 420 |
| atcgaaacaa | gctcttggcc  | gtgcttggtg  | tgtgacaaga | cccgtcattg | cttgctcagt | 480 |
| gaccagcaat | gagggtagcc  | agctgaaaca  | acagatacag | ggtctcaagg | actcgattga | 540 |
| gaagcttctc | atctgattta  | cctaagatct  | ttcagtggtg | tgggcctcgg | cgacacattt | 600 |
| ttcagaggct | tggactgggtg | atgggtgtctt | gtttacatta | cgctttccaa | actatatttg | 660 |
| aacactgcta | agtcaatcat  | atgtgaattg  | tgcttcg    |            |            |     |

(2) INFORMATION FOR SEQ ID NO:3876:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..184

(D) OTHER INFORMATION: / Ceres Seq. ID 1578544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3876:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Ser | Leu | Gly | Leu | Ser | Ser | Arg | Leu | Pro | His | Thr | Ala | Leu | Gln | Pro |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Leu | Ala | Leu | Thr | Gln | Pro | Asp | Asn | Gln | Tyr | Thr | Thr | Ala | Thr | Lys | Pro |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Gly | Pro | Asn | Asn | Ser | Ala | Gly | Gln | Pro | Pro | Pro | Phe | Ala | Gly | Lys | Glu |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Pro | Pro | Asp | Pro | Pro | Arg | Pro | Ala | Met | Glu | Ser | Ala | Val | Asn | Pro |  |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Lys | Ala | Tyr | Pro | Leu | Ala | Asp | Ala | Gln | Leu | Thr | Met | Gly | Ile | Leu | Asp |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Ile | Ile | Gln | Gln | Ala | Asn | Tyr | Lys | Gln | Leu | Lys | Lys | Gly | Ala | Asn |     |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Glu | Ala | Thr | Lys | Thr | Leu | Asn | Arg | Gly | Ile | Ser | Glu | Phe | Val | Val | Met |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ala | Ala | Asp | Thr | Glu | Pro | Leu | Glu | Ile | Leu | Leu | His | Leu | Pro | Leu | Leu |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ala | Glu | Asp | Lys | Asn | Val | Pro | Tyr | Val | Phe | Val | Pro | Ser | Lys | Gln | Ala |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Leu | Gly | Arg | Ala | Cys | Gly | Val | Thr | Arg | Pro | Val | Ile | Ala | Cys | Ser | Val |  |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Thr | Ser | Asn | Glu | Gly | Ser | Gln | Leu | Lys | Gln | Gln | Ile | Gln | Gly | Leu | Lys |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Asp | Ser | Ile | Glu | Lys | Leu | Leu | Ile |     |     |     |     |     |     |     |     |  |
|     |     |     | 180 |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:3877:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

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(2) INFORMATION FOR SEO ID NO:3878:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1578546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3878:

(2) INFORMATION FOR SEQ ID NO:3879:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 472 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..472

(D) OTHER INFORMATION: / Ceres Seq. ID 1578582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3879:

|             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| gatcagtttag | tagttcacca | gagttcacac | aaaaatcaca | agcaagcagt  | cgcgtgtgta | 60  |
| gctcgcaaca  | atggcgacga | acccggcgct | cttcaccgag | tggccgtgga  | agaagctcgg | 120 |
| caacttcagg  | gtagctcccc | gcacggcgcc | cgtctcagta | ccctgcgtgc  | gtacgtccat | 180 |
| ggcacagag   | gggggagaag | gtgaaggaaa | attagcaact | cgtctcttgc  | tcaccggcgg | 240 |
| cgtgcacatc  | catgqcaatc | ttgggcgcac | gttatattgc | acatgtgcggc | acgCagtgtc | 300 |

(2) INFORMATION FOR SEQ ID NO:3880:

(A) LENGTH: 67 amino aci

- (A) LENGTH: 67 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..67  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3880:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..95  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3881:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Thr | Asn | Pro | Gly | Leu | Phe | Thr | Glu | Trp | Pro | Trp | Lys | Lys | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Asn | Phe | Lys | Val | Ala | Pro | Gly | Thr | Gly | Pro | Val | Ser | Val | Pro | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Arg | Thr | Ser | Met | Ala | Gln | Ser | Gly | Gly | Glu | Gly | Glu | Gly | Lys | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Ala | Thr | Arg | Leu | Leu | Leu | Thr | Gly | Gly | Val | Pro | Cys | His | Gly | Asn | Leu |
|     |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Arg | Met | Val | Tyr | Gly | His | Val | Arg | His | Ala | Val | Ser | Glu | His | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Cys | Thr | His | Gly | Leu | Ala | Ile | His | Thr | Cys | Met | His | Arg | Gln | Pro |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..66  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3882:

[illegible]

Met Pro Trp Gln Ser Trp Ala His Gly Ile Trp Pro Cys Ala Ala Arg  
1 5 10 15  
Ser Val Gly Thr Cys Met His Ala Trp Thr Cys Tyr Thr Tyr Met His  
20 25 30  
Ala Pro Ala Ala Val Arg Pro Ser Val His Glu Ser Tyr Ala Pro Val  
35 40 45  
His Leu Met Phe Arg Pro Thr His Glu His Gly Arg Lys Pro Pro Lys  
50 55 60  
Val His  
65

(2) INFORMATION FOR SEQ ID NO:3883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..780
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3883:

aattcacgac cttattgata ctccccactg cacaaagatg acatagagaa acatgtgaag 60  
gagctcttgg cctcgggtat gatcgtcccc agtaatagcc catttgctc cccggttttg 120  
tgtcaattac tggaagttaa actcactatc aaaaaccggt ttccattcc gatcatgat 180  
gaaattctgg acgagttggc aggcacaaaa cttttcacca agctggacat gagatcgggt 240  
taccatcaag tcgggatgca ttcagatgat gagtttaaaa cgacattcaa aatacatcat 300  
ggacattttc agtttcattg ttgacagact tcagttcgca agacctgttg ccggatcaac 360  
ttctggactg tcgcttggtg aagaaaggca gtaaggcggg tccacaagtg ttagtccaat 420  
ggcgcaatct tctagctgct tctgctacgt gggaggactg gtacgtgttg aagaatcact 480  
ttccacacat ggctgcttgg ggacaggcat caactgaagg ggaggagat gtagcgCccg 540  
acgtgtcGgg tgcggtacag gagtctgcag aagccgtgcc caagtgaagg cgtaatgtgt 600  
taggtccgt catttacttt gttaagagtc atttaaggta ccattggtgg gctcaatgta 660  
atgaccagca actatgctgt taaggtcctt gtggtcggaa cctgaggaac attatcatgc 720  
aaaaagaata tacacgaaag tgaactcggg gttgccttgc ctcgcaagtt catcatccct 780

(2) INFORMATION FOR SEQ ID NO:3884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..81
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3884:

Met Ile Val Pro Ser Asn Ser Pro Phe Ala Ser Pro Val Leu Cys Gln  
1 5 10 15  
Leu Leu Glu Val Lys Leu Thr Ile Lys Asn Arg Phe Pro Ile Pro Ile  
20 25 30  
Ile Asp Glu Ile Leu Asp Glu Leu Ala Gly Thr Lys Leu Phe Thr Lys  
35 40 45  
Leu Asp Met Arg Ser Gly Tyr His Gln Val Gly Met His Ser Asp Asp  
50 55 60  
Glu Phe Lys Thr Thr Phe Lys Ile His His Gly His Phe Gln Phe His  
65 70 75 80  
Cys

(2) INFORMATION FOR SEQ ID NO:3885:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 42 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..42  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1578588  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3885:  
Met Met Ser Leu Lys Arg His Ser Lys Tyr Ile Met Asp Ile Phe Ser  
1                  5                  10                  15  
Phe Ile Val Asp Arg Leu Gln Phe Ala Arg Pro Val Ala Gly Ser Thr  
                  20                  25                  30  
Ser Gly Leu Ser Leu Gly Glu Glu Arg Gln  
                  35                  40

(2) INFORMATION FOR SEQ ID NO:3886:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 41 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..41  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1578589  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3886:  
Met Ser Leu Lys Arg His Ser Lys Tyr Ile Met Asp Ile Phe Ser Phe  
1                  5                  10                  15  
Ile Val Asp Arg Leu Gln Phe Ala Arg Pro Val Ala Gly Ser Thr Ser  
                  20                  25                  30  
Gly Leu Ser Leu Gly Glu Glu Arg Gln  
                  35                  40

(2) INFORMATION FOR SEQ ID NO:3887:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 514 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..514  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1578590  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3887:  
atcgcaactcg tagtcgtagc tcaagcatca rcvgcaggag ctctgggcag cgtgcgcacg 60  
trgggtacct agctcgctct gctagcctac catggctgat caccaccggg gcgcgcacggg 120  
argtgscggg ggctacggcg acctccagcg cgggggcggc atgcacggcg aggcgcagCa 180  
gcagcagaag cagggcgcca tgatgacggc gctcaaggcc gcgacggccg cgacctcctt 240  
gaaccactgc cggcgcgggc gcatatggcc cttaaaggcg gtggctgctg ctacgtacgc 300  
tgccgtagag tctcggtcgc cgcgatagCt ctagctagtc gtttatgtgt tgtgctttgt 360  
gtgtgcatgc ttgtgtctgg gggcatgcag tgcagtgcag tactatatgc tgtatgcgtc 420  
tctctttgat cggagaggcg gatgtacagc atgctcgata tgtctagttt ggatgtcatg 480  
tttatgatga ggaataaaat gcagtgttca ggtg

(2) INFORMATION FOR SEQ ID NO:3888:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 66 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..66  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1578591  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3888:  
Arg Thr Arg Ser Arg Ser Ser Ser Ile Xaa Xaa Arg Ser Ser Gly Gln  
1                  5                  10                  15  
Arg Ala His Xaa Gly Tyr Leu Ala Arg Ser Ala Ser Leu Pro Trp Leu  
          20                  25                  30  
Ile Thr Thr Gly Ala Arg Arg Xaa Val Xaa Gly Ala Thr Ala Thr Ser  
          35                  40                  45  
Ser Ala Gly Ala Ala Cys Thr Ala Arg Arg Ser Ser Ser Arg Ser Arg  
50                  55                  60  
Ala Pro  
65

(2) INFORMATION FOR SEQ ID NO:3889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3889:

Met Ala Asp His His Arg Gly Ala Thr Gly Xaa Xaa Gly Gly Tyr Gly  
1                  5                  10                  15  
Asp Leu Gln Arg Gly Gly Gly Met His Gly Glu Ala Gln Gln Gln Gln  
          20                  25                  30  
Lys Gln Gly Ala Met Met Thr Ala Leu Lys Ala Ala Thr Ala Ala Thr  
          35                  40                  45  
Ser Leu Asn His Cys Arg Arg Gly Gly Ile Trp Pro Leu Lys Ala Val  
50                  55                  60  
Ala Ala Ala Thr Tyr Ala Ala Val Glu Ser Arg Ser Pro Arg  
65                  70                  75

(2) INFORMATION FOR SEQ ID NO:3890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..55
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3890:

Met His Gly Glu Ala Gln Gln Gln Gln Lys Gln Gly Ala Met Met Thr  
1                  5                  10                  15  
Ala Leu Lys Ala Ala Thr Ala Ala Thr Ser Leu Asn His Cys Arg Arg  
          20                  25                  30  
Gly Gly Ile Trp Pro Leu Lys Ala Val Ala Ala Ala Thr Tyr Ala Ala  
35                  40                  45  
Val Glu Ser Arg Ser Pro Arg  
50                  55

(2) INFORMATION FOR SEQ ID NO:3891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1077 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1077  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578630  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3891:

gtaccttggtt tcatgctcag ttgatggaat aattgaagtc tgggattatc ttagtggaaa 60  
gcttaaaaag gatcttcaat atcaagccga tgaaagcttt atgatgcacg aggaacctgt 120  
gctgtgtggtt gatttttagta gggattctga aatgctggca totggatcac aggatggaaa 180  
gattaagggtt tggcgtatac gaactgggtca gtgcttgcaa cgccttgagc gtgcacattc 240  
gaaagggtgtt acaagtgtta catttttcacg tgatggaacc caaatattga gtacatcctt 300  
tgacactacc gcgagggtac atggcctcaa gtctggaaag atgctgaaag aatttcgagg 360  
tcattcttca tatgtaaatt atgccatctt cactactgac ggtagccgtg tcattacagc 420  
ttccagtgat tgtactgtta aggtctggGa tactaaaaca acagattgct tgcatacttt 480  
caagccacca cctcctttga ggggaggaga tgcactgttt aattctgtcc atttatttcc 540  
aaaaaatact gatcacattg ttgtctgcaa taagacttca tcaatattca tcatKgactt 600  
tacaaggaca ggttgtgaag agtttctcat caggtaaagcg agaaggggga gattttgttg 660  
cagcttcagt ttcacaaaaa ggagaatgga tatattgtgt tgggtgaagac atgaacatgt 720  
attgcttttag ctaccaatct ggtaaactgg agcatctgat gaagggtgat gagaaggatg 780  
tcataggcat tacgcaccat cctcacagga acttagtagc caccattgct gaggattgta 840  
tgatgaagat atggaagcct tgactttttt tctttttaaa aaaaccttga accgatgatt 900  
aaataggatg tattttgttt tgtaatttag ataactggta ggcgctacag ctatggactc 960  
gttggtgctt atgttgcccc atgtcttact accattgtat cctgtactag atttagggac 1020  
ctttcaatgg tgtaaacaca gcttactacg actcctcgct acaagttcat tatggtc

(2) INFORMATION FOR SEQ ID NO:3892:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 211 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..211  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578631  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3892:

Tyr Leu Val Ser Cys Ser Val Asp Gly Ile Ile Glu Val Trp Asp Tyr  
1 5 10 15  
Leu Ser Gly Lys Leu Lys Lys Asp Leu Gln Tyr Gln Ala Asp Glu Ser  
20 25 30  
Phe Met Met His Glu Glu Pro Val Leu Cys Val Asp Phe Ser Arg Asp  
35 40 45  
Ser Glu Met Leu Ala Ser Gly Ser Gln Asp Gly Lys Ile Lys Val Trp  
50 55 60  
Arg Ile Arg Thr Gly Gln Cys Leu Gln Arg Leu Glu Arg Ala His Ser  
65 70 75 80  
Lys Gly Val Thr Ser Val Thr Phe Ser Arg Asp Gly Thr Gln Ile Leu  
85 90 95  
Ser Thr Ser Phe Asp Thr Thr Ala Arg Val His Gly Leu Lys Ser Gly  
100 105 110  
Lys Met Leu Lys Glu Phe Arg Gly His Ser Ser Tyr Val Asn Tyr Ala  
115 120 125  
Ile Phe Thr Thr Asp Gly Ser Arg Val Ile Thr Ala Ser Ser Asp Cys  
130 135 140  
Thr Val Lys Val Trp Asp Thr Lys Thr Thr Asp Cys Leu His Thr Phe  
145 150 155 160  
Lys Pro Pro Pro Pro Leu Arg Gly Gly Asp Ala Ser Val Asn Ser Val

165 170 175  
His Leu Phe Pro Lys Asn Thr Asp His Ile Val Val Cys Asn Lys Thr  
180 185 190  
Ser Ser Ile Phe Ile Xaa Asp Phe Thr Arg Thr Gly Cys Glu Glu Phe  
195 200 205  
Leu Ile Arg  
210

(2) INFORMATION FOR SEQ ID NO:3893:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1578632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3893:

Met Met His Glu Glu Pro Val Leu Cys Val Asp Phe Ser Arg Asp Ser  
1 5 10 15  
Glu Met Leu Ala Ser Gly Ser Gln Asp Gly Lys Ile Lys Val Trp Arg  
20 25 30  
Ile Arg Thr Gly Gln Cys Leu Gln Arg Leu Glu Arg Ala His Ser Lys  
35 40 45  
Gly Val Thr Ser Val Thr Phe Ser Arg Asp Gly Thr Gln Ile Leu Ser  
50 55 60  
Thr Ser Phe Asp Thr Thr Ala Arg Val His Gly Leu Lys Ser Gly Lys  
65 70 75 80  
Met Leu Lys Glu Phe Arg Gly His Ser Ser Tyr Val Asn Tyr Ala Ile  
85 90 95  
Phe Thr Thr Asp Gly Ser Arg Val Ile Thr Ala Ser Ser Asp Cys Thr  
100 105 110  
Val Lys Val Trp Asp Thr Lys Thr Thr Asp Cys Leu His Thr Phe Lys  
115 120 125  
Pro Pro Pro Pro Leu Arg Gly Asp Ala Ser Val Asn Ser Val His  
130 135 140  
Leu Phe Pro Lys Asn Thr Asp His Ile Val Val Cys Asn Lys Thr Ser  
145 150 155 160  
Ser Ile Phe Ile Xaa Asp Phe Thr Arg Thr Gly Cys Glu Glu Phe Leu  
165 170 175  
Ile Arg

(2) INFORMATION FOR SEQ ID NO:3894:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..177

(D) OTHER INFORMATION: / Ceres Seq. ID 1578633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3894:

Met His Glu Glu Pro Val Leu Cys Val Asp Phe Ser Arg Asp Ser Glu  
1 5 10 15  
Met Leu Ala Ser Gly Ser Gln Asp Gly Lys Ile Lys Val Trp Arg Ile  
20 25 30  
Arg Thr Gly Gln Cys Leu Gln Arg Leu Glu Arg Ala His Ser Lys Gly  
35 40 45



Val Thr Ser Val Thr Phe Ser Arg Asp Gly Thr Gln Ile Leu Ser Thr  
50 55 60  
Ser Phe Asp Thr Thr Ala Arg Val His Gly Leu Lys Ser Gly Lys Met  
65 70 75 80  
Leu Lys Glu Phe Arg Gly His Ser Ser Tyr Val Asn Tyr Ala Ile Phe  
85 90 95  
Thr Thr Asp Gly Ser Arg Val Ile Thr Ala Ser Ser Asp Cys Thr Val  
100 105 110  
Lys Val Trp Asp Thr Lys Thr Thr Asp Cys Leu His Thr Phe Lys Pro  
115 120 125  
Pro Pro Pro Leu Arg Gly Gly Asp Ala Ser Val Asn Ser Val His Leu  
130 135 140  
Phe Pro Lys Asn Thr Asp His Ile Val Val Cys Asn Lys Thr Ser Ser  
145 150 155 160  
Ile Phe Ile Xaa Asp Phe Thr Arg Thr Gly Cys Glu Glu Phe Leu Ile  
165 170 175  
Arg

(2) INFORMATION FOR SEQ ID NO:3895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..906
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3895:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aatgatattc agcttagtat tcgtatgccc agtggaata gactggagat caaactaaca  | 60  |
| aaacaagatg ttttaaggaa agtgaagaat ttcgtggatg aaaaccaagg caatgggctt | 120 |
| ggctcatatg acctttctct ggtttatcct aaaagagttt tctctgaaca agatatggaa | 180 |
| gcaacactat ccgagctggg tattcaaaac cgtcatgcaa tgattgttgt tccacatcgg | 240 |
| cagtctggtc aggtatcaag gcgtcactcc tcggcatcct atgatatggg tgtcaattca | 300 |
| ggtgcggatg atgttggtg caattcagggt gcggggggat actttgggta cctgagaacc | 360 |
| gtcctgtcct atgtgaatcc actctcctac ctgaggggaa ataccaactc atcaaataca | 420 |
| gagctacagt caaatgaagG Cctgcggcag cttagacatg gatctgggtcc atggagtga | 480 |
| ccacggcctc ttggcaatag gggccatgaa gtgactgatg cagactctgc aaacacgctg | 540 |
| cgaaggcggc ctagaccatt tggtgccaat atccacactc tggggagcga ggatcatggt | 600 |
| ccgtctgatg aaagaaatgt tttctggaac gggaactcga cagagtttgg aggcgacgac | 660 |
| agaaaatagg ttgtggcgtg gctggcaggg cctgggacga cactatcaga cagaatcaaa | 720 |
| gttggaata gacagctgaa acaaatgcct cgacaggctt attgaggaat aagtattgag  | 780 |
| attatagtc tgaaataatc gctgaattgt gatgtttaca tttgtggaaa catacggtcg  | 840 |
| ctggatccgt atactcgttg tatagtacat agccacagat atattaaatc cgaactgctt | 900 |

ggttcc

(2) INFORMATION FOR SEQ ID NO:3896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..222
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3896:

Asn Asp Ile Gln Leu Ser Ile Arg Met Pro Ser Gly Asn Arg Leu Glu  
1 5 10 15  
Ile Lys Leu Thr Lys Gln Asp Val Leu Arg Lys Val Lys Asn Phe Val

20 25 30  
Asp Glu Asn Gln Gly Asn Gly Leu Gly Ser Tyr Asp Leu Ser Leu Val  
35 40 45  
Tyr Pro Lys Arg Val Phe Ser Glu Gln Asp Met Glu Ala Thr Leu Ser  
50 55 60  
Glu Leu Gly Ile Gln Asn Arg His Ala Met Ile Val Val Pro His Arg  
65 70 75 80  
Gln Ser Gly Gln Val Ser Arg Arg His Ser Ser Ala Ser Tyr Asp Met  
85 90 95  
Gly Val Asn Ser Gly Ala Asp Asp Val Gly Gly Asn Ser Gly Ala Gly  
100 105 110  
Gly Tyr Phe Gly Tyr Leu Arg Thr Val Leu Ser Tyr Val Asn Pro Leu  
115 120 125  
Ser Tyr Leu Arg Gly Asn Thr Asn Ser Ser Asn Thr Glu Leu Gln Ser  
130 135 140  
Asn Glu Gly Leu Arg Gln Leu Arg His Gly Ser Gly Pro Trp Ser Glu  
145 150 155 160  
Pro Arg Pro Leu Gly Asn Arg Gly His Glu Val Thr Asp Ala Asp Ser  
165 170 175  
Ala Asn Thr Leu Arg Arg Arg Pro Arg Pro Phe Gly Ala Asn Ile His  
180 185 190  
Thr Leu Gly Ser Glu Asp His Gly Pro Ser Asp Glu Arg Asn Val Phe  
195 200 205  
Trp Asn Gly Asn Ser Thr Glu Phe Gly Gly Asp Asp Arg Lys  
210 215 220

(2) INFORMATION FOR SEQ ID NO:3897:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1578676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3897:

Met Pro Ser Gly Asn Arg Leu Glu Ile Lys Leu Thr Lys Gln Asp Val  
1 5 10 15  
Leu Arg Lys Val Lys Asn Phe Val Asp Glu Asn Gln Gly Asn Gly Leu  
20 25 30  
Gly Ser Tyr Asp Leu Ser Leu Val Tyr Pro Lys Arg Val Phe Ser Glu  
35 40 45  
Gln Asp Met Glu Ala Thr Leu Ser Glu Leu Gly Ile Gln Asn Arg His  
50 55 60  
Ala Met Ile Val Val Pro His Arg Gln Ser Gly Gln Val Ser Arg Arg  
65 70 75 80  
His Ser Ser Ala Ser Tyr Asp Met Gly Val Asn Ser Gly Ala Asp Asp  
85 90 95  
Val Gly Gly Asn Ser Gly Ala Gly Gly Tyr Phe Gly Tyr Leu Arg Thr  
100 105 110  
Val Leu Ser Tyr Val Asn Pro Leu Ser Tyr Leu Arg Gly Asn Thr Asn  
115 120 125  
Ser Ser Asn Thr Glu Leu Gln Ser Asn Glu Gly Leu Arg Gln Leu Arg  
130 135 140  
His Gly Ser Gly Pro Trp Ser Glu Pro Arg Pro Leu Gly Asn Arg Gly  
145 150 155 160  
His Glu Val Thr Asp Ala Asp Ser Ala Asn Thr Leu Arg Arg Arg Pro  
165 170 175  
Arg Pro Phe Gly Ala Asn Ile His Thr Leu Gly Ser Glu Asp His Gly  
180 185 190

Pro Ser Asp Glu Arg Asn Val Phe Trp Asn Gly Asn Ser Thr Glu Phe  
195 200 205  
Gly Gly Asp Asp Arg Lys  
210

(2) INFORMATION FOR SEQ ID NO:3898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3898:

Met Glu Ala Thr Leu Ser Glu Leu Gly Ile Gln Asn Arg His Ala Met  
1 5 10 15  
Ile Val Val Pro His Arg Gln Ser Gly Gln Val Ser Arg Arg His Ser  
20 25 30  
Ser Ala Ser Tyr Asp Met Gly Val Asn Ser Gly Ala Asp Asp Val Gly  
35 40 45  
Gly Asn Ser Gly Ala Gly Gly Tyr Phe Gly Tyr Leu Arg Thr Val Leu  
50 55 60  
Ser Tyr Val Asn Pro Leu Ser Tyr Leu Arg Gly Asn Thr Asn Ser Ser  
65 70 75 80  
Asn Thr Glu Leu Gln Ser Asn Glu Gly Leu Arg Gln Leu Arg His Gly  
85 90 95  
Ser Gly Pro Trp Ser Glu Pro Arg Pro Leu Gly Asn Arg Gly His Glu  
100 105 110  
Val Thr Asp Ala Asp Ser Ala Asn Thr Leu Arg Arg Arg Pro Arg Pro  
115 120 125  
Phe Gly Ala Asn Ile His Thr Leu Gly Ser Glu Asp His Gly Pro Ser  
130 135 140  
Asp Glu Arg Asn Val Phe Trp Asn Gly Asn Ser Thr Glu Phe Gly Gly  
145 150 155 160  
Asp Asp Arg Lys

(2) INFORMATION FOR SEQ ID NO:3899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..745
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3899:

cagacaataa tatacaatgc tgtgtttaag gtcataatg ctgttatatc agacatgcgg 60  
cctggagtta attggatgga tatgcacaaa ttagcagaac gggcaatact tgaatctctc 120  
aggaaggaac aaattgtaca aggggatggt gatgatatga tggctcaaag gttaggggct 180  
gttttcatgc ctcatggtct tggccactta cttggtattg acacccatga tccaggaggc 240  
taccctgagg gattggagag gccaaggat ccaggactga actccttgcg gaccacaaga 300  
gaactgaaag aaggaatggt tatcacagt gagccaggct gctatttcat tgatgctttg 360  
ctaactaaaa caagggatga tccaatttcc tcaaagttct tcaactggca agaggttgaa 420  
aagtataaaa gctttggtgg cgttcgcatt gaaagtgatg tgtatgtgac ggctcaagga 480  
tgccggaacc tcacaaactg cccgagagag acctgggaga tcgaggctgt aatGgctggc 540  
gcaccatggc ctctgccggc ttcaaGttct atggtggtag cagcagagAa tagcaatgac 600  
atatctaaag cgtcgtaatt ttctctatgc tcaatccata tcccgagttg aaacaaattc 660

gacctggatt cttatattca ataaatagtg aggcctgagggc gcaaaacatt gttggattga 720  
tggttggaac acatttcata cgccc

(2) INFORMATION FOR SEQ ID NO:3900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..205
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3900:

Gln Thr Ile Ile Tyr Asn Ala Val Phe Lys Ala His Asn Ala Val Ile  
1 5 10 15  
Ser Asp Met Arg Pro Gly Val Asn Trp Met Asp Met His Lys Leu Ala  
20 25 30  
Glu Arg Ala Ile Leu Glu Ser Leu Arg Lys Glu Gln Ile Val Gln Gly  
35 40 45  
Asp Val Asp Asp Met Met Ala Gln Arg Leu Gly Ala Val Phe Met Pro  
50 55 60  
His Gly Leu Gly His Leu Leu Gly Ile Asp Thr His Asp Pro Gly Gly  
65 70 75 80  
Tyr Pro Glu Gly Leu Glu Arg Pro Lys Asp Pro Gly Leu Asn Ser Leu  
85 90 95  
Arg Thr Thr Arg Glu Leu Lys Glu Gly Met Val Ile Thr Val Glu Pro  
100 105 110  
Gly Cys Tyr Phe Ile Asp Ala Leu Thr Lys Thr Arg Asp Asp Pro  
115 120 125  
Ile Ser Ser Lys Phe Phe Asn Trp Gln Glu Val Glu Lys Tyr Lys Ser  
130 135 140  
Phe Gly Gly Val Arg Ile Glu Ser Asp Val Tyr Val Thr Ala Gln Gly  
145 150 155 160  
Cys Arg Asn Leu Thr Asn Cys Pro Arg Glu Thr Trp Glu Ile Glu Ala  
165 170 175  
Val Met Ala Gly Ala Pro Trp Pro Leu Pro Ala Ser Ser Ser Met Val  
180 185 190  
Val Ala Ala Glu Asn Ser Asn Asp Ile Ser Lys Ala Ser  
195 200 205

(2) INFORMATION FOR SEQ ID NO:3901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..187
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3901:

Met Arg Pro Gly Val Asn Trp Met Asp Met His Lys Leu Ala Glu Arg  
1 5 10 15  
Ala Ile Leu Glu Ser Leu Arg Lys Glu Gln Ile Val Gln Gly Asp Val  
20 25 30  
Asp Asp Met Met Ala Gln Arg Leu Gly Ala Val Phe Met Pro His Gly  
35 40 45  
Leu Gly His Leu Leu Gly Ile Asp Thr His Asp Pro Gly Gly Tyr Pro  
50 55 60  
Glu Gly Leu Glu Arg Pro Lys Asp Pro Gly Leu Asn Ser Leu Arg Thr

(B) LOCATION: 1..789

(D) OTHER INFORMATION: / Ceres Seq. ID 1578692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3903:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| aagagccaac | agagcaacgc | ccaggcacac | acgacacgaa | ccargcagcc | agccgcggag  | 60  |
| ggaggaacc  | tagcggaaca | ggtgacggcg | gcgcgctacc | ggtgacgggg | gatacggcgg  | 120 |
| catcgtcccc | tcctccatcc | ccggcgcgcc | ggcgagcag  | ccggcctgca | ggctgtttga  | 180 |
| agagctcgcc | atttaatctc | aatggaagcc | aagtttttcc | gtttcctgaa | gctcgttggg  | 240 |
| gtcggcttca | aagcgaggtc | agagagccaa | ggccgtgagt | tgttccttaa | actgggcttc  | 300 |
| agccatgagg | tgagttcac  | cgctcctcca | gctgtccgtg | tcttctgctt | caaaccacaac | 360 |
| ataatctgct | gcaccggcat | cgataaggac | agggtgcacc | agttcgcccg | cgccatccgg  | 420 |
| agctctaagg | ctccagaggt | gtacaagggg | aaggggatcc | tgtacattga | cgagggttatc | 480 |
| aagctgaagc | ccggaaagaa | gcgaaaaaat | aagtgcagat | ccgaaGgcgt | tacaactttt  | 540 |
| tctgtctttt | Aaccccatcc | ttcgcatctg | tagtgatctg | gatctggggg | ctgctgtgtt  | 600 |
| gtgttggtga | cttgcggttg | gctacacaga | tcaccattat | cttaccttta | cctcagctgc  | 660 |
| atgtaggacc | atgagtgga  | ataagttacc | agtttggtga | tatgagctgg | aacgttgctt  | 720 |
| tgcaatttgg | attggattac | cgagtgggat | gttttggttc | aaacttgaag | tctttcaata  | 780 |

gattgttgc

(2) INFORMATION FOR SEQ ID NO:3904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1578693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3904:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Glu | Pro | Thr | Glu | Gln | Arg | Pro | Gly | Thr | His | Asp | Thr | Asn | Xaa | Ala | Ala |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Ser | Arg | Gly | Gly | Arg | Asn | Pro | Ser | Gly | Thr | Gly | Asp | Gly | Gly | Ala | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Pro | Val | Thr | Gly | Asp | Thr | Ala | Ala | Ser | Ser | Pro | Pro | Pro | Ser | Pro | Ala |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |  |
| Arg | Arg | Arg | Ser | Ser | Arg | Pro | Ala | Gly | Cys | Leu | Lys | Ser | Ser | Pro | Phe |  |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Asn | Leu | Asn | Gly | Ser | Gln | Val | Phe | Pro | Phe | Pro | Glu | Ala | Arg | Trp | Gly |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Arg | Leu | Gln | Ser | Glu | Val | Arg | Glu | Pro | Arg | Pro |     |     |     |     |     |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:3905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1578694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3905:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Ala | Lys | Phe | Phe | Arg | Phe | Leu | Lys | Leu | Val | Gly | Val | Gly | Phe |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Lys | Ala | Arg | Ser | Glu | Ser | Gln | Gly | Arg | Glu | Leu | Phe | Leu | Lys | Leu | Gly |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Phe | Ser | His | Glu | Val | Gln | Phe | Thr | Ala | Pro | Pro | Ala | Val | Arg | Val | Phe |  |
|     |     |     | 35  |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Cys | Phe | Lys | Pro | Asn | Ile | Ile | Cys | Cys | Thr | Gly | Ile | Asp | Lys | Asp | Arg |  |
|     |     |     | 50  |     |     | 55  |     |     | 60  |     |     |     |     |     |     |  |
| Val | His | Gln | Phe | Ala | Gly | Ala | Ile | Arg | Ser | Ser | Lys | Ala | Pro | Glu | Val |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Cys | Leu | Gly | Arg | Phe | Leu | Ile | Leu | Leu | Ala | Ser | Pro | Asn | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Pro | Lys | Pro | Phe | Thr | Arg | Xaa | Arg | Arg | Arg | Arg | Arg | Arg | Arg | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Ile | Arg | Ser | Ala | Gln | Pro | Pro | Glu | Lys | Arg | Arg | Glu | Pro | Ala | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Thr | Met | Gly | Arg | Val | Arg | Thr | Lys | Thr | Val | Lys | Lys | Thr | Ser | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Val | Ile | Glu | Lys | Tyr | Tyr | Ser | Arg | Met | Thr | Leu | Asp | Phe | His | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asn | Lys | Lys | Val | Leu | Glu | Glu | Val | Ser | Ile | Leu | Pro | Ser | Lys | Arg | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Asn | Lys | Val | Ala | Gly | Phe | Thr | Thr | His | Leu | Met | Arg | Arg | Ile | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Gly | Pro | Arg | Pro | Leu | Leu | Arg | Arg | Leu | Gly | Ala | Thr | Glu | Val | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Ala | Thr | Ala | Ala | Ala | Ala | Xaa | Ala | Gly | Gly | Thr | Asp | Val | Trp | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| His | Pro | Gly | Phe | Gly | Arg | Val | Ile | Leu | Ser | Ile | Tyr | Ser | Ile | Val | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Phe | Ala | Ser | Val | Thr | Val | Leu | Val | Ser | Val | Leu | Pro | Leu | Asp |     |

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(2) INFORMATION FOR SEQ ID NO:3909:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..102
 (D) OTHER INFORMATION: / Ceres Seq. ID 1578698
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3909:
Met Thr Leu Asp Phe His Thr Asn Lys Lys Val Leu Glu Glu Val Ser
1 5 10 15
Ile Leu Pro Ser Lys Arg Leu Arg Asn Lys Val Ala Gly Phe Thr Thr
 20 25 30
His Leu Met Arg Arg Ile Gln Arg Gly Pro Arg Pro Leu Leu Arg Arg
 35 40 45
Leu Gly Ala Thr Glu Val Val Ala Ala Thr Ala Ala Ala Ala Xaa Ala
 50 55 60
Gly Gly Thr Asp Val Trp Ala His Pro Gly Phe Gly Arg Val Ile Leu
65 70 75 80
Ser Ile Tyr Ser Ile Val Leu Pro Phe Ala Ser Val Thr Val Leu Val
 85 90 95
Ser Val Leu Pro Leu Asp
 100
```

[illegible]



(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..592

(D) OTHER INFORMATION: / Ceres Seq. ID 1578699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3910:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| acacacacca | tcgtcctctc | ctttgccagc | gccgccgaac | ccgccaccag | ccttctccca | 60  |
| tcctcgaagc | acggaaggct | cccagaagga | gctctcacct | cgcagccatc | tctggcacgt | 120 |
| ccgtccttct | tctccctcgg | tccctcccct | tctccacagc | tatcggattg | gcgttggagt | 180 |
| ggagatcgac | ccgggctcgg | aattcccttc | gttggttaag | aaccctaatt | tggtcagatg | 240 |
| ggatttccaa | cttcgacaaa | gcccgcgagg | tcgatcgatc | tcagttgacg | cgagggattg | 300 |
| gaaaactaag | ttgcgggtgt | agttaatttt | ctaggaagat | tggggtttca | gctcaaactc | 360 |
| ccatgctcga | cgctgaggac | gaccCtggcg | ggagatgacg | aggatottcg | tgcagcgcg  | 420 |
| gaccgcccgc | tcctcgtcca | gctccggccg | ctcggacacg | cagccagtgc | agccggcagc | 480 |
| agctgcccgg | gaggaggagt | tgccgctgca | acctcaacca | cagctgccgg | agctattggc | 540 |
| catagatgat | acaactgata | atttaaata  | gggcagcgag | aatatcagca | at         |     |

(2) INFORMATION FOR SEQ ID NO:3911:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1578700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3911:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | His | Thr | Ile | Val | Leu | Ser | Phe | Ala | Ser | Ala | Ala | Glu | Pro | Ala | Thr |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser | Leu | Leu | Pro | Ser | Ser | Lys | His | Gly | Arg | Leu | Pro | Glu | Gly | Ala | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Thr | Ser | Gln | Pro | Ser | Leu | Ala | Arg | Pro | Ser | Phe | Phe | Ser | Leu | Gly | Pro |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     |     | 45  |     |  |
| Ser | Pro | Ser | Pro | Gln | Leu | Ser | Asp | Trp | Arg | Trp | Ser | Gly | Asp | Arg | Pro |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     |     | 60  |     |     |     |  |
| Gly | Leu | Gly | Ile | Pro | Phe | Val | Gly | Lys | Glu | Pro |     |     |     |     |     |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:3912:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1578701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3912:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| His | Thr | Pro | Ser | Ser | Ser | Pro | Leu | Pro | Ala | Pro | Pro | Asn | Pro | Pro | Pro |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ala | Phe | Ser | His | Pro | Arg | Ser | Thr | Glu | Gly | Ser | Gln | Lys | Glu | Leu | Ser |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Pro | Arg | Ser | His | Leu | Trp | His | Val | Arg | Pro | Ser | Ser | Pro | Ser | Val | Pro |  |
|     |     |     | 35  |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Pro | Leu | Leu | His | Ser | Tyr | Arg | Ile | Gly | Val | Gly | Val | Glu | Ile | Asp | Pro |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gly | Ser | Glu | Phe | Pro | Ser | Leu | Val | Arg | Asn | Pro | Asn | Leu | Val | Arg | Trp |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Asp | Phe | Gln | Leu | Arg | Gln | Ser | Pro | Arg | Gly | Arg | Ser | Ile | Ser | Val | Asp |  |

85 90 95  
Ala Arg Asp Trp Lys Thr Lys Leu Arg Val  
100 105

(2) INFORMATION FOR SEQ ID NO:3913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1578702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3913:

Thr His His Arg Pro Leu Leu Cys Gln Arg Arg Arg Thr Arg His Gln  
1 5 10 15  
Pro Ser Pro Ile Leu Glu Ala Arg Lys Ala Pro Arg Arg Ser Ser His  
20 25 30  
Leu Ala Ala Ile Ser Gly Thr Ser Val Leu Leu Leu Pro Arg Ser Leu  
35 40 45  
Pro Phe Ser Thr Ala Ile Gly Leu Ala Leu Glu Trp Arg Ser Thr Arg  
50 55 60  
Ala Arg Asn Ser Leu Arg Trp  
65 70

(2) INFORMATION FOR SEQ ID NO:3914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1051 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1051

(D) OTHER INFORMATION: / Ceres Seq. ID 1578703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3914:

gagccaccaa gagatccacg aatataaccca tccattccc cacaaggctc cgtcccttcg 60  
gcggcgcgca tgtctctccc cctrgcccg gcggacagtg gcgcccggac cggagacgac 120  
tggttccctcg actgcratc cctcgacgac ctgcccgcgc cggcctgcgg ggccttcccg 180  
tgggacgcgt ccccgctcgt tccaaccccc agtgtggaag tgggcagcta tgtaaacgcc 240  
aatgatgcat tcaaggagcc caatgatgtc ttcaaggagc ctggcagcag taaacgttta 300  
cggtcaggat ccagtatat gccaacatct aaagcttgca gggaaagaat gaggaggaac 360  
aagctgaatg acaggtttct tgaactgggg tctgcattag aacctgggaa gccagtgaac 420  
gctgacaaaag ctgccatccc taagcagatg tactgcgatg gttattcagc tccgttcaga 480  
atcacagcaa ctgaaggaga ctaatggcag cctcgaagaa aagattaaag aactaaaggc 540  
cgagaaggac gagttcgcga cgagaagcag aaactgaaac tggagaagga gagtctagag 600  
caccagatga agctgatggc atcggctcca gcctacatgc cccatccgac cctgatgccg 660  
gcgcctttcg cccaggcgcc cctaactcca ttccatgccc agggccaagc tgcagggcag 720  
aagctgatga tgcccttcgt cggctaccca gggtaaccaa tgtggcagtt catgcgcct 780  
tcagaggtcg acacctcgaa ggacagcgag gcgtgccctc ctgtcgcatg atcaacctga 840  
tggggctggc cctgctcaca ccatgtggat tagccgcaac tagttgtcgt tgcgatcca 900  
ttgatggggt ataactgatg ttcttaggct atctccagca gcctctctat cctattctct 960  
atcttactcc ctattttaaa ttttactctg taaacagtac agtctatagt gtaagacaat 1020  
gttttgcatg tttatatcca cgccttgctg g

(2) INFORMATION FOR SEQ ID NO:3915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1578704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3915:

Glu Pro Pro Arg Asp Pro Arg Ile Tyr Pro Ser His Ser Pro Gln Gly  
1 5 10 15  
Ser Val Pro Ser Ala Ala Ala Met Ser Leu Pro Pro Xaa Pro Ala Asp  
20 25 30  
Ser Gly Ala Gly Thr Gly Asp Asp Trp Phe Leu Asp Cys Xaa Ile Leu  
35 40 45  
Asp Asp Leu Pro Ala Ala Ala Cys Gly Ala Phe Pro Trp Asp Ala Ser  
50 55 60  
Pro Ser Ser Ser Asn Pro Ser Val Glu Val Gly Ser Tyr Val Asn Ala  
65 70 75 80  
Asn Asp Ala Phe Lys Glu Pro Asn Asp Val Phe Lys Glu Pro Gly Ser  
85 90 95  
Ser Lys Arg Leu Arg Ser Gly Ser Ser Asp Met Pro Thr Ser Lys Ala  
100 105 110  
Cys Arg Glu Arg Met Arg Arg Asn Lys Leu Asn Asp Arg Phe Leu Glu  
115 120 125  
Leu Gly Ser Ala Leu Glu Pro Gly Lys Pro Val Lys Ala Asp Lys Ala  
130 135 140  
Ala Ile Pro Lys Arg Cys Tyr Ser His Gly Tyr Ser Ala Pro Phe Arg  
145 150 155 160  
Ile Thr Ala Thr Glu Gly Asp  
165

(2) INFORMATION FOR SEQ ID NO:3916:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1578705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3916:

Met Ser Leu Pro Pro Xaa Pro Ala Asp Ser Gly Ala Gly Thr Gly Asp  
1 5 10 15  
Asp Trp Phe Leu Asp Cys Xaa Ile Leu Asp Asp Leu Pro Ala Ala Ala  
20 25 30  
Cys Gly Ala Phe Pro Trp Asp Ala Ser Pro Ser Ser Ser Asn Pro Ser  
35 40 45  
Val Glu Val Gly Ser Tyr Val Asn Ala Asn Asp Ala Phe Lys Glu Pro  
50 55 60  
Asn Asp Val Phe Lys Glu Pro Gly Ser Ser Lys Arg Leu Arg Ser Gly  
65 70 75 80  
Ser Ser Asp Met Pro Thr Ser Lys Ala Cys Arg Glu Arg Met Arg Arg  
85 90 95  
Asn Lys Leu Asn Asp Arg Phe Leu Glu Leu Gly Ser Ala Leu Glu Pro  
100 105 110  
Gly Lys Pro Val Lys Ala Asp Lys Ala Ala Ile Pro Lys Arg Cys Tyr  
115 120 125  
Ser His Gly Tyr Ser Ala Pro Phe Arg Ile Thr Ala Thr Glu Gly Asp  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3917:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 991 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..991  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1578737  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3917:

aaaaatcgaa tcgagcccat ccatctccat ttccgcccgc gccgcccgcg agagacccca 60  
accccaacca tccaccacca tgtggcgccg cctccacacc ctagcccccg ccttgccgag 120  
ggctacccgc gccgcccgcg gggcccctgc ggcgctccgc tcctctgcag cccgcgccgc 180  
cccgcctctcc tcggcgccgc cgcctttccg ccgcaccagc ccgctcctct caggggacaa 240  
gccggcgagt gtggaggacg tcatgcccac cgccacgggg ctcgagcggg aggagctgga 300  
ggccgagctc aagggggaaga agcgggtttga catggatccc ctggtcggcc ccttcgggtac 360  
caaggaggaa ccatctgtag ttgagtccta ctataacaag cggatagtcg gctgccctgg 420  
tggtgaggga gaggatgaac acgatgttgt atggttcttg ttgaaaaaag atgagccgca 480  
tgagtgtcca gtctgtctgc aatactttgt gcttaaggtc attggtgatG ggtggtgatc 540  
cagatggtca tgacgatgaa gatgatggac atcactaagg atgccttggt gttctgaaaa 600  
taagaatttg gtgaggcaga tgaatccaat acacttcttt ttctagaacc agactgctcc 660  
acggcatcct tgtttatgaa aagacagttg gccatcaagc aggtggtagt tttcacctag 720  
gtattttgtc caaacaaaag ctgtttgaga tttgaccctt gcgtttcttt aagagcatcg 780  
tcgaataaaa gatgactgca gtcagattgc tttcttttga tacctcatat tggcccatcg 840  
ggtgtgatgg acatgtaata ttcagtaatg gaacagcccc atttctatgc ttagcgtgct 900  
gggaattttg caaaaggcct cctatatcat tgacgagttt taagccagag tttgatgatc 960  
caacatgttt atgaccattg ttttaatagc c

(2) INFORMATION FOR SEQ ID NO:3918:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 109 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..109  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1578738  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3918:

Lys Asn Arg Ile Glu Pro Ile His Leu His Phe Arg Arg Arg Arg Arg  
1 5 10 15  
Arg Glu Thr Pro Thr Pro Pro Ile His His His Val Ala Pro Pro Pro  
20 25 30  
His Pro Ser Pro Arg Leu Ala Gln Gly Tyr Arg Arg Arg Arg Arg Gly  
35 40 45  
Pro Cys Gly Val Arg Leu Leu Cys Ser Pro Arg Arg Pro Ala Leu Leu  
50 55 60  
Gly Gly Arg Arg Phe Pro Pro His Gln Pro Ala Pro Leu Arg Gly Gln  
65 70 75 80  
Ala Gly Glu Cys Gly Gly Arg His Ala His Arg His Gly Ala Arg Ala  
85 90 95  
Gly Gly Ala Gly Gly Arg Ala Gln Gly Glu Glu Ala Val  
100 105

(2) INFORMATION FOR SEQ ID NO:3919:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 178 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1578739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3919:

Lys Ile Glu Ser Ser Pro Ser Ile Ser Ile Ser Ala Ala Ala Ala Ala  
1 5 10 15  
Glu Arg Pro Gln Pro His Pro Ser Thr Thr Met Trp Arg Arg Leu His  
20 25 30  
Thr Leu Ala Pro Ala Leu Arg Arg Ala Thr Ala Ala Ala Ala Gly Ala  
35 40 45  
Pro Ala Ala Ser Ala Ser Ser Ala Ala Arg Ala Ala Pro Leu Ser Ser  
50 55 60  
Ala Ala Ala Ala Phe Arg Arg Thr Ser Pro Leu Leu Ser Gly Asp Lys  
65 70 75 80  
Pro Ala Ser Val Glu Asp Val Met Pro Ile Ala Thr Gly Leu Glu Arg  
85 90 95  
Glu Glu Leu Glu Ala Glu Leu Lys Gly Lys Lys Arg Phe Asp Met Asp  
100 105 110  
Pro Leu Val Gly Pro Phe Gly Thr Lys Glu Glu Pro Ser Val Val Glu  
115 120 125  
Ser Tyr Tyr Asn Lys Arg Ile Val Gly Cys Pro Gly Gly Glu Gly Glu  
130 135 140  
Asp Glu His Asp Val Val Trp Phe Trp Leu Lys Lys Asp Glu Pro His  
145 150 155 160  
Glu Cys Pro Val Cys Ser Gln Tyr Phe Val Leu Lys Val Ile Gly Asp  
165 170 175  
Gly Trp

(2) INFORMATION FOR SEQ ID NO:3920:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1578740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3920:

Met Trp Arg Arg Leu His Thr Leu Ala Pro Ala Leu Arg Arg Ala Thr  
1 5 10 15  
Ala Ala Ala Ala Gly Ala Pro Ala Ala Ser Ala Ser Ser Ala Ala Arg  
20 25 30  
Ala Ala Pro Leu Ser Ser Ala Ala Ala Phe Arg Arg Thr Ser Pro  
35 40 45  
Leu Leu Ser Gly Asp Lys Pro Ala Ser Val Glu Asp Val Met Pro Ile  
50 55 60  
Ala Thr Gly Leu Glu Arg Glu Glu Leu Glu Ala Glu Leu Lys Gly Lys  
65 70 75 80  
Lys Arg Phe Asp Met Asp Pro Leu Val Gly Pro Phe Gly Thr Lys Glu  
85 90 95  
Glu Pro Ser Val Val Glu Ser Tyr Tyr Asn Lys Arg Ile Val Gly Cys  
100 105 110  
Pro Gly Gly Glu Gly Glu Asp Glu His Asp Val Val Trp Phe Trp Leu  
115 120 125  
Lys Lys Asp Glu Pro His Glu Cys Pro Val Cys Ser Gln Tyr Phe Val  
130 135 140  
Leu Lys Val Ile Gly Asp Gly Trp  
145 150

(2) INFORMATION FOR SEQ ID NO:3921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 865 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..865
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3921:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gttgacatc  | gcgccctcac | gcgttcgacg | tgcgcgcgtg | cgttactcgt | cgtcgtcggg | 60  |
| ccgcggcgct | tggtgcatca | cactgtagta | tatagaacga | gccatccacg | cacataaagc | 120 |
| tacagcatct | gctcgatcgt | ctagcttgga | cggtggaccg | agagaccagc | cagctagatg | 180 |
| gcgcgcaggg | cggtcggcgt | tctactggcc | gtggccgcgc | tcctcgcggc | ggcgacggcg | 240 |
| agggcgggcg | acgacgacga | caagacgcag | ccctggcagt | gcttcaagtc | atgctccaga | 300 |
| rgctgccacc | accaccacga | ccacgaccac | gacaacggcg | ctgctgccgt | ggcggacttc | 360 |
| ctctccgggg | ccgccgccaa | ggtctccgcc | gccgtcaccc | gcgagtgcaa | gaacaacagc | 420 |
| tgccatgaca | acgcgtgctt | caaggacctg | ccggccatca | cctaccgcga | gtgcgccatc | 480 |
| gccacctgcc | Ctcagccatc | cgcaccatag | cagaaagaaa | acggcgtgct | tgaaggactg | 540 |
| ctgcgagaag | tgcttcatca | atggcccacc | tgcgcctggc | ccacctgcgc | ctggcccgcg | 600 |
| tgtgcctggc | ccacctgcgc | ctggcccgcg | tgtccttggt | cccagcccga | cgccaccatc | 660 |
| tccgccaat  | taagcccatg | ttgcatggat | gctcttggtg | cacatgcatg | aagtagtaga | 720 |
| gagcaacggt | caacttactc | cttatattcc | cataataata | aaatacttag | gagtacttac | 780 |
| ttcaaaaaaa | gaaggatctc | atgactgtaa | ccgaagtgac | attttctctt | gagttggggg | 840 |
| gtaacataaa | cccagcacca | aagcc      |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:3922:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3922:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Arg | Arg | Ala | Val | Gly | Val | Leu | Leu | Ala | Val | Ala | Ala | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ala | Ala | Thr | Ala | Arg | Ala | Ala | Asp | Asp | Asp | Asp | Lys | Thr | Gln | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Trp | Gln | Cys | Phe | Lys | Ser | Cys | Ser | Arg | Xaa | Cys | His | His | His | His | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| His | Asp | His | Asp | Asn | Gly | Ala | Ala | Val | Ala | Asp | Phe | Leu | Ser | Gly |     |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Ala | Ala | Ala | Lys | Val | Ser | Ala | Ala | Val | Thr | Arg | Glu | Cys | Lys | Asn | Asn |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Cys | His | Asp | Asn | Ala | Cys | Phe | Lys | Asp | Leu | Pro | Ala | Ile | Thr | Tyr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Pro | Gln | Cys | Ala | Ile | Ala | Thr | Cys | Pro | Gln | Pro | Ser | Ala | Pro |     |     |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:3923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..82  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3923:

```
Met Thr Thr Arg Ala Ser Arg Thr Cys Arg Pro Ser Pro Thr Arg Ser
1 5 10 15
Ala Pro Ser Pro Pro Ala Leu Ser His Pro His His Ser Arg Lys Lys
 20 25 30
Thr Ala Cys Leu Lys Asp Cys Cys Glu Lys Cys Phe Ile Asn Gly Pro
 35 40 45
Pro Ala Pro Gly Pro Pro Ala Pro Gly Pro Pro Val Pro Gly Pro Pro
 50 55 60
Ala Pro Gly Pro Pro Ala Pro Gly Pro Ser Pro Thr Pro Pro Ser Pro
65 70 75 80
Pro Asn
```

(2) INFORMATION FOR SEQ ID NO:3924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 857 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..857  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3924:

```
acagccgcac agccgcgcgc gtcctcatcca cctctccaca ccatctgacg ctgcttccac 60
cgaggtctcc aaggctcact cctcaccagc ttctgctctc tccctcctca tctctgctct 120
gctctggacc gttaactctc cagctccccc tcgctccggt cccttccgcc caaatcaccg 180
ggaccaccac gccttcttcc aagatcggcg ggccgggcacc ggccggcgat gacatccacc 240
gtcaccacaa ccgttgggtg cgggggggctc cccgtccgcc cgttgtcgac agcgaccaga 300
ggacgcccac gcagatgcCg ccgtccgagc ccaggccgcg ggagcgratg cctccaatga 360
taagtcagtg gaggtcatgc gcaagttctc cgagcagtac gcccgccgct ccaacacttt 420
cttctgcgcc gacaagacag tcaactgccg cgatcatcaag ggacttgctg atcacaggga 480
tactcttgga gctcctctat gccctttagt gcattatgat gacaaagctg cggaggtagc 540
acaaggattt tggaaattgcc catgtgtccc catgcgtgag aggaaggaaat gccactgtat 600
gctttttctt actcccgata atgactttgc tgggaaggat caggttatct ccttcgagga 660
gatcaaagag gcgacatcga agttctaagc ccttgtatgt gtcacggagt gtttacttga 720
cagctaattt tttatatgta tatgtactta agtagcatct ataagatatg ccatcaggaa 780
aattttcata aaatgtgcag taaacagcac ttcgcaaggc tgccgatcat ataagnncg 840
ttcggccttt ttattgc
```

(2) INFORMATION FOR SEQ ID NO:3925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..178  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3925:

```
Ser Arg Thr Ala Ala Ala Pro Ser Thr Ser Pro His His Leu Thr
1 5 10 15
Leu Leu Pro Pro Arg Ser Pro Arg Leu Thr Pro His Gln Leu Leu Leu
 20 25 30
Ser Pro Ser Ser Ser Leu Leu Cys Ser Gly Pro Leu Thr Leu Gln Leu
 35 40 45
```

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Pro Leu Ala Pro Phe Pro Ser Ala Gln Ile Thr Gly Thr Thr Thr Ala  
50 55 60  
Phe Phe Lys Ile Gly Gly Arg Ala Pro Ala Gly Asp Asp Ile His Arg  
65 70 75 80  
His His Asn Arg Trp Val Arg Gly Ala Pro Arg Pro Pro Val Val Asp  
85 90 95  
Ser Asp Gln Arg Thr Pro Thr Gln Met Pro Pro Ser Glu Pro Arg Pro  
100 105 110  
Arg Glu Xaa Met Pro Pro Met Ile Ser Gln Trp Arg Ser Cys Ala Ser  
115 120 125  
Ser Pro Ser Ser Thr Pro Ala Ala Pro Thr Leu Ser Ser Ala Pro Thr  
130 135 140  
Arg Gln Ser Leu Pro Ser Ser Arg Asp Leu Leu Ile Thr Gly Ile  
145 150 155 160  
Leu Leu Glu Leu Leu Tyr Ala Leu Val Gly Ile Met Met Thr Lys Leu  
165 170 175  
Arg Arg

(2) INFORMATION FOR SEQ ID NO:3926:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1578756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3926:

Met Arg Lys Phe Ser Glu Gln Tyr Ala Arg Arg Ser Asn Thr Phe Phe  
1 5 10 15  
Cys Ala Asp Lys Thr Val Thr Ala Val Val Ile Lys Gly Leu Ala Asp  
20 25 30  
His Arg Asp Thr Leu Gly Ala Pro Leu Cys Pro Cys Arg His Tyr Asp  
35 40 45  
Asp Lys Ala Ala Glu Val Ala Gln Gly Phe Trp Asn Cys Pro Cys Val  
50 55 60  
Pro Met Arg Glu Arg Lys Glu Cys His Cys Met Leu Phe Leu Thr Pro  
65 70 75 80  
Asp Asn Asp Phe Ala Gly Lys Asp Gln Val Ile Ser Phe Glu Glu Ile  
85 90 95  
Lys Glu Ala Thr Ser Lys Phe  
100

(2) INFORMATION FOR SEQ ID NO:3927:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 713 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..713

(D) OTHER INFORMATION: / Ceres Seq. ID 1578759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3927:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| acacatatata | accttctctc | ttcgccgtgc | tccgatttga | cacacctccc | aaaccctaca | 60  |
| ctcccggcgg  | cggcggcgcc | ggcgcasagc | ggcagcagca | tccgaagatg | gtgaagttcc | 120 |
| tcaagcccg   | caaggccgtt | atcctcctcc | agggccgCtt | cgccggcagg | aaggcagtta | 180 |
| tcgtgcgcgt  | gttcgaggag | ggcaccgcgc | accgccccta | tggccactgc | ctcgtcgag  | 240 |
| gcctcgccaa  | gtacccaaag | aagtgatcc  | gcaaggactc | cgccaagaag | actgcgaaga | 300 |



agtcgcgcgt caagtgttcc atcaagctcg tcaacttcac tcacctcatg cccacccgct 360  
acaccctcga cgtcgatttc aaggatgtcg ccaccggtgg gcccgacgca ctctctaccc 420  
acgacaagaa ggtcgcccgc tgcaagacgg ccaaagcgcg ccttgaggag aggttcaaga 480  
ccggcaagaa cagggtggttc ttaccaaGc tccgcttcta gatgctcggc ctcccgaata 540  
gtcctgtctt agctgtcgat ttgttgtatc ggacacactc catctctgtt ttcgtattac 600  
catgaatatt tcgtgTttta gtccctggggc tctcagagat aaatttgcta agatatgccg 660  
ttgttgtgtt acatgttttc gtgataggtc tggttaaaat tttgttctgt ttc

(2) INFORMATION FOR SEQ ID NO:3928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..137
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3928:

Met Val Lys Phe Leu Lys Pro Gly Lys Ala Val Ile Leu Leu Gln Gly  
1 5 10 15  
Arg Phe Ala Gly Arg Lys Ala Val Ile Val Arg Val Phe Glu Glu Gly  
20 25 30  
Thr Arg Asp Arg Pro Tyr Gly His Cys Leu Val Ala Gly Leu Ala Lys  
35 40 45  
Tyr Pro Lys Lys Val Ile Arg Lys Asp Ser Ala Lys Lys Thr Ala Lys  
50 55 60  
Lys Ser Arg Val Lys Cys Phe Ile Lys Leu Val Asn Phe Thr His Leu  
65 70 75 80  
Met Pro Thr Arg Tyr Thr Leu Asp Val Asp Phe Lys Asp Val Ala Thr  
85 90 95  
Gly Gly Pro Asp Ala Leu Ser Thr His Asp Lys Lys Val Ala Ala Cys  
100 105 110  
Lys Thr Ala Lys Ala Arg Leu Glu Glu Arg Phe Lys Thr Gly Lys Asn  
115 120 125  
Arg Trp Phe Phe Thr Lys Leu Arg Phe  
130 135

(2) INFORMATION FOR SEQ ID NO:3929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 889 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..889
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3929:

catgaggatg gaaactttta ccctggaact ggagctgctc atgaggtggg agttcttgat 60  
ggtcaaggat tctcagttaa tataccttgg agccgtgggtg gtgttgagga tgatgactac 120  
atctttgctt ttcagactgt ggtgcttcca atagcttcag agtttgccgc agacatcact 180  
ataatatctg caggattcga tgcagctaga ggtgaccctc tgggttggtg tgacgtcact 240  
ccaactggat actcttggat gacatccctg ctgactgggtt cctcaaattg aagattgttg 300  
gtgatacttg agggaggata caatctccgg tcgatatcct catcagctac tgaagtgtt 360  
aaggtcctac ttggggaggg tccaatcgt gttcatttg tagtttcacc atcaaaagag 420  
gccttgcgta ctgtttctca agtccctgaag attcaacaac aattttggcc agttttaggt 480  
ccaacatacg catcactaca ggcgcaGcag gggtcggttt cttccaatca tagcaatgag 540  
ctgaagaaaa ggaagcggtt aggaggagga ccagggccct tctggtggaa gatgggaagc 600  
aaaaggcttc tatacgaagc gcttattgag cctcgagcc gtccgaggaa actcaagggg 660  
tcaactgggt cagcagcgcc ttagatgtgg gcagtttgct ggccgttgat cttctagaca 720

tgaacagggt agctcgctga ccgcgtttcc tcaagcagag taggctgcgt ttacgtagaa 780  
aacctacttt tggctgggta cttgcatgat ggtagaccgt ttcagatgga gtttgacagc 840  
aaaccggttg tgtaaccat gcgtggcgta tcagccgatg tttcatgcc

(2) INFORMATION FOR SEQ ID NO:3930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..227
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3930:

His Glu Asp Gly Asn Phe Tyr Pro Gly Thr Gly Ala Ala His Glu Val  
1 5 10 15  
Gly Val Leu Asp Gly Gln Gly Phe Ser Val Asn Ile Pro Trp Ser Arg  
20 25 30  
Gly Gly Val Gly Asp Asp Asp Tyr Ile Phe Ala Phe Gln Thr Val Val  
35 40 45  
Leu Pro Ile Ala Ser Glu Phe Ala Ala Asp Ile Thr Ile Ile Ser Ala  
50 55 60  
Gly Phe Asp Ala Ala Arg Gly Asp Pro Leu Gly Cys Cys Asp Val Thr  
65 70 75 80  
Pro Thr Gly Tyr Ser Trp Met Thr Ser Leu Leu Ala Gly Ser Ser Asn  
85 90 95  
Gly Arg Leu Leu Val Ile Leu Glu Gly Gly Tyr Asn Leu Arg Ser Ile  
100 105 110  
Ser Ser Ser Ala Thr Glu Val Val Lys Val Leu Leu Gly Glu Gly Pro  
115 120 125  
Asn Arg Ala Ser Phe Val Val Ser Pro Ser Lys Glu Ala Leu Arg Thr  
130 135 140  
Val Ser Gln Val Leu Lys Ile Gln Gln Gln Phe Trp Pro Val Leu Gly  
145 150 155 160  
Pro Thr Tyr Ala Ser Leu Gln Ala Gln Gln Gly Ser Val Ser Ser Asn  
165 170 175  
His Ser Asn Glu Leu Lys Lys Arg Lys Arg Ser Gly Gly Gly Pro Gly  
180 185 190  
Pro Phe Trp Trp Lys Met Gly Ser Lys Arg Leu Leu Tyr Glu Ala Leu  
195 200 205  
Ile Glu Pro Arg Ser Arg Pro Arg Lys Leu Lys Gly Ser Thr Gly Ser  
210 215 220  
Ala Ala Pro  
225

(2) INFORMATION FOR SEQ ID NO:3931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3931:

Met Thr Ser Leu Leu Ala Gly Ser Ser Asn Gly Arg Leu Leu Val Ile  
1 5 10 15  
Leu Glu Gly Gly Tyr Asn Leu Arg Ser Ile Ser Ser Ser Ala Thr Glu  
20 25 30

Val Val Lys Val Leu Leu Gly Glu Gly Pro Asn Arg Ala Ser Phe Val  
35 40 45  
Val Ser Pro Ser Lys Glu Ala Leu Arg Thr Val Ser Gln Val Leu Lys  
50 55 60  
Ile Gln Gln Gln Phe Trp Pro Val Leu Gly Pro Thr Tyr Ala Ser Leu  
65 70 75 80  
Gln Ala Gln Gln Gly Ser Val Ser Ser Asn His Ser Asn Glu Leu Lys  
85 90 95  
Lys Arg Lys Arg Ser Gly Gly Gly Pro Gly Pro Phe Trp Trp Lys Met  
100 105 110  
Gly Ser Lys Arg Leu Leu Tyr Glu Ala Leu Ile Glu Pro Arg Ser Arg  
115 120 125  
Pro Arg Lys Leu Lys Gly Ser Thr Gly Ser Ala Ala Pro  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..810
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578782

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3932:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gatggatatt tgcagattag tctacacgag tcacgatagg aggaagactg gaagaggagg  | 60  |
| cgagcacggt tgcggtgccc accctcaccg tccactccaa aaccccaa at ccagttccgt | 120 |
| tccaatcgcc gagaagggca gcaaagggga gaaaaaaaag gaaaacgatr gmngrgccc   | 180 |
| gcggcgagaa cagcggcgcg gngcgagggc gagggcgagt tttacctgcg ctactacgtg  | 240 |
| ggtcacaaag gcaagttcgg gcacgagttc ctcgagttcg agttccgccc cgacggcaag  | 300 |
| ctccgCtacc ccaacaactc caactacaag aacgacacca tgatccgcaa ggaggtcttc  | 360 |
| gtctcgccct ccgtcctccg cgaggccagg aggatcatcc aggagtccga catcatgaag  | 420 |
| gaggacgaca gcaactggcc cgagcccgcg cgcacgcggc gccaggagct cgagatcgtc  | 480 |
| atgggcaacg agcacatttc attcaccact tccaagatcg gtcctcctcg cgatgtccag  | 540 |
| tccagcaagg acccgaggagg cctccggatc ttctactacc ttgtccagga tctgaagtgt | 600 |
| ttcgtgttct cgtcctatcaa ccttcacttc aagatcaagc caatccagtc ttgagctcca | 660 |
| tcccaagcct tcatgtagct ggtttgtgag actgcgagtg ttttgagaga gaacctttta  | 720 |
| accatgtaag atgatgttga tattgtggac gatgcgcgag atcgaccctg tgtggtgcac  | 780 |
| ttagtggaag tggaaccccc ctttgcattt                                   |     |

(2) INFORMATION FOR SEQ ID NO:3933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3933:

Met Asp Ile Cys Arg Leu Val Tyr Thr Ser His Asp Arg Arg Lys Thr  
1 5 10 15  
Gly Arg Gly Gly Glu His Val Cys Gly Ala His Pro His Arg Pro Leu  
20 25 30  
Gln Asn Pro Lys Ser Ser Ser Val Pro Ile Ala Glu Lys Gly Ser Lys  
35 40 45  
Gly Glu Lys Lys Lys Glu Asn Asp Xaa Xaa Xaa Arg Arg Arg Glu Gln  
50 55 60  
Arg Arg Xaa Ala Arg Ala Arg Ala Ser Phe Thr Cys Ala Thr Thr Trp

(2) INFORMATION FOR SEQ ID NO:3934:

(A) LENGTH: 104 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1578785

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 653 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1578786

| (X1) SEQUENCE DESCRIPTION: SEQ ID: 1 |            |             |            |             |             |     |
|--------------------------------------|------------|-------------|------------|-------------|-------------|-----|
| aagactggcg                           | aaacgcgttg | ttttcctctt  | ttcccaagc  | caaccaaac   | atctcgattc  | 60  |
| tcgactcgcg                           | gggaagtttc | gctctcrccg  | gcgtcgacgg | cctaggggtc  | gaggaacgtc  | 120 |
| cgtcggtccg                           | tccggggaag | gagcggtagg  | gaggcggaga | tgatcgaggt  | ggtgctcaac  | 180 |
| gaccgcctgg                           | ggaagaaggt | gcgggtcaag  | tgcaacgagg | acgacaccat  | cggcgacctc  | 240 |
| aagaagctgg                           | tggcggcgca | gacggggacg  | cgccccgaga | agatccgcat  | ccagaagtgg  | 300 |
| tacaacatct                           | acaaggacca | catcaccctc  | aaggactacg | aggtccacga  | cggcctgggc  | 360 |
| ctcgagctct                           | actacaactg | agcgcgcgcc  | cctctctccc | ttctgtcagg  | tgggtctgaa  | 420 |
| ttctgaagtc                           | atgggtgcaa | ttCkcttcgc  | ggtgatctct | taagctcatc  | acatatataa  | 480 |
| aagcaacctc                           | agtgggctat | gtaagacatg  | gcgtgccaaa | ctatcagtga  | ccactgacag  | 540 |
| ctttgcaata                           | cgttggtgta | tggctaacct  | gcaaaacttg | tgtactgcta  | ctcgtaactat | 600 |
| aaataacata                           | gggttttaac | cttggttggtg | gtaatggtca | tctttttctca | ttc         |     |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3937:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Trp | Arg | Asn | Ala | Leu | Phe | Ser | Ser | Phe | Pro | Gln | Gly | Asn | Gln | Thr |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Ser | Ile | Leu | Asp | Ser | Trp | Gly | Ser | Phe | Ala | Leu | Xaa | Gly | Val | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Leu | Gly | Phe | Glu | Glu | Arg | Pro | Ser | Val | Arg | Pro | Gly | Lys | Glu | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |

(D) OTHER INFORMATION: / Ceres Seq. ID 1578789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3938:

[illegible]

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 713 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..713  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1578793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3939:

```
gctagcggctc cgcaccact caccggttgc ctccaaactc atttctccc agcgccgccg 60
cgagcctctg ttccagcttc gttcatggct tccctcaccg gatccgctct ctcttttgcg 120
aggcccgctca aggcaatcag cattaagtct gtctctttCc tctgggtctaa ggaaggataa 180
tgtagccttc cgcttgccagc cagtgcacaa aagattcgct gtctgctgtc ctgctaaaaa 240
ggagactgtg gatcggggtt gtgatattgt caagaagcag cttgcacttc ctgagggcac 300
tgaggtctgt ggctcctcta agtttcaaga cctcggtgct gattcggttg acactgttga 360
gattgttatg ggccttgagg aggctttcaa gatcactgta gaggagtcga gcgcgcagtc 420
aatcgcaact gtggaagatg ctgctaactc catcgacgaa cttgttgagc gagcagcaaa 480
atcgtgttaa actcgtgggtc gtattgcgtt ggggtgctgta ccagggcatc acttgttgtt 540
ctatgcccc ttccctacta gattttcttt tctaccctgg gcctggagag atgtttctgt 600
catgactgtc attgtggatc tcgcgatatt gttatattga agcttttgtg cttgttcaag 660
aaaagaaaat gttgttgcca tatatatgtt attatattga attttttttt gtc
```

(2) INFORMATION FOR SEQ ID NO:3940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..162  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3940:

```
Leu Ala Val Arg Thr His Ser Pro Val Ala Ser Lys Leu Ile Ser Pro
1 5 10 15
Glu Arg Arg Arg Glu Pro Leu Phe Gln Leu Arg Ser Trp Leu Pro Ser
20 25 30
Pro Asp Pro Leu Ser Pro Leu Arg Gly Pro Ser Arg Gln Ser Ala Leu
35 40 45
Ser Leu Ser Leu Ser Ser Gly Leu Arg Lys Asp Asn Val Ala Phe Arg
50 55 60
Leu Gln Pro Val Pro Gln Arg Phe Ala Val Cys Cys Pro Ala Lys Lys
65 70 75 80
Glu Thr Val Asp Arg Val Cys Asp Ile Val Lys Lys Gln Leu Ala Leu
85 90 95
Pro Glu Gly Thr Glu Val Cys Gly Ser Lys Phe Gln Asp Leu Gly
100 105 110
Ala Asp Ser Leu Asp Thr Val Glu Ile Val Met Gly Leu Glu Glu Ala
115 120 125
Phe Lys Ile Thr Val Glu Glu Ser Ser Ala Gln Ser Ile Ala Thr Val
130 135 140
Glu Asp Ala Ala Asn Leu Ile Asp Glu Leu Val Ala Gly Ala Ala Lys
145 150 155 160
Ser Cys
```

(2) INFORMATION FOR SEQ ID NO:3941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(A) NAME/KEY: -  
(B) LOCATION: 1..674  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578799

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| attagctcagc | agatttgtgaa | gaaacagctg | tctccaaagc | gagaagaoga | agaaagggga | 60  |
| aatcgagaga  | tgagctacca  | gagagtccct | cccagggaac | cctaccctoc | tccaggacat | 120 |
| cctogatctc  | aGgcgcacc   | ttaccaccog | ccaccagatg | tgtaccgcgc | tccccctcgg | 180 |
| ggccatggac  | atccaccacc  | accccatggc | gtgtaccgcg | cgccgcgcga | gggtccttac | 240 |
| ccccaccacc  | agcagccttc  | acccgggtac | cagggtactt | tcaacgacca | cgagcgtcct | 300 |
| tactaccgcg  | cgccgatgg   | agagcataaa | cacaaccacc | accagggaaa | ccagggtagc | 360 |
| tcctctgggt  | tcctcaaagg  | atgtttggct | gctctctctg | ctgctgcgtg | ctggaggaat | 420 |
| gctgcggctg  | cttctgagac  | gtgagatgtc | cggaatccg  | atcgcaagtt | atcgtcgcta | 480 |
| gaattcggga  | gcaccccagt  | tattatcata | taatagtaac | tgtgcttgta | aataatctgg | 540 |
| agcagcagtg  | ttcatgagct  | cccagccccg | catttatatt | ctcataaatt | gtagtagctt | 600 |
| ctatgattta  | tcogaaaata  | aaggactcta | tatatgggat | tctaaataag | gtatttgcat | 660 |
| atttcattggg | attc        |            |            |            |            |     |

(A) LENGTH: 147 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(A) NAME/KEY: peptide  
(B) LOCATION: 1..147  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578800

[illegible]

(A) LENGTH: 124 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(A) NAME/KEY: peptide  
(B) LOCATION: 1..124  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3943:

Met Ser Tyr Gln Arg Val Pro Pro Glu Glu Pro Tyr Pro Pro Pro Gly  
1 5 10 15  
His Pro Arg Ser Gln Ala His Pro Tyr Pro Pro Pro Asp Val Tyr  
20 25 30  
Pro Pro Pro Pro Arg Gly His Gly His Pro Pro Pro Pro His Gly Val  
35 40 45  
Tyr Pro Pro Pro Pro Gln Gly Pro Tyr Pro Pro Pro Gln Gln Pro Pro  
50 55 60  
Pro Gly Tyr Gln Gly Tyr Phe Asn Asp Gln Gln Arg Pro Tyr Tyr Pro  
65 70 75 80  
Pro Pro His Gly Glu His Gln His Asn His His Gln Gly Asn Gln Gly  
85 90 95  
Ser Ser Ser Gly Phe Leu Lys Gly Cys Leu Ala Ala Leu Ser Ala Ala  
100 105 110  
Ala Cys Trp Arg Asn Ala Ala Ala Ala Ser Glu Thr  
115 120

(2) INFORMATION FOR SEQ ID NO:3944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3944:

Met Cys Thr Arg Leu Pro Leu Gly Ala Met Asp Ile His His His Pro  
1 5 10 15  
Met Ala Cys Thr Arg Arg Arg Arg Arg Val Leu Thr Pro His His Ser  
20 25 30  
Ser Leu His Arg Gly Thr Arg Ala Thr Ser Thr Thr Ser Ser Val Leu  
35 40 45  
Thr Thr Arg Arg Arg Met Glu Ser Ile Asn Thr Thr Thr Thr Arg Glu  
50 55 60  
Thr Arg Val Ala Pro Leu Gly Ser Ser Lys Asp Val Trp Leu Leu Ser  
65 70 75 80  
Leu Leu Leu Arg Ala Gly Gly Met Leu Arg Leu Leu Leu Arg Arg Glu  
85 90 95  
Met Ser Gly Asn Pro Ile Ala Ser Tyr Arg Arg  
100 105

(2) INFORMATION FOR SEQ ID NO:3945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..923
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3945:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| agaagctcct ccggtcctcc cttctctccg tagaaacatt tcccgaacggg tgtttccac | 60  |
| gccggaatgg accagccggc accataagcc caagattcgt ttgatgagtt tgtacgatac | 120 |
| tggtctaca gttaggagaa cacatttaac ctaccttcac tagcattcag taatgccttt  | 180 |
| gcctaaatca gacctggggt cataactctt tagtagagaa ccaagaagat gcaggcatct | 240 |
| agggaaggc ttttcaagga gtacaaggag gtacagcgag agaagtcagc tgaccctgat  | 300 |
| atccaattaa tatgtgatga ttctaacata ttcaagtga ctgctcttat caaGggccct  | 360 |
| tctgaaacac cttatgaagg tgggtgtgtt caacttgcac tcgcaattcc agagcagtat | 420 |



(2) INFORMATION FOR SEQ ID NO:3946:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1578818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3946:

| (X1) SEQUENCE DESCRIPTION: Big 1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|----------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met                              | Gln | Ala | Ser | Arg | Ala | Arg | Leu | Phe | Lys | Glu | Tyr | Lys | Glu | Val | Gln |  |
| 1                                |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Arg                              | Glu | Lys | Ser | Ala | Asp | Pro | Asp | Ile | Gln | Leu | Ile | Cys | Asp | Asp | Ser |  |
|                                  |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asn                              | Ile | Phe | Lys | Trp | Thr | Ala | Leu | Ile | Lys | Gly | Pro | Ser | Glu | Thr | Pro |  |
|                                  |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Tyr                              | Glu | Gly | Gly | Val | Phe | Gln | Leu | Ala | Phe | Ala | Ile | Pro | Glu | Gln | Tyr |  |
|                                  | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Pro                              | Leu | Leu | Pro | Pro | Gln | Val | Arg | Phe | Leu | Thr | Lys | Thr | Phe | His | Pro |  |
| 65                               |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Asn                              | Val | His | Phe | Lys | Thr | Gly | Glu | Ile | Cys | Leu | Asp | Ile | Leu | Lys | Glu |  |
|                                  |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Cys                              | Met | Glu | Pro | Tyr | Met | Asp | Pro | Ser | Val | Cys | Leu |     |     |     |     |  |
|                                  |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:3947:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1578819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3947:

[illegible]

(2) INFORMATION FOR SEQ ID NO:3948:

(A) LENGTH: 626 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..626
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1578834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3948:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| gatgcaacca | gaacccatag | ctgacgacac | caccgtgtgg | tgcacaaaat  | aaaaaggaga | 60  |
| gagagagaga | tggctctgtc | gtctcgccgt | atggccgccg | caccattctt  | cgtcgtcgtc | 120 |
| cttctcgctc | tcgtggcggc | agagaggacg | atgggcaggg | tgggtggtgga | agagacgctc | 180 |
| tgcttgctgc | agagccatgc | cttcaaaggc | gtgtgcctca | gcaacaccaa  | ctgcgacaac | 240 |
| gtatgcaaga | cggagaagtt | cacaggcggc | gagtgcaaga | tggacggcgt  | catgcgcaag | 300 |
| tgctactgca | agaaggtctg | ctagggcatg | accggcagca | agNCCCCag   | ccgtacggct | 360 |
| gggGtgatcc | ggttgcacac | cgtttgggca | cgcggtcatg | ttccggcttc  | tcggctttat | 420 |
| ttatttcttc | tttggtataa | taaatagact | ctgttagtca | gggtcggttt  | agtctgggtc | 480 |
| gtacgttatt | aattctctag | tgtattgtat | ttRcgcaaCG | cgcgctgtac  | ttaacgtagc | 540 |
| caggcatgta | ttcgcgttgc | gtggtcgaga | ggccaacgat | ttatcttgat  | tgtacaaaaa | 600 |
| aattatatat | atttgtgatg | gtggtc     |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:3949:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 84 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..84
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1578835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3949:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Ser | Ser | Arg | Arg | Met | Ala | Ala | Ala | Pro | Phe | Phe | Val | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Leu | Leu | Val | Leu | Val | Ala | Ala | Glu | Arg | Thr | Met | Gly | Arg | Val | Val |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Val | Glu | Glu | Thr | Leu | Cys | Leu | Ser | Gln | Ser | His | Ala | Phe | Lys | Gly | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Leu | Ser | Asn | Thr | Asn | Cys | Asp | Asn | Val | Cys | Lys | Thr | Glu | Lys | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Gly | Gly | Glu | Cys | Lys | Met | Asp | Gly | Val | Met | Arg | Lys | Cys | Tyr | Cys |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Lys | Val | Cys |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3950:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 77 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..77
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1578836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3950:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Ala | Pro | Phe | Phe | Val | Val | Val | Leu | Leu | Val | Leu | Val | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Glu | Arg | Thr | Met | Gly | Arg | Val | Val | Val | Glu | Glu | Thr | Leu | Cys | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Gln | Ser | His | Ala | Phe | Lys | Gly | Val | Cys | Leu | Ser | Asn | Thr | Asn | Cys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..232

(D) OTHER INFORMATION: / Ceres Seq. ID 1578846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3953:

Ser Gly Thr Gln Ala Pro His Ala Thr Xaa Thr Ser Thr Arg Trp Ile  
1 5 10 15  
Ala Asn Pro Gln His Val Ser Ile Ser Gly Leu Thr Ala Ala Ala Ala  
20 25 30  
Ala Leu Arg Gly Tyr Ala Arg Arg Arg Gly Leu Arg Arg His Phe Arg  
35 40 45  
Arg Gln Ala Leu Thr Arg Tyr Ser Ala Met Val Phe Leu Glu Ala Glu  
50 55 60  
Met Ser Trp Asn Val Leu Ile Ser Pro Ser Gln Leu Asp Arg Lys Xaa  
65 70 75 80  
Leu Leu Leu Arg Lys Ala Ile Ile Val Arg Leu Leu Glu Asp Val Thr  
85 90 95  
Asn Arg Arg Ala Ser Lys Glu His Gly Tyr Tyr Ile Ala Val Asn Gln  
100 105 110  
Leu Lys Ala Ile Ser Glu Gly Lys Val Arg Glu Leu Thr Gly Asp Val  
115 120 125  
Leu Phe Pro Val Ser Phe Thr Cys Ile Thr Gln Lys Pro Met Lys Gly  
130 135 140  
Glu Val Met Val Gly His Val Asp Arg Ile Leu Lys His Gly Val Phe  
145 150 155 160  
Leu Lys Ser Gly Pro Val Glu Ser Ile Phe Leu Ala Glu Lys Ser Met  
165 170 175  
Ser Asn Tyr Lys Tyr Ile Gly Gly Glu Asn Ala Met Phe Met Asn Asp  
180 185 190  
His Ser Lys Leu Glu Lys Asp Thr Ala Val Arg Phe Lys Val Leu Gly  
195 200 205  
Phe Arg Trp Met Glu Ala Asp Arg Gln Phe Gln Leu Leu Ala Thr Ile  
210 215 220  
Ala Gly Asp Phe Leu Gly Pro Leu  
225 230

(2) INFORMATION FOR SEQ ID NO:3954:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1578847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3954:

Met Val Phe Leu Glu Ala Glu Met Ser Trp Asn Val Leu Ile Ser Pro  
1 5 10 15  
Ser Gln Leu Asp Arg Lys Xaa Leu Leu Leu Arg Lys Ala Ile Ile Val  
20 25 30  
Arg Leu Leu Glu Asp Val Thr Asn Arg Arg Ala Ser Lys Glu His Gly  
35 40 45  
Tyr Tyr Ile Ala Val Asn Gln Leu Lys Ala Ile Ser Glu Gly Lys Val  
50 55 60  
Arg Glu Leu Thr Gly Asp Val Leu Phe Pro Val Ser Phe Thr Cys Ile  
65 70 75 80  
Thr Gln Lys Pro Met Lys Gly Glu Val Met Val Gly His Val Asp Arg  
85 90 95  
Ile Leu Lys His Gly Val Phe Leu Lys Ser Gly Pro Val Glu Ser Ile  
100 105 110

Phe Leu Ala Glu Lys Ser Met Ser Asn Tyr Lys Tyr Ile Gly Gly Glu  
115 120 125  
Asn Ala Met Phe Met Asn Asp His Ser Lys Leu Glu Lys Asp Thr Ala  
130 135 140  
Val Arg Phe Lys Val Leu Gly Phe Arg Trp Met Glu Ala Asp Arg Gln  
145 150 155 160  
Phe Gln Leu Leu Ala Thr Ile Ala Gly Asp Phe Leu Gly Pro Leu  
165 170 175

(2) INFORMATION FOR SEQ ID NO:3955:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..168

(D) OTHER INFORMATION: / Ceres Seq. ID 1578848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3955:

Met Ser Trp Asn Val Leu Ile Ser Pro Ser Gln Leu Asp Arg Lys Xaa  
1 5 10 15  
Leu Leu Leu Arg Lys Ala Ile Ile Val Arg Leu Leu Glu Asp Val Thr  
20 25 30  
Asn Arg Arg Ala Ser Lys Glu His Gly Tyr Tyr Ile Ala Val Asn Gln  
35 40 45  
Leu Lys Ala Ile Ser Glu Gly Lys Val Arg Glu Leu Thr Gly Asp Val  
50 55 60  
Leu Phe Pro Val Ser Phe Thr Cys Ile Thr Gln Lys Pro Met Lys Gly  
65 70 75 80  
Glu Val Met Val Gly His Val Asp Arg Ile Leu Lys His Gly Val Phe  
85 90 95  
Leu Lys Ser Gly Pro Val Glu Ser Ile Phe Leu Ala Glu Lys Ser Met  
100 105 110  
Ser Asn Tyr Lys Tyr Ile Gly Gly Glu Asn Ala Met Phe Met Asn Asp  
115 120 125  
His Ser Lys Leu Glu Lys Asp Thr Ala Val Arg Phe Lys Val Leu Gly  
130 135 140  
Phe Arg Trp Met Glu Ala Asp Arg Gln Phe Gln Leu Leu Ala Thr Ile  
145 150 155 160  
Ala Gly Asp Phe Leu Gly Pro Leu  
165

(2) INFORMATION FOR SEQ ID NO:3956:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 686 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..686

(D) OTHER INFORMATION: / Ceres Seq. ID 1578852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3956:

gctccggcct gtagccgtga cggtgacggc gtcaggctca gctcgctcgc cccccccacg 60  
aaaaccctaa tggcgtcccg cctccttcac ctccgcgcgc tcattactcc tccccccacc 120  
gtccccgcgc cttcctttctc caccgccgctc agcgcgaccc cgs gcgtctc cgcgctcgtc 180  
gacgagatct gcgggctcac cctcctcgag gcctcttccc tggccgatgc cctgcgcggc 240  
cgcctcggcg tcgaccagtt gccgccacta gctatcctca cgggcggcgg cgcaccgctc 300  
gtcggcggcg gagtaggtcc cggcgcggcc ggccgaggagg cgaaggccaa ggaggagaag 360  
atggcgttcg acgtgaagct ggagggggttc gacgccgcgc cgaaGctcaa gatcatcaag 420

gagctgaggg cgttcacgaa tctgggtctg aaggaggcca aggatctcgt ggagaaggcg 480  
ccccccgtgc tgaaggctgg agttcccaag gaggaggcgg agagtatcgc cgagaagatg 540  
cggcgctcgg cgccaagatt gttctcgagt gaacgacgag agctgtgtat gccctcgttt 600  
cttgatttgt ttctgtgttc ttgtatgaaa aaaagagaga attttggaac aaggagataa 660  
taattagtaa atttgactag agatcc

(2) INFORMATION FOR SEQ ID NO:3957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..219
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3957:

Ala Pro Ala Cys Ser Arg Asp Gly Asp Gly Val Arg Leu Ser Ser Leu  
1 5 10 15  
Ala Pro Pro Thr Lys Thr Leu Met Ala Ser Arg Leu Leu His Leu Arg  
20 25 30  
Arg Leu Ile Thr Pro Pro Pro Thr Val Pro Ala Ala Ser Phe Ser Thr  
35 40 45  
Ala Val Ser Ala Thr Pro Xaa Val Ser Ala Leu Val Asp Glu Ile Cys  
50 55 60  
Gly Leu Thr Leu Leu Glu Ala Ser Ser Leu Ala Asp Ala Leu Arg Gly  
65 70 75 80  
Arg Leu Gly Val Asp Gln Leu Pro Pro Leu Ala Ile Leu Thr Gly Gly  
85 90 95  
Gly Ala Pro Leu Val Gly Gly Gly Val Gly Pro Gly Ala Ala Gly Glu  
100 105 110  
Glu Ala Lys Ala Lys Glu Glu Lys Met Ala Phe Asp Val Lys Leu Glu  
115 120 125  
Gly Phe Asp Ala Ala Ala Lys Leu Lys Ile Ile Lys Glu Leu Arg Ala  
130 135 140  
Phe Thr Asn Leu Gly Leu Lys Glu Ala Lys Asp Leu Val Glu Lys Ala  
145 150 155 160  
Pro Ala Val Leu Lys Ala Gly Val Pro Lys Glu Glu Ala Glu Ser Ile  
165 170 175  
Ala Glu Lys Met Arg Arg Ser Ala Pro Arg Leu Phe Ser Ser Glu Arg  
180 185 190  
Arg Glu Leu Cys Met Pro Ser Phe Leu Asp Leu Phe Arg Val Ser Cys  
195 200 205  
Met Lys Lys Arg Glu Asn Phe Gly Thr Arg Arg  
210 215

(2) INFORMATION FOR SEQ ID NO:3958:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3958:

Met Ala Ser Arg Leu Leu His Leu Arg Arg Leu Ile Thr Pro Pro Pro  
1 5 10 15  
Thr Val Pro Ala Ala Ser Phe Ser Thr Ala Val Ser Ala Thr Pro Xaa  
20 25 30

Val Ser Ala Leu Val Asp Glu Ile Cys Gly Leu Thr Leu Leu Glu Ala  
35 40 45  
Ser Ser Leu Ala Asp Ala Leu Arg Gly Arg Leu Gly Val Asp Gln Leu  
50 55 60  
Pro Pro Leu Ala Ile Leu Thr Gly Gly Gly Ala Pro Leu Val Gly Gly  
65 70 75 80  
Gly Val Gly Pro Gly Ala Ala Gly Glu Glu Ala Lys Ala Lys Glu Glu  
85 90 95  
Lys Met Ala Phe Asp Val Lys Leu Glu Gly Phe Asp Ala Ala Lys  
100 105 110  
Leu Lys Ile Ile Lys Glu Leu Arg Ala Phe Thr Asn Leu Gly Leu Lys  
115 120 125  
Glu Ala Lys Asp Leu Val Glu Lys Ala Pro Ala Val Leu Lys Ala Gly  
130 135 140  
Val Pro Lys Glu Glu Ala Glu Ser Ile Ala Glu Lys Met Arg Arg Ser  
145 150 155 160  
Ala Pro Arg Leu Phe Ser Ser Glu Arg Arg Glu Leu Cys Met Pro Ser  
165 170 175  
Phe Leu Asp Leu Phe Arg Val Ser Cys Met Lys Lys Arg Glu Asn Phe  
180 185 190  
Gly Thr Arg Arg  
195

(2) INFORMATION FOR SEQ ID NO:3959:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..772
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3959:

|             |            |             |             |            |            |     |
|-------------|------------|-------------|-------------|------------|------------|-----|
| aatcaaaccc  | tcacagcgaa | ggacacaaaa  | acacaggtag  | ggttaggcga | cgcggcggcg | 60  |
| agagcrcgag  | agtaggagga | ggcgctcgcc  | atgacgggga  | aggcgaacrn | angaagcaca | 120 |
| cggcgaagga  | gatcgccgcg | aagatcgacg  | cggcgacgac  | gaaccgnrgc | ggcggaagg  | 180 |
| tcgggcaggc  | ggatcggtca | gggcaggaca  | aggrcgggca  | cgcgaaactg | cgtgcccgt  | 240 |
| ctgcccgcacc | ccggcgcccg | acatcaagtc  | catgcagatc  | caccacgagg | cgcgccatcc | 300 |
| caagctccct  | ttcgagccgg | agaagctcgt  | caacctgcac  | tcctccaccc | ccgcccgcgc | 360 |
| cgaggccacc  | acctccaagc | ccaagcccg   | ggtccgcggc  | aGcctcaaga | agtagctggc | 420 |
| tggcttgcc   | gcctgactgc | ctggggtaat  | tcccttcgat  | ttcaatccca | tccaccgacc | 480 |
| cgatctacaa  | tcaatcaaag | taccgcccgc  | cctccggctg  | cggtgtactg | ttagtctgct | 540 |
| gctgcttctt  | attgttggtt | tattgtctgat | acatgtctcg  | cgtgatagat | gtgcaactat | 600 |
| atatcagtct  | cgtcgccggc | aacactggca  | tgcttaaaca  | tgtgtcgctg | ctgctccgtg | 660 |
| atgccggcka  | ckgctgctat | tagcggtta   | gttagtgtcg  | atcggtctc  | cttgaacaat | 720 |
| ggcaggaatc  | tggtgcttgt | ttactttctt  | ctaattggcaa | gtaaagttcc | ct         |     |

(2) INFORMATION FOR SEQ ID NO:3960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3960:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Asn | Pro | His | Ser | Glu | Gly | His | Lys | Asn | Thr | Gly | Arg | Val | Arg | Arg |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

Arg Gly Gly Glu Ser Xaa Arg Val Gly Gly Gly Val Gly His Asp Gly  
20 25 30  
Glu Gly Glu Xaa Xaa Lys His Thr Ala Lys Glu Ile Ala Ala Lys Ile  
35 40 45  
Asp Ala Ala Thr Thr Asn Xaa Xaa Gly Gly Lys Val Gly Gln Ala Asp  
50 55 60  
Arg Leu Gly Gln Asp Lys Xaa Gly His Ala Asn Trp Arg Ala Arg Ser  
65 70 75 80  
Ala Ala Pro Arg Arg Pro Thr Ser Ser Pro Cys Arg Ser Thr Thr Arg  
85 90 95  
Arg Ala Ile Pro Ser Ser Leu Ser Ser Arg Arg Ser Ser Ser Thr Cys  
100 105 110  
Thr Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Ser Pro Ser  
115 120 125  
Pro Gly Ser Ala Ala Ala Ser Arg Ser Ser Trp Leu Ala Cys Leu Pro  
130 135 140  
Asp Cys Leu Gly  
145

(2) INFORMATION FOR SEQ ID NO:3961:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..825
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3961:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| actcccaagc | cccaatacac | agcacagcag | catcaacaca  | acctcagagg | agcactactg | 60  |
| cgagtcaatc | agcgaccagc | acagcaaccg | aactcaaaaag | caagagccca | agatccgagc | 120 |
| ggtaggagaa | tccggacatg | gcggcggcag | cgagggcgtc  | gtggatggtg | gcgatgagcg | 180 |
| tccggcgcgt | ggaggcgctc | aaggaccagg | caggcctctg  | ccgctggaac | tacgccggcg | 240 |
| tggtcggttg | aggagtggac | gtggaacasa | acagctcctg  | cgcgaagagc | gctgccagga | 300 |
| ggagcatgga | gagcgtcgtc | ggcgccggcg | ccgctgtggc  | ggtcgtcgtc | gtcgtccagg | 360 |
| tatatgttgg | agctggtgta | gacgaggagc | gaggcgtaga  | tgatggcgtg | ctcgtggttc | 420 |
| ggcaGccgct | caggcgggat | ggagccgtcg | gcgcggaacg  | gcacggcga  | gtaggcgagc | 480 |
| atctgggttg | ccagcccgtg | scctccgcgg | ccagcatggc  | gatgggctcg | aggcgacgca | 540 |
| cccgtggcg  | ccgggaacca | tgctgccggc | gcgaggacga  | cgacgcgcga | cgatgaggac | 600 |
| gacggggtcg | gggcgaggga | gaccaagagc | ctcatgtggt  | tgaagaggtg | ccataggccg | 660 |
| aggcctgaga | gcacgcgcgc | tgccagggtg | tggctgatga  | ttttatccgc | ggcgccgcgg | 720 |
| ggcagcatcg | tcacgcgat  | cgatgtcagt | cgtctaaact  | gttgatgctg | gcttgctgat | 780 |
| ttctttgttt | gcaatgcatg | ctcgatcggg | aaggatttat  | tctct      |            |     |

(2) INFORMATION FOR SEQ ID NO:3962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3962:

Met Ala Ala Ala Arg Ala Ser Trp Met Val Ala Met Ser Val Gly  
1 5 10 15  
Ala Val Glu Ala Leu Lys Asp Gln Ala Gly Leu Cys Arg Trp Asn Tyr  
20 25 30  
Ala Gly Val Val Gly Gly Gly Val Asp Val Glu Xaa Asn Ser Ser Cys

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35 40 45  
Ala Lys Ser Ala Ala Arg Arg Ser Met Glu Ser Val Val Gly Ala Gly  
50 55 60  
Ala Ala Trp Ala Val Val Val Val Val Gln Val Tyr Val Gly Ala Gly  
65 70 75 80  
Val Asp Glu Glu Arg Gly Val Asp Asp Gly Val Leu Val Val Arg Gln  
85 90 95  
Pro Leu Arg Arg Asp Gly Ala Val Gly Ala Glu Arg His Arg Arg Val  
100 105 110  
Gly Glu His Leu Gly Gly Gln Pro Val Xaa Pro Ala Ala Ser Met Ala  
115 120 125  
Met Gly Ser Arg Arg Arg Thr Pro Trp Arg Arg Glu Pro Cys Cys Arg  
130 135 140  
Arg Glu Asp Asp Asp Ala Arg Arg  
145 150

(2) INFORMATION FOR SEQ ID NO:3963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1578911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3963:

Met Val Ala Met Ser Val Gly Ala Val Glu Ala Leu Lys Asp Gln Ala  
1 5 10 15  
Gly Leu Cys Arg Trp Asn Tyr Ala Gly Val Val Gly Gly Gly Val Asp  
20 25 30  
Val Glu Xaa Asn Ser Ser Cys Ala Lys Ser Ala Ala Arg Arg Ser Met  
35 40 45  
Glu Ser Val Val Gly Ala Gly Ala Ala Trp Ala Val Val Val Val Val  
50 55 60  
Gln Val Tyr Val Gly Ala Gly Val Asp Glu Glu Arg Gly Val Asp Asp  
65 70 75 80  
Gly Val Leu Val Val Arg Gln Pro Leu Arg Arg Asp Gly Ala Val Gly  
85 90 95  
Ala Glu Arg His Arg Arg Val Gly Glu His Leu Gly Gly Gln Pro Val  
100 105 110  
Xaa Pro Ala Ala Ser Met Ala Met Gly Ser Arg Arg Arg Thr Pro Trp  
115 120 125  
Arg Arg Glu Pro Cys Cys Arg Arg Glu Asp Asp Asp Ala Arg Arg  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3964:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1578912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3964:

Met Ser Val Gly Ala Val Glu Ala Leu Lys Asp Gln Ala Gly Leu Cys  
1 5 10 15  
Arg Trp Asn Tyr Ala Gly Val Val Gly Gly Gly Val Asp Val Glu Xaa  
20 25 30

Asn Ser Ser Cys Ala Lys Ser Ala Ala Arg Arg Ser Met Glu Ser Val  
35 40 45  
Val Gly Ala Gly Ala Ala Trp Ala Val Val Val Val Val Gln Val Tyr  
50 55 60  
Val Gly Ala Gly Val Asp Glu Glu Arg Gly Val Asp Asp Gly Val Leu  
65 70 75 80  
Val Val Arg Gln Pro Leu Arg Arg Asp Gly Ala Val Gly Ala Glu Arg  
85 90 95  
His Arg Arg Val Gly Glu His Leu Gly Gly Gln Pro Val Xaa Pro Ala  
100 105 110  
Ala Ser Met Ala Met Gly Ser Arg Arg Arg Thr Pro Trp Arg Arg Glu  
115 120 125  
Pro Cys Arg Arg Glu Asp Asp Asp Ala Arg Arg  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 869 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..869
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3965:

|             |            |             |             |            |            |     |
|-------------|------------|-------------|-------------|------------|------------|-----|
| ctagcatttta | cgcggnvgag | ctcgagccgg  | cggcgctcgac | gggcggcggt | ggcgacgacc | 60  |
| acaacctgga  | cctgtcgctg | gggagctcgg  | cggggaacaa  | aaggggcagc | cttgacgacg | 120 |
| gctccccac   | tcagaaaacc | cagccgcccgc | cgcacgcggc  | tcccaggtaa | gcagtagcgt | 180 |
| ccacccagc   | cgccgccatg | aagcgcaacc  | cccgcgtcac  | gagctcccgc | cggaagtgcc | 240 |
| gcaagggcan  | cttcacggcc | ccgtcctccg  | tccgcgcgct  | gctcatgtcc | gcggcgctat | 300 |
| cgacggagCt  | ccgccacaag | tacaatgtgc  | gttccatccc  | gatccgcaag | gacgacgagg | 360 |
| tgcaggtcgt  | gcgcggcacc | tacaagggcc  | gtgagggcaa  | agtggtgca  | gtgtaccgcc | 420 |
| gtcgctgggt  | catccaagtt | gagcggatca  | cccgcgagaa  | ggtgaacggc | tccaccgtga | 480 |
| acgtgggcat  | ccacccttcc | aaggtcatgg  | ttacaaagct  | gaagcttgac | aaggaccgca | 540 |
| aggcgctcct  | cgaccgcaag | gcccggggcc  | gcgcgcgccg  | caaggctaag | ggcaagttta | 600 |
| ctgcccagca  | cgtcgccgcc | gctgctgggt  | gcgcgcgccg  | cactggcgcg | tctctccagg | 660 |
| agatcgacta  | ggcttcgcgg | ggatctgatg  | gtggtcctac  | cgcctattac | tccttatcgc | 720 |
| tctagttttt  | gctatcaatg | attatgtgct  | aggagtttta  | tgttacttat | aaactgcttt | 780 |
| gagcctcgat  | gggagttgaa | cttaatgtgg  | agtgtatctg  | agatatgaag | aactcattat | 840 |
| atggctaata  | tctctgtgtg | tggtctgct   |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:3966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3966:

Met Lys Arg Asn Pro Arg Val Thr Ser Ser Arg Arg Lys Cys Arg Lys  
1 5 10 15  
Gly Xaa Phe Thr Ala Pro Ser Ser Val Arg Arg Val Leu Met Ser Ala  
20 25 30  
Ala Leu Ser Thr Glu Leu Arg His Lys Tyr Asn Val Arg Ser Ile Pro  
35 40 45  
Ile Arg Lys Asp Asp Glu Val Gln Val Val Arg Gly Thr Tyr Lys Gly  
50 55 60

Arg Glu Gly Lys Val Val Gln Val Tyr Arg Arg Arg Trp Val Ile His  
65 70 75 80  
Val Glu Arg Ile Thr Arg Glu Lys Val Asn Gly Ser Thr Val Asn Val  
85 90 95  
Gly Ile His Pro Ser Lys Val Met Val Thr Lys Leu Lys Leu Asp Lys  
100 105 110  
Asp Arg Lys Ala Leu Leu Asp Arg Lys Ala Arg Gly Arg Ala Ala Asp  
115 120 125  
Lys Ala Lys Gly Lys Phe Thr Ala Asp Asp Val Ala Ala Ala Gly  
130 135 140  
Gly Ala Ala Ala Thr Gly Ala Ser Leu Gln Glu Ile Asp  
145 150 155

(2) INFORMATION FOR SEQ ID NO:3967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3967:

Met Ser Ala Ala Leu Ser Thr Glu Leu Arg His Lys Tyr Asn Val Arg  
1 5 10 15  
Ser Ile Pro Ile Arg Lys Asp Asp Glu Val Gln Val Val Arg Gly Thr  
20 25 30  
Tyr Lys Gly Arg Glu Gly Lys Val Val Gln Val Tyr Arg Arg Arg Trp  
35 40 45  
Val Ile His Val Glu Arg Ile Thr Arg Glu Lys Val Asn Gly Ser Thr  
50 55 60  
Val Asn Val Gly Ile His Pro Ser Lys Val Met Val Thr Lys Leu Lys  
65 70 75 80  
Leu Asp Lys Asp Arg Lys Ala Leu Leu Asp Arg Lys Ala Arg Gly Arg  
85 90 95  
Ala Ala Asp Lys Ala Lys Gly Lys Phe Thr Ala Asp Asp Val Ala Ala  
100 105 110  
Ala Ala Gly Gly Ala Ala Ala Thr Gly Ala Ser Leu Gln Glu Ile Asp  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..557
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3968:

agtctaataca ctattgcagt cggcttctct aatactgggc cactggtttc gctccgcact 60  
tccgccgcta tggccgcgc aaccttctcc gccgcggcc gccggtcct ctcacccgcc 120  
gcggcaggca ngnagaaaac cgagctcccc gtccctatcg cccgtmttcg ccagctcgcc 180  
cgcgctggcc gctcgacga catcgacgcg actctcgcg cctgttccc tccccacccc 240  
gtcgccgcgc tctcgccct ctccacggtg ggctccccc ancCgcgcct ccgcgctgct 300  
cggcaccatg acgtcgcca ataccgcga cctgaacgcg gtccctcggtc cactcctccg 360  
ccgcgcgcgc ctgAgccggg ctgctgcct caatcctcgc cgcgcacgac tctgtccgcg 420

gggacgccgt cacggacagc atcctcgcca agtcgctctg cctcacctcg ggcgccgact 480  
ccgcgctcca cctcctccgg aagccttcgt cgggagcgcc gccgnygctc cagctcttca 540  
caaccatcat cgactcc

(2) INFORMATION FOR SEQ ID NO:3969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..185
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3969:

Ser Leu Ile Thr Ile Ala Val Gly Phe Ser Asn Thr Gly Pro Leu Val  
1 5 10 15  
Ser Leu Arg Thr Ser Ala Ala Met Ala Ala Ala Thr Phe Ser Ala Ala  
20 25 30  
Gly Arg Arg Leu Leu Ser Thr Ala Ala Gly Xaa Xaa Lys Thr Glu  
35 40 45  
Leu Pro Val Pro Ile Ala Arg Xaa Arg Gln Leu Ala Arg Ala Gly Arg  
50 55 60  
Leu Asp Asp Ile Asp Ala Thr Leu Ala Pro Leu Phe Pro Ser His Pro  
65 70 75 80  
Val Ala Ala Leu Ser Ala Leu Ser Thr Val Gly Leu Pro Xaa Pro Arg  
85 90 95  
Leu Arg Ala Ala Arg His His Asp Val Ala Gln Tyr Arg Ala Pro Glu  
100 105 110  
Arg Gly Pro Arg Ser Thr Pro Pro Pro Pro Pro Glu Pro Gly Ser  
115 120 125  
Cys Pro Gln Ser Ser Pro Arg Met Pro Leu Ser Arg Gly Thr Pro Ser  
130 135 140  
Arg Thr Ala Ser Ser Pro Ser Arg Ser Ala Ser Pro Arg Ala Pro Thr  
145 150 155 160  
Pro Arg Ser Thr Ser Ser Gly Ser Leu Arg Arg Glu Arg Arg Xaa Xaa  
165 170 175  
Ser Ser Ser Ser Gln Pro Ser Ser Thr  
180 185

(2) INFORMATION FOR SEQ ID NO:3970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3970:

Met Ala Ala Ala Thr Phe Ser Ala Ala Gly Arg Arg Leu Leu Ser Thr  
1 5 10 15  
Ala Ala Ala Gly Xaa Xaa Lys Thr Glu Leu Pro Val Pro Ile Ala Arg  
20 25 30  
Xaa Arg Gln Leu Ala Arg Ala Gly Arg Leu Asp Asp Ile Asp Ala Thr  
35 40 45  
Leu Ala Pro Leu Phe Pro Ser His Pro Val Ala Ala Leu Ser Ala Leu  
50 55 60  
Ser Thr Val Gly Leu Pro Xaa Pro Arg Leu Arg Ala Ala Arg His His  
65 70 75 80

Asp Val Ala Gln Tyr Arg Ala Pro Glu Arg Gly Pro Arg Ser Thr Pro  
85 90 95  
Pro Pro Pro Pro Pro Glu Pro Gly Ser Cys Pro Gln Ser Ser Pro Arg  
100 105 110  
Met Pro Leu Ser Arg Gly Thr Pro Ser Arg Thr Ala Ser Ser Pro Ser  
115 120 125  
Arg Ser Ala Ser Pro Arg Ala Pro Thr Pro Arg Ser Thr Ser Ser Gly  
130 135 140  
Ser Leu Arg Arg Glu Arg Arg Xaa Xaa Ser Ser Ser Ser Gln Pro Ser  
145 150 155 160  
Ser Thr

(2) INFORMATION FOR SEQ ID NO:3971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..752
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3971:

|             |             |             |            |             |            |     |
|-------------|-------------|-------------|------------|-------------|------------|-----|
| gactagggtt  | ctgtccacct  | tccaggtcct  | tcgaacttcc | acgcattcct  | actactcctg | 60  |
| gctcccgcca  | cctaacgccg  | ccactcctga  | cttcgccatc | cggcgatcac  | cagagcccta | 120 |
| gctccggcgt  | ctctagcgat  | ccccaaaaAc  | ccactccgcc | gcattttctgc | cgacttggcc | 180 |
| ggatttggtcg | cttattgaaN  | atgGCTacgc  | cacttatagc | aggacttgca  | gttgcagcaa | 240 |
| ctgctcttgc  | tggtcgatat  | ggtgtccaag  | catggcaagc | ttataaggca  | aggcctatag | 300 |
| ttccaaggat  | gcgcaaattc  | tatgaagggtg | gctttcaacc | tacaatgaac  | cgaaggraag | 360 |
| ctgcattaat  | ccttggtgtc  | agggaaactg  | ccaacgcaga | gaaggtaaaa  | gaggcgcaca | 420 |
| agaggggttat | ggtgcgccaac | catccagatg  | ctggtggaag | tcattacctt  | gcgtcaaaga | 480 |
| ttaatgaggc  | gaaggatgtg  | ttgtcaggga  | aaacaaaagg | aggtgggtcg  | gccttctgat | 540 |
| tgtagaatta  | agaatgcact  | ctctgctaga  | aggataattt | tgtgcctcta  | aatttagcat | 600 |
| taKTTgaaga  | tactgtagac  | cgcagtttag  | tcttggtatt | gcggaaattt  | ctggacaaag | 660 |
| catattgggc  | cttctgtgaa  | gtagttatcc  | agtgcctatt | aatactcagc  | tgtgcctgct | 720 |
| tctataaaga  | tatacatgat  | gaaggttaca  | tc         |             |            |     |

(2) INFORMATION FOR SEQ ID NO:3972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3972:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Leu Gly Phe Cys Pro Pro Ser Arg Ser Phe Glu Leu Pro Arg Ile Pro |  |
| 1 5 10 15                                                       |  |
| Thr Thr Pro Gly Ser Arg Asp Leu Thr Pro Pro Leu Leu Thr Ser Pro |  |
| 20 25 30                                                        |  |
| Ser Gly Asp His Gln Ser Pro Ser Ser Gly Val Ser Ser Asp Pro Gln |  |
| 35 40 45                                                        |  |
| Lys Pro Thr Pro Pro His Phe Cys Arg Leu Gly Arg Ile Gly Arg Leu |  |
| 50 55 60                                                        |  |
| Leu Xaa Met Ala Thr Pro Leu Ile Ala Gly Leu Ala Val Ala Ala Thr |  |
| 65 70 75 80                                                     |  |
| Ala Leu Ala Gly Arg Tyr Gly Val Gln Ala Trp Gln Ala Tyr Lys Ala |  |
| 85 90 95                                                        |  |

Arg Pro Ile Val Pro Arg Met Arg Lys Phe Tyr Glu Gly Gly Phe Gln  
100 105 110  
Pro Thr Met Asn Arg Arg Xaa Ala Ala Leu Ile Leu Gly Val Arg Glu  
115 120 125  
Thr Ala Asn Ala Glu Lys Val Lys Glu Ala His Lys Arg Val Met Val  
130 135 140  
Ala Asn His Pro Asp Ala Gly Gly Ser His Tyr Leu Ala Ser Lys Ile  
145 150 155 160  
Asn Glu Ala Lys Asp Val Leu Ser Gly Lys Thr Lys Gly Gly Gly Ser  
165 170 175  
Ala Phe

(2) INFORMATION FOR SEQ ID NO:3973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3973:

Met Ala Thr Pro Leu Ile Ala Gly Leu Ala Val Ala Ala Thr Ala Leu  
1 5 10 15  
Ala Gly Arg Tyr Gly Val Gln Ala Trp Gln Ala Tyr Lys Ala Arg Pro  
20 25 30  
Ile Val Pro Arg Met Arg Lys Phe Tyr Glu Gly Gly Phe Gln Pro Thr  
35 40 45  
Met Asn Arg Arg Xaa Ala Ala Leu Ile Leu Gly Val Arg Glu Thr Ala  
50 55 60  
Asn Ala Glu Lys Val Lys Glu Ala His Lys Arg Val Met Val Ala Asn  
65 70 75 80  
His Pro Asp Ala Gly Gly Ser His Tyr Leu Ala Ser Lys Ile Asn Glu  
85 90 95  
Ala Lys Asp Val Leu Ser Gly Lys Thr Lys Gly Gly Gly Ser Ala Phe  
100 105 110

(2) INFORMATION FOR SEQ ID NO:3974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..848
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3974:

aaaaagataa agttaggctc ggcaccgggg gctcatccgc aagcctgtgg acgcgagtga 60  
gtgaacacca gccgtattgt cccgaccccg accgatcctc gcctgctgca gccatggcga 120  
cctccgcggc gctctctacc gccgccaatc ccacccagct ctgccgggcc cgcgcttcgc 180  
tgggcaagcc ggtgaagggg cttggcctga gcatggggcc cgagcgcgcc cagcggagca 240  
ttgtgtgccg ggcggcgagc agcatctccg ccgaccgcgt ccccgacatg gagaagcgga 300  
agctgatgaa cctcctcctc ctcggcgcca tctcgttgcc caccgtcggc atggtcgtcc 360  
cctacggcgc cttcttcgtc cctgccggct ccgggaacgc cggcggCggg acctacgcga 420  
aggacaagct gggcaacgac atcacggtgg aggcgtggct caacacgcac ggtcccaacg 480  
accgcacgct cgcgcagggg ctcaagggtg accccacgta cctggtggtg gagcaggaca 540

(2) INFORMATION FOR SEQ ID NO:3975:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(A) NAM

(B) LOCATION: 1..246

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:3975:

Asp Lys Val Arg Leu Gly Thr Gly Gly Ser Se

(2) INFORMATION FOR SEQ ID NO:3976:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..209

(D) OTHER INFORMATION: / Ceres Seq. ID 1579006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3976:

Met Ala Thr Ser Ala Ala Leu Ser Thr Ala Ala Asn Pro Thr Gln Leu  
1 5 10 15  
Cys Arg Ser Arg Ala Ser Leu Gly Lys Pro Val Lys Gly Leu Gly Leu  
20 25 30  
Ser Met Gly Arg Glu Arg Ala Gln Arg Ser Ile Val Cys Gln Ala Ala  
35 40 45  
Ser Ser Ile Ser Ala Asp Arg Val Pro Asp Met Glu Lys Arg Lys Leu  
50 55 60  
Met Asn Leu Leu Leu Leu Gly Ala Ile Ser Leu Pro Thr Val Gly Met  
65 70 75 80  
Val Val Pro Tyr Gly Ala Phe Phe Val Pro Ala Gly Ser Gly Asn Ala  
85 90 95  
Gly Gly Gly Thr Tyr Ala Lys Asp Lys Leu Gly Asn Asp Ile Thr Val  
100 105 110  
Glu Ala Trp Leu Asn Thr His Gly Pro Asn Asp Arg Thr Leu Ala Gln  
115 120 125  
Gly Leu Lys Gly Asp Pro Thr Tyr Leu Val Val Glu Gln Asp Lys Thr  
130 135 140  
Leu Ala Thr Tyr Gly Ile Asn Ala Val Cys Thr His Leu Gly Cys Val  
145 150 155 160  
Val Pro Trp Asn Gly Ala Glu Asn Lys Phe Ile Cys Pro Cys His Gly  
165 170 175  
Ser Gln Tyr Asn Asn Gln Gly Lys Val Val Ala Gly Pro Phe Glu Ser  
180 185 190  
Met Lys Val Lys His Gly Arg Ser Lys Arg Val Trp Lys Asp Cys Arg  
195 200 205  
Cys

(2) INFORMATION FOR SEQ ID NO:3977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3977:

Met Gly Arg Glu Arg Ala Gln Arg Ser Ile Val Cys Gln Ala Ala Ser  
1 5 10 15  
Ser Ile Ser Ala Asp Arg Val Pro Asp Met Glu Lys Arg Lys Leu Met  
20 25 30  
Asn Leu Leu Leu Leu Gly Ala Ile Ser Leu Pro Thr Val Gly Met Val  
35 40 45  
Val Pro Tyr Gly Ala Phe Phe Val Pro Ala Gly Ser Gly Asn Ala Gly  
50 55 60  
Gly Gly Thr Tyr Ala Lys Asp Lys Leu Gly Asn Asp Ile Thr Val Glu  
65 70 75 80  
Ala Trp Leu Asn Thr His Gly Pro Asn Asp Arg Thr Leu Ala Gln Gly  
85 90 95  
Leu Lys Gly Asp Pro Thr Tyr Leu Val Val Glu Gln Asp Lys Thr Leu  
100 105 110  
Ala Thr Tyr Gly Ile Asn Ala Val Cys Thr His Leu Gly Cys Val Val  
115 120 125  
Pro Trp Asn Gly Ala Glu Asn Lys Phe Ile Cys Pro Cys His Gly Ser  
130 135 140  
Gln Tyr Asn Asn Gln Gly Lys Val Val Ala Gly Pro Phe Glu Ser Met  
145 150 155 160



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Cys | Ser | Lys | Ser | Gln | Ile | Leu | Ala | Xaa | Gly | Arg | Arg | Pro | Arg | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ser | Leu | Asp | Asp | Leu | Pro | Ser | Ala | Glu | Ala | Ser | Lys | Thr | Arg | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Cys | Lys | Leu | Pro | Ser | Ala | Ala | Ala | Met | Ala | Gly | Ala | Glu | Val | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Asp | Lys | Tyr | Arg | Ser | Phe | Ile | His | Gly | Glu | Gly | Glu | Arg | Asp | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Trp | Arg | Tyr | Gly | Ala | Pro | Pro | Asn | Tyr | Asp | Val | Val | Asn | Lys | Leu |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Phe | Glu | Glu | Glu | Arg | Thr | Gln | Val | Trp | Pro | Glu | Gly | Ser | Leu | Glu | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Val | Gln | Arg | Leu | Leu | Lys | Ser | Trp | Glu | Met | Glu | Leu | Val | His | Xaa |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Arg | Pro | Glu | Asp | Gln | Lys | Thr | Val | Asn | Ser | Glu | Lys | Tyr | Ser | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

Ser Thr Asn Gly Met Xaa Ala Xaa Thr Arg Ala Glu Val Met Ala Ile  
130 135 140  
Gly Gly Tyr Asn Asn Phe Leu Arg Thr Lys Leu Pro Pro Glu His Arg  
145 150 155 160  
Ile Tyr Asp Pro Asp Ser Glu Thr Val Glu Ser Ala Met Ala Thr Phe  
165 170 175  
Thr Thr Ala Phe Pro Arg Gly Phe Ala Ile Glu Val Leu Asp Val Tyr  
180 185 190  
Ser Gly Pro Pro Arg Ile Ala Phe Lys Phe Arg His Trp Gly Tyr Met  
195 200 205  
Glu Gly Pro Ser Arg Ala Thr Arg Arg Thr Ala Ser Gly Ser Ser Ser  
210 215 220  
Ser Ala Ser Ala Ser Ser Met Leu Thr Lys Thr  
225 230 235

(2) INFORMATION FOR SEQ ID NO:3980:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..194
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3980:

Met Ala Gly Ala Glu Val Gly Glu Asp Lys Tyr Arg Ser Phe Ile His  
1 5 10 15  
Gly Glu Gly Glu Arg Asp Thr Val Trp Arg Tyr Gly Ala Pro Pro Asn  
20 25 30  
Tyr Asp Val Val Asn Lys Leu Phe Glu Glu Glu Arg Thr Gln Val Trp  
35 40 45  
Pro Glu Gly Ser Leu Glu Glu Lys Val Gln Arg Leu Leu Lys Ser Trp  
50 55 60  
Glu Met Glu Leu Val His Xaa Val Arg Pro Glu Asp Gln Lys Thr Val  
65 70 75 80  
Asn Ser Glu Lys Tyr Ser Ala Ser Thr Asn Gly Met Xaa Ala Xaa Thr  
85 90 95  
Arg Ala Glu Val Met Ala Ile Gly Gly Tyr Asn Asn Phe Leu Arg Thr  
100 105 110  
Lys Leu Pro Pro Glu His Arg Ile Tyr Asp Pro Asp Ser Glu Thr Val  
115 120 125  
Glu Ser Ala Met Ala Thr Phe Thr Thr Ala Phe Pro Arg Gly Phe Ala  
130 135 140  
Ile Glu Val Leu Asp Val Tyr Ser Gly Pro Pro Arg Ile Ala Phe Lys  
145 150 155 160  
Phe Arg His Trp Gly Tyr Met Glu Gly Pro Ser Arg Ala Thr Arg Arg  
165 170 175  
Thr Ala Ser Gly Ser Ser Ser Ser Ala Ser Ala Ser Ser Met Leu Thr  
180 185 190  
Lys Thr

(2) INFORMATION FOR SEQ ID NO:3981:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

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(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1579015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3981:

Met Glu Leu Val His Xaa Val Arg Pro Glu Asp Gln Lys Thr Val Asn  
1 5 10 15  
Ser Glu Lys Tyr Ser Ala Ser Thr Asn Gly Met Xaa Ala Xaa Thr Arg  
20 25 30  
Ala Glu Val Met Ala Ile Gly Gly Tyr Asn Asn Phe Leu Arg Thr Lys  
35 40 45  
Leu Pro Pro Glu His Arg Ile Tyr Asp Pro Asp Ser Glu Thr Val Glu  
50 55 60  
Ser Ala Met Ala Thr Phe Thr Thr Ala Phe Pro Arg Gly Phe Ala Ile  
65 70 75 80  
Glu Val Leu Asp Val Tyr Ser Gly Pro Pro Arg Ile Ala Phe Lys Phe  
85 90 95  
Arg His Trp Gly Tyr Met Glu Gly Pro Ser Arg Ala Thr Arg Arg Thr  
100 105 110  
Ala Ser Gly Ser Ser Ser Ser Ala Ser Ser Ser Met Leu Thr Lys  
115 120 125  
Thr

(2) INFORMATION FOR SEQ ID NO:3982:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1205 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1205

(D) OTHER INFORMATION: / Ceres Seq. ID 1579027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3982:

ctctctgtcg catttcccgt cctgtccttc ccttaccgg cggtttaaac cctagttctc 60  
actcccatcg ccgcttcagc tccgccgcag cagatggagt tctgggggtct cgagggtcaag 120  
cctgggttcca ctgttaagtg tgagcctgga tatggctttg tgctgcacct ttcccaggct 180  
gctcttgggg aatcgaagaa gagtataat gccttgatgt atgtcaaaat tgatgatcag 240  
aaacttgcca ttggaaccct ctctgttgac aagaaccac acatacaatt tgatctgggt 300  
ttogataaag agtttgagct gtgcacaca tcaaaaacta ccagcgtctt cttcactggc 360  
tacaaggttg agcagccatt cgaggaagat gagccttctt ccacaatgga tcttgattct 420  
gaagatgaag acgaggagcg ggatgttcca gtatgcaagg aaaatggcaa agctgatggg 480  
aagaacaga aaagtcaaga aaaggcagtt gctgcacctt caaatcaag tccggattcc 540  
aagaagagca asgaTgacTg atgattctga tgaggaygag ackgaygatt ctgatgaggg 600  
tttatcttct gaagaaggcg atgatgattc aagtgatgaa gatgatacca gtgacgatga 660  
ggaggaagac actccaactc ctaagaagcc tgaggtaggc aagaagagag ctgctgaaag 720  
ttcctgtctg aaaactctc tatctgataa gaaagcaaag gttgccacac cgtcatctca 780  
gaagacaggt ggcaagaagg gcgcgcgct ccatgtggca actccacacc cagcaaaagg 840  
caagaccatt gtaaacaatg acaaatcggt caagtctcca aaatctgcgc caaatctgg 900  
tgtcccttgc aaatcgtgca gcaagtcatt catcagtcag acggcacttc aggctcactc 960  
gaaggcgaag catgggggca agtgagtcgc aggtccaata gagtcaacaa caaatgcaaa 1020  
acatgggaga ggagggtgaa cgagagtcctc gaaagagtg cggtggaagt aggcctaacc 1080  
ttattttgtt tagagacggg ctatgcgttc gatgtagcaa aacaaggctg tggtttgtgt 1140  
acttcaatat ttgggttgtg tgtttcgaat ttttttttga acgtgtctcg gattgttgtg 1200  
gtgcc

(2) INFORMATION FOR SEQ ID NO:3983:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1579028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3983:

Met Glu Phe Trp Gly Leu Glu Val Lys Pro Gly Ser Thr Val Lys Cys  
1 5 10 15  
Glu Pro Gly Tyr Gly Phe Val Leu His Leu Ser Gln Ala Ala Leu Gly  
20 25 30  
Glu Ser Lys Lys Ser Asp Asn Ala Leu Met Tyr Val Lys Ile Asp Asp  
35 40 45  
Gln Lys Leu Ala Ile Gly Thr Leu Ser Val Asp Lys Asn Pro His Ile  
50 55 60  
Gln Phe Asp Leu Val Phe Asp Lys Glu Phe Glu Leu Ser His Thr Ser  
65 70 75 80  
Lys Thr Thr Ser Val Phe Phe Thr Gly Tyr Lys Val Glu Gln Pro Phe  
85 90 95  
Glu Glu Asp Glu Pro Ser Ser Thr Met Asp Leu Asp Ser Glu Asp Glu  
100 105 110  
Asp Glu Glu Arg Asp Val Pro Val Lys Glu Asn Gly Lys Ala Asp  
115 120 125  
Gly Lys Lys Gln Lys Ser Gln Glu Lys Ala Val Ala Ala Pro Ser Lys  
130 135 140  
Ser Ser Pro Asp Ser Lys Lys Ser Xaa Asp Asp  
145 150 155

(2) INFORMATION FOR SEQ ID NO:3984:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1579029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3984:

Met Ala Lys Leu Met Gly Arg Asn Arg Lys Val Lys Lys Arg Gln Leu  
1 5 10 15  
Leu His Leu Gln Asn Gln Val Arg Ile Pro Arg Arg Ala Xaa Met Thr  
20 25 30  
Asp Asp Ser Asp Glu Xaa Glu Xaa Xaa Asp Ser Asp Glu Gly Leu Ser  
35 40 45  
Ser Glu Glu Gly Asp Asp Asp Ser Ser Asp Glu Asp Asp Thr Ser Asp  
50 55 60  
Asp Glu Glu Glu Asp Thr Pro Thr Pro Lys Lys Pro Glu Val Gly Lys  
65 70 75 80  
Lys Arg Ala Ala Glu Ser Ser Val Leu Lys Thr Pro Leu Ser Asp Lys  
85 90 95  
Lys Ala Lys Val Ala Thr Pro Ser Ser Gln Lys Thr Gly Gly Lys Lys  
100 105 110  
Gly Ala Ala Val His Val Ala Thr Pro His Pro Ala Lys Gly Lys Thr  
115 120 125  
Ile Val Asn Asn Asp Lys Ser Val Lys Ser Pro Lys Ser Ala Pro Lys  
130 135 140  
Ser Gly Val Pro Cys Lys Ser Cys Ser Lys Ser Phe Ile Ser Gln Thr  
145 150 155 160  
Ala Leu Gln Ala His Ser Lys Ala Lys His Gly Gly Lys  
165 170

(2) INFORMATION FOR SEQ ID NO:3985:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..169  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579030  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3985:

Met Gly Arg Asn Arg Lys Val Lys Lys Arg Gln Leu Leu His Leu Gln  
1 5 10 15  
Asn Gln Val Arg Ile Pro Arg Arg Ala Xaa Met Thr Asp Asp Ser Asp  
20 25 30  
Glu Xaa Glu Xaa Xaa Asp Ser Asp Glu Gly Leu Ser Ser Glu Glu Gly  
35 40 45  
Asp Asp Asp Ser Ser Asp Glu Asp Asp Thr Ser Asp Asp Glu Glu Glu  
50 55 60  
Asp Thr Pro Thr Pro Lys Lys Pro Glu Val Gly Lys Lys Arg Ala Ala  
65 70 75 80  
Glu Ser Ser Val Leu Lys Thr Pro Leu Ser Asp Lys Lys Ala Lys Val  
85 90 95  
Ala Thr Pro Ser Ser Gln Lys Thr Gly Gly Lys Lys Gly Ala Ala Val  
100 105 110  
His Val Ala Thr Pro His Pro Ala Lys Gly Lys Thr Ile Val Asn Asn  
115 120 125  
Asp Lys Ser Val Lys Ser Pro Lys Ser Ala Pro Lys Ser Gly Val Pro  
130 135 140  
Cys Lys Ser Cys Ser Lys Ser Phe Ile Ser Gln Thr Ala Leu Gln Ala  
145 150 155 160  
His Ser Lys Ala Lys His Gly Gly Lys  
165

(2) INFORMATION FOR SEQ ID NO:3986:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 835 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..835  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3986:

attgtwcccg ccgctcttccc caattcgccg ccagscaggg taaaaaaaaa aaagaggaag 60  
aaaacctcct gcaattccca ttccatcgat ccagctccgg tccaagccaa agctttcttc 120  
gccccaaacc ttgttcaact ccaatgtcgg acttcttctt cgggagcccg ttccgcccgc 180  
tcttccacgc gcgccccttc catgcgctcg actggctctc cgccgcggcg gcggccatgg 240  
actgggtgga gaccccgctc tcccaogtgc tgcgcgtcaa cgtgccggga ctcggaagg 300  
acgacgtcaa ggtccaggtc gacgagggca aagtgtcac catcaggggc gccccgccc 360  
cggccaagga gaaggggaag gaggacgagg aggaggggac ggtgtggcac gtggcggaGc 420  
gcggcaagcc ggagttcgcg cgggccgtgg cgctgccgga gaacgtgcgc gtggacggga 480  
tcagggccgg cttggagaac ggggttctca ccgtcgttgt gccaaggaa gtcgccccg 540  
cccggcccaa gccaggtcc atcgccgtct ccagcaagct ctgatgagtc tgaggcgatg 600  
agtggcagag tgtacgggtc agtgtaaac catgccgcaa atggcgggta cgtctgaatt 660  
ctggtcgtgt gtgtgtccgt gtcacctaga aaacgcgcac cccgtgtaaa ttgcgataca 720  
atttcatgca agtaatccga gtgagtgaag atggctgcta gccaaaaacg gtcgattctg 780  
aatatgcagt ttgcaataaa ctaaattaaa aggaaaaggc atgtttgaat atgtg

(2) INFORMATION FOR SEQ ID NO:3987:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 218 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..218  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579043  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3987:

Ile Xaa Pro Ala Val Phe Pro Asn Ser Pro Pro Xaa Arg Val Lys Lys  
1 5 10 15  
Lys Lys Arg Lys Lys Thr Ser Cys Asn Ser His Ser Ile Asp Pro Ala  
20 25 30  
Pro Val Gln Ala Lys Ala Phe Phe Ala Pro Asn Leu Val Gln Leu Gln  
35 40 45  
Cys Arg Thr Ser Ser Ser Gly Ala Arg Ser Ala Ala Ser Ser Thr Arg  
50 55 60  
Ala Pro Ser Met Pro Ser Thr Gly Pro Pro Pro Arg Arg Arg Pro Trp  
65 70 75 80  
Thr Gly Trp Arg Pro Arg Pro Pro Thr Cys Cys Ala Ser Thr Cys Arg  
85 90 95  
Asp Ser Ala Arg Thr Thr Ser Arg Ser Arg Ser Thr Arg Ala Lys Cys  
100 105 110  
Ser Pro Ser Gly Ala Pro Arg Pro Arg Pro Arg Arg Arg Gly Arg Arg  
115 120 125  
Thr Arg Arg Arg Gly Arg Cys Gly Thr Trp Arg Ser Ala Ala Ser Arg  
130 135 140  
Ser Ser Arg Gly Pro Trp Arg Cys Arg Arg Thr Cys Ala Trp Thr Gly  
145 150 155 160  
Ser Gly Pro Ala Trp Arg Thr Gly Phe Ser Pro Ser Leu Cys Pro Arg  
165 170 175  
Lys Ser Pro Arg Pro Gly Pro Ser Pro Gly Pro Ser Pro Ser Pro Ala  
180 185 190  
Ser Ser Asp Glu Ser Glu Ala Met Ser Gly Arg Val Tyr Gly Ala Val  
195 200 205  
Leu Asn His Ala Ala Asn Gly Gly Tyr Val  
210 215

(2) INFORMATION FOR SEQ ID NO:3988:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 193 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..193  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579044  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3988:

Cys Xaa Arg Arg Leu Pro Gln Phe Ala Ala Xaa Gln Gly Lys Lys Lys  
1 5 10 15  
Lys Glu Glu Glu Asn Leu Leu Gln Phe Pro Phe His Arg Ser Ser Ser  
20 25 30  
Gly Pro Ser Gln Ser Phe Leu Arg Pro Lys Pro Cys Ser Thr Pro Met  
35 40 45  
Ser Asp Phe Phe Phe Gly Ser Pro Phe Arg Arg Leu Phe His Ala Arg  
50 55 60  
Pro Phe His Ala Val Asp Trp Ser Ser Ala Ala Ala Ala Met Asp  
65 70 75 80  
Trp Val Glu Thr Pro Ser Ser His Val Leu Arg Val Asn Val Pro Gly  
85 90 95

(2) INFORMATION FOR SEQ ID NO:3989:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1579045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3989:

(2) INFORMATION FOR SEQ ID NO:3990:

(A) LENGTH: 827 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..827

(D) OTHER INFORMATION: / Ceres Seq. ID 1579078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3990:

(X1) SEQUENCE DESCRIPTION: SEQ ID:101

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gtcgccccc  | cgtagtcgc  | ccaaactacg | caaccgatat | attccccagc | acccccgttc | 60  |
| cagccgtcca | accgagacac | cgcgtgcgaa | ccaagcagac | cccagcagaa | gaagcgaagt | 120 |
| cgctgcggga | gcaggaggaa | gagcgagcag | caagatgtcg | tggcaggcgt | acgtcgatga | 180 |

ccacctgctg tgcgacatcg aaggccagca cctcagcgcc gccgccatcg tcggccacga 240  
Cggcagcgtc tgggcacagt ccgagaactt ccccagagta aagcctgagg aggttgctgg 300  
gatgataaag gactttgatg aacctggaac tcttgaccca actggtcttt ttgttgaggg 360  
tacgAagtac atggtgatcc aaggtgaacc tggagttgtc atccgaggaa agaagggcac 420  
tggaggcatt actatcaaga aaactggcat gtccttgatt atcggtatct atgatgagcc 480  
aatgactcca gggcaatgca atatggtggg ggagaggctc gccgattacc tgatcgaaca 540  
Ggggcttcta agtttgtcat aatgctatth tggtcattgg gcacttaagt ttgcacctca 600  
tttggttctg taatatgtgg gcttgtgcat gtgcttggcg tattgcatgc agtgaataat 660  
ttatcttcgc gttgggttgg tgacaatgtt gggaacggat ttgaattggg gtttatgctt 720  
gccatctcct catatctcga actcagctgc tgtttcactg agtaatgtac atttcocctgg 780  
taatggtact tgtgcactct gctgctttat gaaaagagt gcatttt

(2) INFORMATION FOR SEQ ID NO:3991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579079

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3991:

Arg Pro His Ala Ser Arg Pro Asn Tyr Ala Thr Asp Ile Phe Pro Ser  
1 5 10 15  
Thr Pro Val Pro Ala Val Gln Pro Arg His Arg Val Arg Thr Lys Gln  
20 25 30  
Thr Pro Ala Glu Glu Ala Lys Ser Ser Pro Glu Gln Glu Glu Arg  
35 40 45  
Ala Ala Arg Cys Arg Gly Arg Arg Thr Ser Met Thr Thr Cys Cys Ala  
50 55 60  
Thr Ser Lys Ala Ser Thr Ser Ala Pro Pro Pro Ser Ser Ala Thr Thr  
65 70 75 80  
Ala Ala Ser Gly His Ser Pro Arg Thr Ser Pro Ser  
85 90

(2) INFORMATION FOR SEQ ID NO:3992:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3992:

Met Ser Trp Gln Ala Tyr Val Asp Asp His Leu Leu Cys Asp Ile Glu  
1 5 10 15  
Gly Gln His Leu Ser Ala Ala Ala Ile Val Gly His Asp Gly Ser Val  
20 25 30  
Trp Ala Gln Ser Glu Asn Phe Pro Glu Leu Lys Pro Glu Glu Val Ala  
35 40 45  
Gly Met Ile Lys Asp Phe Asp Glu Pro Gly Thr Leu Ala Pro Thr Gly  
50 55 60  
Leu Phe Val Gly Gly Thr Lys Tyr Met Val Ile Gln Gly Glu Pro Gly  
65 70 75 80  
Val Val Ile Arg Gly Lys Lys Gly Thr Gly Gly Ile Thr Ile Lys Lys  
85 90 95  
Thr Gly Met Ser Leu Ile Ile Gly Ile Tyr Asp Glu Pro Met Thr Pro  
100 105 110



Gly Gln Cys Asn Met Val Val Glu Arg Leu Gly Asp Tyr Leu Ile Glu  
115 120 125  
Gln Gly Leu Leu Ser Leu Ser  
130 135

(2) INFORMATION FOR SEQ ID NO:3993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3993:

Met Ile Lys Asp Phe Asp Glu Pro Gly Thr Leu Ala Pro Thr Gly Leu  
1 5 10 15  
Phe Val Gly Gly Thr Lys Tyr Met Val Ile Gln Gly Glu Pro Gly Val  
20 25 30  
Val Ile Arg Gly Lys Lys Gly Thr Gly Ile Thr Ile Lys Lys Thr  
35 40 45  
Gly Met Ser Leu Ile Ile Gly Ile Tyr Asp Glu Pro Met Thr Pro Gly  
50 55 60  
Gln Cys Asn Met Val Val Glu Arg Leu Gly Asp Tyr Leu Ile Glu Gln  
65 70 75 80  
Gly Leu Leu Ser Leu Ser  
85

(2) INFORMATION FOR SEQ ID NO:3994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..833
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3994:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| atcctagaag gaaacaggaa caggcagctc tgaaagactg aaactcacgg ccatggccat   | 60  |
| cctgggcgcc ctcaggctcg cgccgtctcc acccgccctc gccggcgctg cgccaccggc   | 120 |
| tacgtcgccg tctgcggctg tacgtcctc cgtgcacttc cacctcgcca atgccggcgc    | 180 |
| cgccgcgctc ngtcgccgcc tcgtcctctg ccgccgaccc cgccgtggct ttcattggag   | 240 |
| gaggaccgta cgggaagcag gtgacgcggg ggcaggacct caccggcaag gacttcagcg   | 300 |
| gccagacact catcaagcag gacttcaaga cgtctatact gaggcaggcg aacttcaaag   | 360 |
| gcgcgaacct gctcggcgcg aGcttcttcg atgcagacct cacaagcgct gatctctctg   | 420 |
| acgtgatct tagaggcgct gatttgctgc tggcgaattt aacgaaggca aacttatcaa    | 480 |
| atgccaactt agaaggggca cttgccactg ggaacacttc tttcaaaggt gccgacataa   | 540 |
| ctggggcaga ttttaccgat gtgccgctgc gagatgatca acgggagtac ctctgcaaaa   | 600 |
| tcgctgacgg agtaaattca accactggaa acccaacaaa ggagactctg ttctgcagct   | 660 |
| gatcgacgga aggacctggg acttggtgact tattcaacgt cttgataaac ttgcattctgc | 720 |
| tgctgtaagc acgtgaggaa tgtaaattga gttatagagg gttcctagaa ataataactg   | 780 |
| gtaattacgt gtaaatcaac caacaataaa agtgtgtgct gccctttgaa tgt          |     |

(2) INFORMATION FOR SEQ ID NO:3995:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(A) NAME/KEY: peptide  
(B) LOCATION: 1..119  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579083

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(A) NAME/KEY: peptide  
(B) LOCATION: 1..163  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579084

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 871 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..871

(D) OTHER INFORMATION: / Ceres Seq. ID 1579106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3997:

```
atcgatcgag cttggttgct cggcagcagc tagcaatggc cgccaagggg ggtgatgagc 60
tgaagctgct gggcgtgtgg aacagcccgt acgtcaacag ggtccagatc gtgctcaacc 120
tcaagggcct cagctacgag tacgtggagg aggacctcct cagcaagagc gagctcctcc 180
tcaagtccaa cccgggtgcac aagaaagtgc ccggtgctcat ccacgccggc aagccggctg 240
ccgagtcgca ggccatcatt cagtacctcg acgaggcttt ccccgccggc acgttcccgt 300
cggtcctccc agccgacccc tacgcacgtg ccaactgccg cttctggggc gccttcgctg 360
acgacaaggt cgggtctcca tggcacacgg tcctgttcgc gcgggaccac gggaagaagg 420
cggacgccgc gtcgcggatc gtcgcggcgc tggagacgct ggagggcgcg ttcaaggact 480
gtcgcggcgg gagggactac ttcggcggcg gcgCcatcgg cttcgtggac gtggctcctg 540
gcagctacct gggctgggtt aaggtgttcg agaagatggt cggcgctcagg gtcctggacg 600
tgggcaggac gccgctcctc gccgcgtggg gggagcggtt cggcgccggc gaagcggcca 660
aggacgtcct gccggatgac gttgacaagg tgctcgagtt ccttcagaag ttccctggact 720
aggtgcgcgc cagcgccacc atgtgctccg gtgtccaact cccaatgttt gtttgctttg 780
gtcattttcg gtgcgctggt aatggccctc agatgtttgc cagttgattt tatagaatta 840
agagctaatt tggtaatcac atttttttc g
```

(2) INFORMATION FOR SEQ ID NO:3998:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1579107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3998:

```
Arg Ser Ser Leu Val Ala Arg Gln Gln Leu Ala Met Ala Ala Lys Gly
1 5 10 15
Gly Asp Glu Leu Lys Leu Leu Gly Val Trp Asn Ser Pro Tyr Val Asn
20 25 30
Arg Val Gln Ile Val Leu Asn Leu Lys Gly Leu Ser Tyr Glu Tyr Val
35 40 45
Glu Glu Asp Leu Leu Ser Lys Ser Glu Leu Leu Leu Lys Ser Asn Pro
50 55 60
Val His Lys Lys Val Pro Val Leu Ile His Ala Gly Lys Pro Val Ala
65 70 75 80
Glu Ser Gln Ala Ile Ile Gln Tyr Leu Asp Glu Ala Phe Pro Gly Gly
85 90 95
Thr Phe Pro Ser Val Leu Pro Ala Asp Pro Tyr Ala Arg Ala Thr Ala
100 105 110
Arg Phe Trp Ala Ala Phe Val Asp Asp Lys Val Gly Ser Pro Trp His
115 120 125
Thr Val Leu Phe Ala Arg Asp His Gly Lys Lys Ala Asp Ala Ala Ser
130 135 140
Arg Ile Val Ala Ala Leu Glu Thr Leu Glu Gly Ala Phe Lys Asp Cys
145 150 155 160
Ser Gly Gly Arg Asp Tyr Phe Gly Gly Gly Ala Ile Gly Phe Val Asp
165 170 175
Val Val Leu Gly Ser Tyr Leu Gly Trp Phe Lys Val Phe Glu Lys Met
180 185 190
Val Gly Val Arg Val Leu Asp Val Ala Arg Thr Pro Leu Leu Ala Ala
195 200 205
Trp Gly Glu Arg Phe Ala Ala Glu Ala Ala Lys Asp Val Leu Pro
210 215 220
```

(2) INFORMATION FOR SEQ ID NO:3999:

(D) TOPOLOGY: linear

(D) OTHER INFORMATION: / Ceres Seq. ID 1579108

Lys Phe Leu Asp  
225

(D) TOPOLOGY: linear

(D) OTHER INFORMATION: / Ceres Seq. ID 1579116

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| acttctctcc | tttttacagc | cgcgcgcgc  | gcattcccagc | ctccatcacc  | gtttccgtct | 60  |
| cgttgccatg | ggtaaggtgc | acggatcggt | ggcgcgcgc   | gggaaggtcc  | gcgggcagac | 120 |
| ccccaaagtg | gcgaaGcagg | acaagaagaa | gaagccccc   | ggccgcgcgc  | acaagaggat | 180 |
| gcagtacaac | cgcgcgtctg | tcaccgcgct | cgtcggttc   | ggcgaagaagc | gcgggcccac | 240 |
| ctctctcgag | aagtaggcgc | cgtcgcgctc | gtaccggttc  | ctcatccttc  | ctgctctcgg | 300 |

tatgcttatg ctcttgatgg tactagtttc gttgttcgca agcagaggaa gaaccttctg 360  
tagattcggg tttgttgctc atgtgctcag atgggaactt gagattgtat gaatttgaga 420  
tatgggtgata tgagctgatg atttttatta tgctt

(2) INFORMATION FOR SEQ ID NO:4001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4001:

Leu Pro Pro Phe Leu Gln Pro Pro Pro Pro His Pro Ser Leu His His  
1 5 10 15  
Arg Phe Arg Leu Val Ala Met Gly Lys Val His Gly Ser Leu Ala Arg  
20 25 30  
Ala Gly Lys Val Arg Gly Gln Thr Pro Lys Val Ala Lys Gln Asp Lys  
35 40 45  
Lys Lys Lys Pro Arg Gly Arg Ala His Lys Arg Met Gln Tyr Asn Arg  
50 55 60  
Arg Phe Val Thr Ala Val Val Gly Phe Gly Lys Lys Arg Gly Pro Asn  
65 70 75 80  
Ser Ser Glu Lys

(2) INFORMATION FOR SEQ ID NO:4002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4002:

Phe Leu Pro Ser Tyr Ser Arg Arg Arg Arg Ile Pro Ala Ser Ile Thr  
1 5 10 15  
Val Ser Val Ser Leu Pro Trp Val Arg Cys Thr Asp Arg Trp Arg Ala  
20 25 30  
Pro Gly Arg Ser Ala Gly Arg Pro Arg Trp Arg Ser Arg Thr Arg  
35 40 45  
Arg Arg Ser Pro Ala Ala Ala Arg Thr Arg Gly Cys Ser Thr Thr Ala  
50 55 60  
Ala Ser Ser Pro Pro Ser Ser Ala Ser Ala Arg Ser Ala Gly Pro Thr  
65 70 75 80  
Pro Pro Arg Ser Arg Arg Arg Ser Ala Arg Thr Gly Ser Ser Ser Phe  
85 90 95  
Leu Leu Ser Val Cys Leu Cys Ser  
100

(2) INFORMATION FOR SEQ ID NO:4003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(2) INFORMATION FOR SEQ ID NO:4006:

(B) LOCATION: 1..1051

(D) OTHER INFORMATION: / Ceres Seq. ID 1579182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4008:

|             |            |            |             |            |            |      |
|-------------|------------|------------|-------------|------------|------------|------|
| aatccaacga  | actgaccaca | actacctaag | ctaaaagcta  | accaccgtac | ccccggccat | 60   |
| ggcgctcgcg  | cccacctccg | ctgccgtgct | caagaccccg  | ttcctcgggg | ccaggcgcg  | 120  |
| gctcgccaag  | cccgcgcctc | gccgcgcgct | cgatcatgcc  | gccgcggccg | ccgccaagaa | 180  |
| gtcgtggatc  | ccggccatca | agagcgacgc | cgagatcgct  | aaccgcacct | ggctcgacgg | 240  |
| ctcgctcccc  | ggcgacttcg | ggttcgaccc | gctggggctg  | ggcaaggacc | cgcggttcct | 300  |
| caagtgtgtac | cgggaggcgg | astgatccac | gggcggtggg  | cgatggcggc | cggtgtgggc | 360  |
| atcttcgtgg  | ggcaggcgtg | gagcggcatc | ccgtgggttcg | argccggcgc | ggacccgagc | 420  |
| gccatcgcg   | ccttctCctt | cgggtcgctg | ctgggcacgc  | agctgctgct | gatgggggtg | 480  |
| gtggagtcga  | agcggtggtg | ggacttcctt | aaccgcgact  | cccaggccgt | ggagtgggcc | 540  |
| acgccgtggt  | cgcgcaccgc | tgagaacttc | gccaacttca  | ccggcgagca | gggctacccg | 600  |
| ggcggcaagt  | tcttcgaccc | gctcggcctc | gccggcaccc  | tcaaggacgc | cgtctacatc | 660  |
| cccgcgctcg  | acaagctcga | gcggctcaag | ctggccgaga  | tcaagcacgc | ccgcatcgcc | 720  |
| atgcttgcca  | tgctcgctt  | ctacttcgag | gccgggcagg  | gcaagacgcc | gctcggcgcg | 780  |
| ctcggcctat  | gatttgcatg | ctgccggcga | ccgagtcagt  | tctcgattgc | gcgggggtgg | 840  |
| tgagctccta  | gggacgtacg | gctgcagcgg | atcagacgcc  | ttgcctcgca | gattggaggc | 900  |
| gaaagaagag  | cgtagcagca | atctactgtc | tgtgttggtg  | gtttagcgtg | cgtgaaccag | 960  |
| atgggggtgtt | cctctctgtt | ttttctttct | ttcttttctg  | tgtatgtatg | taccatgtaa | 1020 |
| tgtatagtat  | ggatcgattt | tcattgcatt | g           |            |            |      |

(2) INFORMATION FOR SEQ ID NO:4009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1579183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4009:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Ala | Pro | Thr | Ser | Ala | Ala | Val | Leu | Lys | Thr | Pro | Phe | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ala | Arg | Arg | Ala | Leu | Ala | Lys | Pro | Ala | Pro | Arg | Arg | Ala | Leu | Val |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Ile | Ala | Ala | Ala | Ala | Ala | Ala | Lys | Lys | Ser | Trp | Ile | Pro | Ala | Ile | Lys |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Ser | Asp | Ala | Glu | Ile | Val | Asn | Pro | Pro | Trp | Leu | Asp | Gly | Ser | Leu | Pro |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Gly | Asp | Phe | Gly | Phe | Asp | Pro | Leu | Gly | Leu | Gly | Lys | Asp | Pro | Ala | Phe |
|     |     |     |     |     |     |     | 70  |     |     | 75  |     |     |     |     | 80  |
| Leu | Lys | Trp | Tyr | Arg | Glu | Ala | Xaa |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     | 85  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:4010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1579184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4010:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Val | Leu | Gly | Ile | Phe | Val | Gly | Gln | Ala | Trp | Ser | Gly | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Trp | Phe | Xaa | Ala | Gly | Ala | Asp | Pro | Ser | Ala | Ile | Ala | Pro | Phe | Ser |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Phe | Gly | Ser | Leu | Leu | Gly | Thr | Gln | Leu | Leu | Leu | Met | Gly | Trp | Val | Glu |



35 40 45  
Ser Lys Arg Trp Val Asp Phe Phe Asn Pro Asp Ser Gln Ala Val Glu  
50 55 60  
Trp Ala Thr Pro Trp Ser Arg Thr Ala Glu Asn Phe Ala Asn Phe Thr  
65 70 75 80  
Gly Glu Gln Gly Tyr Pro Gly Gly Lys Phe Phe Asp Pro Leu Gly Leu  
85 90 95  
Ala Gly Thr Val Lys Asp Gly Val Tyr Ile Pro Asp Val Asp Lys Leu  
100 105 110  
Glu Arg Leu Lys Leu Ala Glu Ile Lys His Ala Arg Ile Ala Met Leu  
115 120 125  
Ala Met Leu Ala Phe Tyr Phe Glu Ala Gly Gln Gly Lys Thr Pro Leu  
130 135 140  
Gly Ala Leu Gly Leu  
145

(2) INFORMATION FOR SEQ ID NO:4011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1579185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4011:

Met Gly Trp Val Glu Ser Lys Arg Trp Val Asp Phe Phe Asn Pro Asp  
1 5 10 15  
Ser Gln Ala Val Glu Trp Ala Thr Pro Trp Ser Arg Thr Ala Glu Asn  
20 25 30  
Phe Ala Asn Phe Thr Gly Glu Gln Gly Tyr Pro Gly Gly Lys Phe Phe  
35 40 45  
Asp Pro Leu Gly Leu Ala Gly Thr Val Lys Asp Gly Val Tyr Ile Pro  
50 55 60  
Asp Val Asp Lys Leu Glu Arg Leu Lys Leu Ala Glu Ile Lys His Ala  
65 70 75 80  
Arg Ile Ala Met Leu Ala Met Leu Ala Phe Tyr Phe Glu Ala Gly Gln  
85 90 95  
Gly Lys Thr Pro Leu Gly Ala Leu Gly Leu  
100 105

(2) INFORMATION FOR SEQ ID NO:4012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..760

(D) OTHER INFORMATION: / Ceres Seq. ID 1579249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4012:

atgaggaggc aagtrcgacg gagccaata aaaagaacaa gaaaaagaag gcacatgata 60  
taagcagaag tgaagtcag gcaggaactg gacttggtga gtcagatagc aaggaaccac 120  
tccaaacacg gacgtttgcc aatggtatga tgattcagga gttagagatg ggcaaacctg 180  
atggtaaaaa ggccagccgt gggaagaagg tttctgttag atatattggc aagctaaaga 240  
atggcactat tttcgactcc aacgtcagtg gaagaccttt tgagtttaga ctaggtgttg 300  
ggcaggttat cagtggctgg gacgttggcg tcaatggtat gcgggttggg gacaaaagga 360  
gactcaccat tccaccttcc atggggtatg ggagcaaaaag agtggggcag ataccacaga 420  
actcaactct catcttcgat gtggagctgg tgaacgtaaa atgaagtgaag aagatccacg 480

agaaaactgcg gcagttttcac aaatttttGct acgcatcatt ttccttgggc aatgctgttt 540  
cgtaggcata ggggcatgtt aagtggattc atctctgtcg ctatcatact ttcgaactga 600  
gtttcagaag gaaaaaaact gtggactgtt gccatctggg ataattcctg ggctgcagca 660  
ttcgccatcc ttctcccggt tccttcaggg tcattttgac attcttgtga taccctcaga 720  
accttttgaa ctgatgaaat ggtaaggtg gagtacgtgc

(2) INFORMATION FOR SEQ ID NO:4013:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1579250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4013:

Glu Glu Ala Ser Xaa Gln Glu Ala Asn Lys Lys Asn Lys Lys Lys Lys  
1 5 10 15  
Ala His Asp Ile Ser Arg Ser Glu Ser Gln Ala Gly Thr Gly Leu Gly  
20 25 30  
Glu Ser Asp Ser Lys Glu Pro Leu Gln Thr Arg Thr Phe Ala Asn Gly  
35 40 45  
Met Met Ile Gln Glu Leu Glu Met Gly Lys Pro Asp Gly Lys Lys Ala  
50 55 60  
Ser Arg Gly Lys Lys Val Ser Val Arg Tyr Ile Gly Lys Leu Lys Asn  
65 70 75 80  
Gly Thr Ile Phe Asp Ser Asn Val Ser Gly Arg Pro Phe Glu Phe Arg  
85 90 95  
Leu Gly Val Gly Gln Val Ile Ser Gly Trp Asp Val Gly Val Asn Gly  
100 105 110  
Met Arg Val Gly Asp Lys Arg Arg Leu Thr Ile Pro Pro Ser Met Gly  
115 120 125  
Tyr Gly Ser Lys Arg Val Gly Gln Ile Pro Gln Asn Ser Thr Leu Ile  
130 135 140  
Phe Asp Val Glu Leu Val Asn Val Lys  
145 150

(2) INFORMATION FOR SEQ ID NO:4014:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1579251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4014:

Met Met Ile Gln Glu Leu Glu Met Gly Lys Pro Asp Gly Lys Lys Ala  
1 5 10 15  
Ser Arg Gly Lys Lys Val Ser Val Arg Tyr Ile Gly Lys Leu Lys Asn  
20 25 30  
Gly Thr Ile Phe Asp Ser Asn Val Ser Gly Arg Pro Phe Glu Phe Arg  
35 40 45  
Leu Gly Val Gly Gln Val Ile Ser Gly Trp Asp Val Gly Val Asn Gly  
50 55 60  
Met Arg Val Gly Asp Lys Arg Arg Leu Thr Ile Pro Pro Ser Met Gly  
65 70 75 80  
Tyr Gly Ser Lys Arg Val Gly Gln Ile Pro Gln Asn Ser Thr Leu Ile  
85 90 95

(2) INFORMATION FOR SEQ ID NO:4015:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..104  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4015:

[illegible]

(2) INFORMATION FOR SEQ ID NO:4016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..525  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4016:

| (X1) SEQUENCE DELETION |            |             |            |            | Score      |     |
|------------------------|------------|-------------|------------|------------|------------|-----|
| acacggaatcg            | aaaacgaatt | acccNtcgGt  | gccctccctc | tcggcggcgg | cggcgaagt  | 60  |
| cccttcatc              | tccggcgcg  | caaattggcag | gcggcagggt | tgcacatgct | accctcaagg | 120 |
| gccccagcgt             | ggtgaaggag | atcttcattg  | gactgacct  | gggtctgac  | gctggaggta | 180 |
| tgtggaagat             | gcaccactgg | aacgagcaga  | ggaaaactag | atcctctac  | gacatgcttg | 240 |
| acaagggcc              | gatcagcgtc | gtcgtcgagg  | accaggacga | ccagaagcaa | gagcagccgc | 300 |
| cgtgcccgc              | cgtatgaatc | aaacccgatt  | ccttgcttgt | actagctgct | actgctgtta | 360 |
| tgtgcgcaa              | taaagtctgt | tgtgcgtgtg  | cagtcagtac | tactgctctg | ctgctactat | 420 |
| cctagtcccta            | gtatatagtg | atattataca  | gtcctctctg | tgaatttga  | atcgactcga | 480 |
| aaatcaaac              | ccaccaatat | gagcttggtta | atatttgtcc | tcccg      |            |     |

(2) INFORMATION FOR SEQ ID NO:4017:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..72  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4017:

(2) INFORMATION FOR SEQ ID NO:4018:

(A) LENGTH: 104 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1579258

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1579259

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Gly | Arg | Val | Ala | His | Ala | Thr | Leu | Lys | Gly | Pro | Ser | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Lys | Glu | Ile | Phe | Ile | Gly | Leu | Thr | Leu | Gly | Leu | Ile | Ala | Gly | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Trp | Lys | Met | His | His | Trp | Asn | Glu | Gln | Arg | Lys | Thr | Arg | Ser | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Asp | Met | Leu | Asp | Lys | Gly | Gln | Ile | Ser | Val | Val | Val | Glu | Asp | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Asp | Gln | Lys | Gln | Glu | Gln | Pro | Pro | Leu | Pro | Pro | Val |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 906 base pairs

| Variable                       | Mean | Standard deviation | Minimum | Maximum |
|--------------------------------|------|--------------------|---------|---------|
| Age                            | 34.5 | 10.5               | 20      | 55      |
| Gender                         | 0.5  | 0.5                | 0       | 1       |
| Marital status                 | 0.5  | 0.5                | 0       | 1       |
| Education                      | 12.5 | 1.5                | 10      | 15      |
| Income                         | 15.5 | 5.5                | 10      | 25      |
| Occupation                     | 1.5  | 1.5                | 0       | 3       |
| Health status                  | 1.5  | 1.5                | 0       | 3       |
| Life satisfaction              | 4.5  | 1.5                | 1       | 7       |
| Subjective well-being          | 5.5  | 1.5                | 1       | 7       |
| Life expectancy                | 75.5 | 5.5                | 60      | 90      |
| Quality of life                | 6.5  | 1.5                | 1       | 10      |
| Health-related quality of life | 5.5  | 1.5                | 1       | 10      |
| Physical health                | 5.5  | 1.5                | 1       | 10      |
| Mental health                  | 5.5  | 1.5                | 1       | 10      |
| Social health                  | 5.5  | 1.5                | 1       | 10      |
| Environmental health           | 5.5  | 1.5                | 1       | 10      |
| Overall health                 | 5.5  | 1.5                | 1       | 10      |
| Life satisfaction              | 4.5  | 1.5                | 1       | 7       |
| Subjective well-being          | 5.5  | 1.5                | 1       | 7       |
| Life expectancy                | 75.5 | 5.5                | 60      | 90      |
| Quality of life                | 6.5  | 1.5                | 1       | 10      |
| Health-related quality of life | 5.5  | 1.5                | 1       | 10      |
| Physical health                | 5.5  | 1.5                | 1       | 10      |
| Mental health                  | 5.5  | 1.5                | 1       | 10      |
| Social health                  | 5.5  | 1.5                | 1       | 10      |
| Environmental health           | 5.5  | 1.5                | 1       | 10      |
| Overall health                 | 5.5  | 1.5                | 1       | 10      |

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..906  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579263  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4020:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| attatctatt | tatctcgtag  | tatctcttct | taacagaacc | cctataaatt | ccctacgac  | 60  |
| gaccccttgg | ctccacctat  | cacttttctt | tccgatcaga | tcctctcagt | tatcatggcg | 120 |
| ggcggcgctt | tcaccgagaa  | gggcaagcaa | tatccgggga | agatgacggg | gttcgtcttc | 180 |
| ctgcctgcc  | tcgtcgcttc  | ctccggcggc | ctcatcttcg | gatacgacat | tggcatctca | 240 |
| ggcggcggtg | cgtccatgga  | ccggttcttg | aagcgcttct | tcccgtcggt | gtacgccaa  | 300 |
| gagcaggagg | tgggtggagac | caaccagtag | tgcaagttcg | acagcgtgct | gCtgacgctc | 360 |
| ttcacctctt | cgctctacct  | cgcgcgcttc | gtcgctctcc | tcttcgccgg | ctacatcacc | 420 |
| aagaggtgog | gocgcaggGt  | gtccatgctc | ggcggcgggc | cCatcttctt | cgtcggcgcc | 480 |
| gtcctcaacg | gcctcgccca  | gaacgtggcc | atgctcatca | tcggcaggat | ctttctcggc | 540 |
| attggcgctg | gattcagcaa  | tcagccggat | gcatggatct | gcgtcgcgat | ttatttttgg | 600 |
| aaccgtttct | ctgatcggtt  | ggccttttta | gcgggcaact | gaaacttgct | gccaaagtgc | 660 |
| aacagagacc | aaacttccct  | gcactgtaga | gtatgctgca | tgtgttgtgt | gcagccgcac | 720 |
| ctggaagagc | atgcactgcc  | agaagctcct | agatttattt | ntcacttacg | ttttttcagt | 780 |
| gctagccagt | atttcacatt  | tctacttacg | gttatttttg | aaccgtcatc | acaaatgggt | 840 |
| ttcttaagtc | aactgtcaat  | aaaaatagca | tttttatttg | cggttttctt | tatgaaaccc | 900 |
| aagtgg     |             |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:4021:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 175 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..175  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579264  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4021:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Gly | Phe | Thr | Glu | Lys | Gly | Lys | Gln | Tyr | Pro | Gly | Lys |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Met | Thr | Val | Phe | Val | Phe | Leu | Ala | Cys | Leu | Val | Ala | Ser | Ser | Gly |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  | Gly |
| Leu | Ile | Phe | Gly | Tyr | Asp | Ile | Gly | Ile | Ser | Gly | Gly | Val | Thr | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  | Met |
| Asp | Pro | Phe | Leu | Lys | Arg | Phe | Phe | Pro | Ser | Val | Tyr | Ala | Lys | Gln |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Glu | Val | Val | Glu | Thr | Asn | Gln | Tyr | Cys | Lys | Phe | Asp | Ser | Val | Leu |
|     |     |     |     |     |     |     | 70  |     |     |     |     |     |     | 80  |
| Thr | Leu | Phe | Thr | Ser | Ser | Leu | Tyr | Leu | Ala | Ala | Leu | Val | Ala | Ser |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 95  |
| Phe | Ala | Gly | Tyr | Ile | Thr | Lys | Arg | Cys | Gly | Arg | Arg | Val | Ser | Met |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 110 |
| Gly | Gly | Gly | Ala | Ile | Phe | Leu | Val | Gly | Ala | Val | Leu | Asn | Gly | Leu |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 125 |
| Gln | Asn | Val | Ala | Met | Leu | Ile | Gly | Arg | Ile | Phe | Leu | Gly | Ile | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 140 |
| Val | Gly | Phe | Ser | Asn | Gln | Pro | Asp | Ala | Trp | Ile | Cys | Val | Ala | Ile |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 160 |
| Phe | Trp | Asn | Arg | Phe | Ser | Asp | Arg | Leu | Ala | Phe | Leu | Ala | Gly | Asn |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 175 |

(2) INFORMATION FOR SEQ ID NO:4022:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..159  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579265  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4022:

Met Thr Val Phe Val Phe Leu Ala Cys Leu Val Ala Ser Ser Gly Gly  
1 5 10 15  
Leu Ile Phe Gly Tyr Asp Ile Gly Ile Ser Gly Gly Val Thr Ser Met  
20 25 30  
Asp Pro Phe Leu Lys Arg Phe Phe Pro Ser Val Tyr Ala Lys Glu Gln  
35 40 45  
Glu Val Val Glu Thr Asn Gln Tyr Cys Lys Phe Asp Ser Val Leu Leu  
50 55 60  
Thr Leu Phe Thr Ser Ser Leu Tyr Leu Ala Ala Leu Val Ala Ser Leu  
65 70 75 80  
Phe Ala Gly Tyr Ile Thr Lys Arg Cys Gly Arg Arg Val Ser Met Leu  
85 90 95  
Gly Gly Gly Ala Ile Phe Leu Val Gly Ala Val Leu Asn Gly Leu Ala  
100 105 110  
Gln Asn Val Ala Met Leu Ile Ile Gly Arg Ile Phe Leu Gly Ile Gly  
115 120 125  
Val Gly Phe Ser Asn Gln Pro Asp Ala Trp Ile Cys Val Ala Ile Tyr  
130 135 140  
Phe Trp Asn Arg Phe Ser Asp Arg Leu Ala Phe Leu Ala Gly Asn  
145 150 155

(2) INFORMATION FOR SEQ ID NO:4023:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 128 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..128  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579266  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4023:

Met Asp Pro Phe Leu Lys Arg Phe Phe Pro Ser Val Tyr Ala Lys Glu  
1 5 10 15  
Gln Glu Val Val Glu Thr Asn Gln Tyr Cys Lys Phe Asp Ser Val Leu  
20 25 30  
Leu Thr Leu Phe Thr Ser Ser Leu Tyr Leu Ala Ala Leu Val Ala Ser  
35 40 45  
Leu Phe Ala Gly Tyr Ile Thr Lys Arg Cys Gly Arg Arg Val Ser Met  
50 55 60  
Leu Gly Gly Gly Ala Ile Phe Leu Val Gly Ala Val Leu Asn Gly Leu  
65 70 75 80  
Ala Gln Asn Val Ala Met Leu Ile Ile Gly Arg Ile Phe Leu Gly Ile  
85 90 95  
Gly Val Gly Phe Ser Asn Gln Pro Asp Ala Trp Ile Cys Val Ala Ile  
100 105 110  
Tyr Phe Trp Asn Arg Phe Ser Asp Arg Leu Ala Phe Leu Ala Gly Asn  
115 120 125

(2) INFORMATION FOR SEQ ID NO:4024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..783
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4024:

|             |            |             |            |            |             |     |
|-------------|------------|-------------|------------|------------|-------------|-----|
| atgtgtgtgt  | cccaacagct | gagtggcatg  | gacatggacc | aaaggcttca | gtgcatgttt  | 60  |
| aagagagttcc | gggagacctt | cgacgctgcg  | acagaaggca | tcaagacaaa | ctactatggc  | 120 |
| ataaagcatg  | tgatcgaagc | cttgcctgct  | ctgcttcaag | cttcctccga | tgggaggatc  | 180 |
| gttaacgtct  | cctctgagtt | cggcctgcta  | aggctgatca | acaacgagga | gctaaggcag  | 240 |
| gagctaaacg  | acgtggagan | gctcaccgar  | gagargctgg | acgargtgct | ggccgcgtac  | 300 |
| ctgaragact  | tgcagcccvr | cnargtkggg  | gcrcgcgggt | kgccggtgga | cttctcgccc  | 360 |
| tacaargtgg  | ccaaggtggc | catgaacgcg  | tacacgagga | tcctagcgag | gaggcaccs   | 420 |
| gggstgcgcg  | tcaactgcgc | gcaccccgcc  | tacgtgagca | ccgacatgac | cgtccacacc  | 480 |
| gggcytytca  | cgcccgagca | aggcgcgccc  | aacgtcgtga | aggtggcgct | gatgccggag  | 540 |
| ggcgcccgca  | ccggcgcgta | cttcgcgttg  | ggagaggagg | cgtcctttgt | gtgacgaaag  | 600 |
| caccgtcgtc  | gttaagttcg | tcgttggttcg | ccaactccct | gtcagtcgat | ttctaaatcg  | 660 |
| acgtacaatg  | aaatacatca | tcgctgcaaa  | ctcacaatg  | aaaacagtta | agggaaacctt | 720 |
| ttgtagcaaa  | aaaaaaagtg | gacagaataa  | tgaataatca | tgtcaaatat | cgcttgagta  | 780 |
| tct         |            |             |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:4025:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4025:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Val | Ser | Gln | Leu | Ser | Gly | Met | Asp | Met | Asp | Gln | Arg | Leu |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gln | Cys | Met | Phe | Lys | Arg | Val | Arg | Glu | Thr | Tyr | Asp | Ala | Ala | Thr |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ile | Lys | Thr | Asn | Tyr | Tyr | Gly | Ile | Lys | His | Val | Ile | Glu | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Leu | Pro | Leu | Leu | Gln | Ala | Ser | Ser | Asp | Gly | Arg | Ile | Val | Asn | Val |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Ser | Glu | Phe | Gly | Leu | Leu | Arg | Leu | Ile | Asn | Asn | Glu | Glu | Leu | Arg |
|     |     |     |     |     |     |     | 70  |     |     |     | 75  |     |     | 80  |
| Glu | Leu | Asn | Asp | Val | Glu | Xaa | Leu | Thr | Xaa | Glu | Xaa | Leu | Asp | Xaa |
|     |     |     |     |     |     |     | 85  |     |     |     | 90  |     |     | 95  |
| Leu | Ala | Ala | Tyr | Leu | Xaa | Asp | Phe | Asp | Ala | Xaa | Xaa | Xaa | Gly | Xaa |
|     |     |     |     |     |     |     | 100 |     |     |     | 105 |     |     | 110 |
| Gly | Xaa | Pro | Val | Asp | Phe | Ser | Ala | Tyr | Xaa | Val | Ala | Lys | Val | Ala |
|     |     |     |     |     |     |     | 115 |     |     |     | 120 |     |     | 125 |
| Asn | Ala | Tyr | Thr | Arg | Ile | Leu | Ala | Arg | Arg | His | Xaa | Gly | Xaa | Arg |
|     |     |     |     |     |     |     | 130 |     |     |     | 135 |     |     | 140 |
| Asn | Cys | Ala | His | Pro | Gly | Tyr | Val | Ser | Thr | Asp | Met | Thr | Val | His |
|     |     |     |     |     |     |     | 145 |     |     |     | 150 |     |     | 155 |
| Gly | Xaa | Xaa | Thr | Pro | Glu | Gln | Gly | Ala | Ala | Asn | Val | Val | Lys | Val |
|     |     |     |     |     |     |     | 165 |     |     |     | 170 |     |     | 175 |
| Leu | Met | Pro | Glu | Gly | Gly | Pro | Thr | Gly | Ala | Tyr | Phe | Ala | Leu | Gly |
|     |     |     |     |     |     |     | 180 |     |     |     | 185 |     |     | 190 |

Glu Ala Ser Phe Val  
195

(2) INFORMATION FOR SEQ ID NO:4026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..188
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4026:

Met Asp Met Asp Gln Arg Leu Gln Cys Met Phe Lys Arg Val Arg Glu  
1 5 10 15  
Thr Tyr Asp Ala Ala Thr Glu Gly Ile Lys Thr Asn Tyr Tyr Gly Ile  
20 25 30  
Lys His Val Ile Glu Ala Leu Leu Pro Leu Leu Gln Ala Ser Ser Asp  
35 40 45  
Gly Arg Ile Val Asn Val Ser Ser Glu Phe Gly Leu Leu Arg Leu Ile  
50 55 60  
Asn Asn Glu Glu Leu Arg Gln Glu Leu Asn Asp Val Glu Xaa Leu Thr  
65 70 75 80  
Xaa Glu Xaa Leu Asp Xaa Val Leu Ala Ala Tyr Leu Xaa Asp Phe Asp  
85 90 95  
Ala Xaa Xaa Xaa Gly Xaa Arg Gly Xaa Pro Val Asp Phe Ser Ala Tyr  
100 105 110  
Xaa Val Ala Lys Val Ala Met Asn Ala Tyr Thr Arg Ile Leu Ala Arg  
115 120 125  
Arg His Xaa Gly Xaa Arg Val Asn Cys Ala His Pro Gly Tyr Val Ser  
130 135 140  
Thr Asp Met Thr Val His Thr Gly Xaa Xaa Thr Pro Glu Gln Gly Ala  
145 150 155 160  
Ala Asn Val Val Lys Val Ala Leu Met Pro Glu Gly Gly Pro Thr Gly  
165 170 175  
Ala Tyr Phe Ala Leu Gly Glu Glu Ala Ser Phe Val  
180 185

(2) INFORMATION FOR SEQ ID NO:4027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..655
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4027:

cactaccacc agtaccacac cactccgcgc tastgaggac ggtacagcgg cacagaggtg 60  
cgacgtacga cgacgacgac gcargcgcca cacatggcat cccagctctc cgccgccgtg 120  
ccccggttcc acggcctccg gggctacgcc gcgcccaggt ccgcggtggc agcgtgccc 180  
tccgtgaggg tgggcaggaa gaggtcgctg tcgcagggca tccgctgcga ctacatybgC 240  
tccgccacca acctgatcat ggtgacgacg acgacgctga tgctgttcgc rgggcggttc 300  
GggctggCgc cgtcggCgaa ccgcaaggcg acggcggggc tgaagctgga ggcgcgcgac 360  
tccggcctgc agacgggtga ccccgccggg ttaccctcg ccgacacgct gGCctgcggc 420  
gccgtcggcc acatcctcgg cgtcggcatc gtgctcgggc tcaagaacac cggcgccctc 480  
gaccagatca tcggctagat ccctacgtcg tcgttggttaa gatcagactc agcagcctcg 540  
atcgcgccgc cggccggcag gtgcctgcag gtggtgactt tgtaacgtgt gtgcgtgctg 600  
acgtgtacat tgcatccatc ttggttccaa tggacatata gtcctgttg ctctct



(2) INFORMATION FOR SEQ ID NO:4028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4028:

Leu Pro Pro Val Pro His His Ser Ala Leu Xaa Arg Thr Val Gln Arg  
1 5 10 15  
His Arg Gly Ala Thr Tyr Asp Asp Asp Ala Xaa Ala Thr His Gly  
20 25 30  
Ile Pro Ala Leu Arg Arg Arg Ala Pro Val Pro Arg Pro Gly Leu  
35 40 45  
Arg Arg Ala Gln Val Arg Gly Gly Ser Ala Ala Val Arg Glu Gly Gly  
50 55 60  
Gln Glu Glu Val Val Val Ala Gly His Pro Leu Arg Leu His Xaa Leu  
65 70 75 80  
Arg His Gln Pro Asp His Gly Asp Asp Asp Ala Asp Ala Val Arg  
85 90 95  
Xaa Ala Val Arg Ala Gly Ala Val Gly Glu Pro Gln Gly Asp Gly Gly  
100 105 110  
Ala Glu Ala Gly Gly Ala Arg Leu Arg Pro Ala Asp Gly  
115 120 125

(2) INFORMATION FOR SEQ ID NO:4029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4029:

Met Ala Ser Gln Leu Ser Ala Ala Val Pro Arg Phe His Gly Leu Arg  
1 5 10 15  
Gly Tyr Ala Ala Pro Arg Ser Ala Val Ala Ala Leu Pro Ser Val Arg  
20 25 30  
Val Gly Arg Lys Arg Ser Ser Ser Gln Gly Ile Arg Cys Asp Tyr Xaa  
35 40 45  
Xaa Ser Ala Thr Asn Leu Ile Met Val Thr Thr Thr Thr Leu Met Leu  
50 55 60  
Phe Xaa Gly Arg Phe Gly Leu Ala Pro Ser Ala Asn Arg Lys Ala Thr  
65 70 75 80  
Ala Gly Leu Lys Leu Glu Ala Arg Asp Ser Gly Leu Gln Thr Gly Asp  
85 90 95  
Pro Ala Gly Phe Thr Leu Ala Asp Thr Leu Ala Cys Gly Ala Val Gly  
100 105 110  
His Ile Leu Gly Val Gly Ile Val Leu Gly Leu Lys Asn Thr Gly Ala  
115 120 125  
Leu Asp Gln Ile Ile Gly  
130

(2) INFORMATION FOR SEQ ID NO:4030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..79
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1579277
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4030:

```
Met Val Thr Thr Thr Thr Leu Met Leu Phe Xaa Gly Arg Phe Gly Leu
1 5 10 15
Ala Pro Ser Ala Asn Arg Lys Ala Thr Ala Gly Leu Lys Leu Glu Ala
 20 25 30
Arg Asp Ser Gly Leu Gln Thr Gly Asp Pro Ala Gly Phe Thr Leu Ala
 35 40 45
Asp Thr Leu Ala Cys Gly Ala Val Gly His Ile Leu Gly Val Gly Ile
 50 55 60
Val Leu Gly Leu Lys Asn Thr Gly Ala Leu Asp Gln Ile Ile Gly
65 70 75
```

(2) INFORMATION FOR SEQ ID NO:4031:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 851 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..851
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4031:

```
ctccccaatc cccaggtcct catcggcctc ctctctctcg gtctcgccag atctcccccac 60
ggaaccctac ccgagcatca gccatggcaa tcgcggcgcg cgccctgcgc cgcctcccgc 120
ttcacctctc cccctcgatc tcccgctcct tctgcgcggt ttccccggcc gccgcctcgg 180
ctacctcggc ccccgccgcc gcgtccgcca aggtcgctga ccgcatcggt cgcgtcctcg 240
ccatcgatcc cgacggggcg cgcccgatg tggtcggcct ctcggggcag acactccttc 300
gcgctctggc caacgcgggG ctcatcgagc cggcctccca ccgcctcgag gatatcgacg 360
cgtgCtccgc cgagtgcgag gtccacatcg cgcaggagtg gcttgacaag ctgccaccac 420
cgctctacga ggagcgatac gtgtctacgc gcgcgtccag gaaccgcgag ctcaacaagy 480
acgcgcgcct gggctgccag gtggtcctcg cgccggagct gcaggggatg gtgctcgcca 540
tccccgagcc taagccgtgg gacatcccat aatggcctgc cgacgaaagg taaggtgcgg 600
cttttgacgc tgtgagcctt ccttaattcc cttggctcgg tcaagctgtg cgcctgtgcc 660
atcccccttt atatgttacg gatttagtga agaataataa tttgatgagc aaaacttggc 720
attggttaac ttttgttcct agtatatgga tgctctaata tggaatcctt ttgcaactac 780
cgcagtttaa tgtttcatgg tttgaagttt tgtacattgt gatgaatggt tgattaatct 840
tttcatttcc t
```

(2) INFORMATION FOR SEQ ID NO:4032:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 204 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..204
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4032:

```
Leu Pro Asn Pro Gln Val Leu Ile Gly Leu Leu Ser Leu Gly Leu Ala
1 5 10 15
Arg Ser Pro His Gly Thr Leu Pro Glu His Gln Pro Trp Gln Ser Arg
```

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20 25 30  
Arg Ala Pro Cys Ala Ala Ser Arg Phe Thr Ser Pro Pro Arg Ser Pro  
35 40 45  
Ala Pro Ser Ala Arg Phe Pro Arg Pro Pro Pro Arg Leu Pro Arg Pro  
50 55 60  
Pro Pro Pro Arg Pro Pro Arg Ser Leu Thr Ala Ser Cys Ala Ser Ser  
65 70 75 80  
Pro Ser Ile Pro Thr Gly Arg Ala Ala Met Trp Ser Ala Ser Arg Gly  
85 90 95  
Arg His Ser Phe Ala Leu Trp Pro Thr Arg Gly Ser Ser Ser Arg Pro  
100 105 110  
Pro Thr Ala Ser Arg Ile Ser Thr Arg Ala Pro Pro Ser Ala Arg Ser  
115 120 125  
Thr Ser Arg Arg Ser Gly Leu Thr Ser Cys His His Arg Pro Thr Arg  
130 135 140  
Ser Asp Thr Cys Ser Arg Ala Arg Pro Gly Thr Ala Ser Ser Thr Xaa  
145 150 155 160  
Thr Arg Ala Trp Ala Ala Arg Ser Ser Ser Arg Arg Ser Cys Arg Gly  
165 170 175  
Trp Ser Ser Pro Ser Pro Ser Leu Ser Arg Gly Thr Ser His Asn Gly  
180 185 190  
Leu Pro Thr Lys Gly Lys Val Arg Leu Leu Thr Leu  
195 200

(2) INFORMATION FOR SEQ ID NO:4033:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..189

(D) OTHER INFORMATION: / Ceres Seq. ID 1579280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4033:

Pro Gln Ser Pro Gly Pro His Arg Pro Pro Leu Ser Arg Ser Arg Gln  
1 5 10 15  
Ile Ser Pro Arg Asn Pro Thr Arg Ala Ser Ala Met Ala Ile Ala Ala  
20 25 30  
Arg Ala Leu Arg Arg Leu Pro Leu His Leu Ser Pro Ser Ile Ser Arg  
35 40 45  
Ser Phe Cys Ala Val Ser Pro Ala Ala Ala Ser Ala Thr Ser Ala Pro  
50 55 60  
Ala Ala Ala Ser Ala Lys Val Ala Asp Arg Ile Val Arg Val Leu Ala  
65 70 75 80  
Ile Asp Pro Asp Gly Ala Arg Arg Asp Val Val Gly Leu Ser Gly Gln  
85 90 95  
Thr Leu Leu Arg Ala Leu Ala Asn Ala Gly Leu Ile Glu Pro Ala Ser  
100 105 110  
His Arg Leu Glu Asp Ile Asp Ala Cys Ser Ala Glu Cys Glu Val His  
115 120 125  
Ile Ala Gln Glu Trp Leu Asp Lys Leu Pro Pro Pro Ser Tyr Glu Glu  
130 135 140  
Arg Tyr Val Leu Thr Arg Ala Ser Arg Asn Arg Glu Leu Asn Lys Xaa  
145 150 155 160  
Ala Arg Leu Gly Cys Gln Val Val Leu Ala Pro Glu Leu Gln Gly Met  
165 170 175  
Val Val Ala Ile Pro Glu Pro Lys Pro Trp Asp Ile Pro  
180 185

(2) INFORMATION FOR SEQ ID NO:4034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..162  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579281  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4034:

Met Ala Ile Ala Ala Arg Ala Leu Arg Leu Pro Leu His Leu Ser  
1 5 10 15  
Pro Ser Ile Ser Arg Ser Phe Cys Ala Val Ser Pro Ala Ala Ala Ser  
20 25 30  
Ala Thr Ser Ala Pro Ala Ala Ala Ser Ala Lys Val Ala Asp Arg Ile  
35 40 45  
Val Arg Val Leu Ala Ile Asp Pro Asp Gly Ala Arg Arg Asp Val Val  
50 55 60  
Gly Leu Ser Gly Gln Thr Leu Leu Arg Ala Leu Ala Asn Ala Gly Leu  
65 70 75 80  
Ile Glu Pro Ala Ser His Arg Leu Glu Asp Ile Asp Ala Cys Ser Ala  
85 90 95  
Glu Cys Glu Val His Ile Ala Gln Glu Trp Leu Asp Lys Leu Pro Pro  
100 105 110  
Pro Ser Tyr Glu Glu Arg Tyr Val Leu Thr Arg Ala Ser Arg Asn Arg  
115 120 125  
Glu Leu Asn Lys Xaa Ala Arg Leu Gly Cys Gln Val Val Leu Ala Pro  
130 135 140  
Glu Leu Gln Gly Met Val Val Ala Ile Pro Glu Pro Lys Pro Trp Asp  
145 150 155 160  
Ile Pro

(2) INFORMATION FOR SEQ ID NO:4035:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 843 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..843  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4035:

tcttcaccca cattataaag atcctccact tcgcactttc gccgccgcct ctctccttcc 60  
cgagcaggag gcgacaagg taagcagcaa tcgcaggaac cctagcgccg ccgcacccgc 120  
aggaatgggt atcgacctcg tcgccggtgg gaggrrkaag aagaccaagc gcactgcgcc 180  
caagtctgac gatgtctacc tcAagctcct cgtcaagctc taccgtttcN ttggtcagga 240  
ggaccaagag caatttcaac gctgtcattc tcaagaggct tttcatgagt aaaaccaacc 300  
gaccaccaat ctccatgcgc cgccttgta agtttatgga aggaaaggag aagaacattg 360  
ctgtcattgt tggcacagtc acagatgaca aaaggatcca ggaggttcca gcaatgaagg 420  
ttactgccct gaggttcacg gagacagcaa gggccaggat tgtcaatgct ggtggcgagt 480  
gcttcacatt tgaccagctt gctcttcgtg ctccacttgg cgagaacacg gtcctcttga 540  
ggggcccaaa gaatgccgt gaggcagtga ggcactttgg caaggctcct ggagtgccgc 600  
acagccacac caagccgtat gtgcgctcca agggaaggaa gttcgagaag gctcgtggca 660  
ggaggaacag ccgtggattc aagggtttaa acaaattgtg gccctccgtg ttscatcag 720  
catmstgcaa ccgttgtgtt tgatcagtcg acagtaatta gtcatcactc tgtaccgaga 780  
ttmstagcac aatttgttgt cctggytga attytsgaag atatttgatg tcgtctccyt 840  
att

(2) INFORMATION FOR SEQ ID NO:4036:

- (i) SEQUENCE CHARACTERISTICS:

[illegible]

130

(2) INFORMATION FOR SEQ ID NO:4038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4038:

Met Arg Arg Leu Val Lys Phe Met Glu Gly Lys Glu Lys Asn Ile Ala  
1 5 10 15  
Val Ile Val Gly Thr Val Thr Asp Asp Lys Arg Ile Gln Glu Val Pro  
20 25 30  
Ala Met Lys Val Thr Ala Leu Arg Phe Thr Glu Thr Ala Arg Ala Arg  
35 40 45  
Ile Val Asn Ala Gly Gly Glu Cys Leu Thr Phe Asp Gln Leu Ala Leu  
50 55 60  
Arg Ala Pro Leu Gly Glu Asn Thr Val Leu Leu Arg Gly Pro Lys Asn  
65 70 75 80  
Ala Arg Glu Ala Val Arg His Phe Gly Lys Ala Pro Gly Val Pro His  
85 90 95  
Ser His Thr Lys Pro Tyr Val Arg Ser Lys Gly Arg Lys Phe Glu Lys  
100 105 110  
Ala Arg Gly Arg Arg Asn Ser Arg Gly Phe Lys Val  
115 120

(2) INFORMATION FOR SEQ ID NO:4039:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..819
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4039:

aaatccccac gaaaacccta aaccctcgct acccggcggc ggctacaagc tcttcgctcg 60  
ttcagcacca tgargccacc ggctagagga ggacgtggtg ggaggggtgg caggttcgat 120  
ggcggcgggc tctgtcgcgg cggecggttg atcgccccct gcctcaccgt tctcttcctt 180  
ctcgcgctcg cggggttcct cctctggccc gcggaaccgg acatctccct ggccgcctc 240  
cacctagcgc acgtctccgt cgtggcacgc cctgccgtcg ccgtcactat atCcgccacg 300  
ctcaaggttc gcgttcgcaa tctgacctc ttgcgctcg actacaccgg cctcgacgtc 360  
gctatcggct aCcgcggtgc Ggggcttggc cgggtaacat ccggcgggcg acgggtccgg 420  
gcgcgcgctg tctcgtagct cgacgccaac ctgcagctcg acggcatacg cgtcgtcgag 480  
gacgcgatgt acctgctcga ggacctcgcg caaggatccg tgcccttcga caccatcgcc 540  
gaggtcgagg gccacctcca ctcccttttc ctcagcatcc cgggtcaaggg gagaatatct 600  
tgcgtaatgc atattaatcc acacaaccaa accatagtag atcaggactg ctatcctgag 660  
tgaattgctt atggcggtga aatgtggaag ggtgtaagct atgttgctt gcgaatggat 720  
cgtttgattt gtttctaacc tttgcttcca gtcgtggttg taaaagtaag aaccaactaa 780  
ggggtgtttg aatgtaatta agctaatagt tagttcgct

(2) INFORMATION FOR SEQ ID NO:4040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..197  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579308  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4040:

Met Xaa Pro Pro Ala Arg Gly Gly Arg Gly Gly Arg Gly Gly Arg Phe  
1                  5                  10                  15  
Asp Gly Gly Gly Leu Cys Arg Gly Gly Arg Cys Ile Val Pro Cys Leu  
                  20                  25                  30  
Thr Val Leu Phe Leu Leu Ala Leu Ala Gly Phe Leu Leu Trp Pro Ala  
                  35                  40                  45  
Asp Pro Asp Ile Ser Leu Ala Arg Leu His Leu Ala His Val Ser Val  
                  50                  55                  60  
Val Ala Arg Pro Ala Val Ala Val Thr Ile Ser Ala Thr Leu Lys Val  
65                  70                  75                  80  
Arg Val Arg Asn Pro Asp Leu Phe Ala Leu Asp Tyr Thr Arg Leu Asp  
                  85                  90                  95  
Val Ala Ile Gly Tyr Arg Gly Ala Gly Leu Gly Arg Val Thr Ser Gly  
                  100                 105                 110  
Gly Gly Arg Val Arg Ala Arg Ala Val Ser Tyr Val Asp Ala Asn Leu  
                 115                 120                 125  
Gln Leu Asp Gly Ile Arg Val Val Glu Asp Ala Met Tyr Leu Leu Glu  
130                 135                 140  
Asp Leu Ala Gln Gly Ser Val Pro Phe Asp Thr Ile Ala Glu Val Glu  
145                 150                 155                 160  
Gly His Leu His Phe Leu Phe Leu Ser Ile Pro Val Lys Gly Arg Ile  
                 165                 170                 175  
Ser Cys Val Met His Ile Asn Pro His Asn Gln Thr Ile Val His Gln  
                 180                 185                 190  
Asp Cys Tyr Pro Glu  
                 195

(2) INFORMATION FOR SEQ ID NO:4041:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 628 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
    (B) LOCATION: 1..628  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4041:

ataaaaaagct gttcttctcc cctcatcgca tacggcatac cacactagaa ccgccgccgc          60  
tgccgtttcg cgcaccgtac cctagccctc gtcagcggcg gcttcgagct cctccagcca         120  
tgacgttcaa gcggaggaat ggcggacgca acaagcacgg gcgcggccac gtcaagtaca         180  
tccgctgctc caactgcgcc aagtgcgtgcc ccaaggataa ggctatcaag cggttcttgg         240  
tgaggaaacat tgttgagcag gctgccgtga gagatgtgca ggaggcctgt gtacatgatg         300  
gatatgttct acccaaattg tatgcaaagg ttcatcactg tgtctcatgc gcaatccatg         360  
cgcacattgt ccgtgtccgc tctcgtgaga acaggaggaa ccgtgagccc ccgcagcgct         420  
tcagacgccg ggatgatggc ccaaggcctg gtcagggccc gccgcgcccc ggcggtgcag         480  
ctcctgCagc tgcagctgct getgctcctc gtacctaaagt tctggaatta gtttcggggc         540  
ttagttttgt gaaacattac ctgttttgag aaaccattgt tactgtatcc ccttgatgtc         600  
aaacttttta gcacaatttg tggttctg

(2) INFORMATION FOR SEQ ID NO:4042:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 171 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

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(A) LENGTH: 85 amino acids

[illegible]



- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..85  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579354  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4044:

Met Cys Arg Arg Pro Val Tyr Met Met Asp Met Phe Tyr Pro Asn Cys  
1 5 10 15  
Met Gln Arg Phe Ile Thr Val Ser His Ala Gln Ser Met Arg Thr Leu  
20 25 30  
Ser Val Ser Ala Leu Val Arg Thr Gly Gly Thr Val Ser Pro Arg Ser  
35 40 45  
Ala Ser Asp Ala Gly Met Met Ala Gln Gly Leu Val Arg Ala Arg Arg  
50 55 60  
Ala Gln Ala Val Gln Leu Leu Gln Leu Gln Leu Leu Leu Leu Val  
65 70 75 80  
Pro Lys Phe Trp Asn  
85

(2) INFORMATION FOR SEQ ID NO:4045:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 804 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..804  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579355  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4045:

tttgcgtgaag tacaccaaac aaggcatact cctgtacagt ctcagatttg ggtcggttgt 60  
gttgcagcag tcatggcagg cctctttaat gtgcgtgtgc tctcacatat tctttccgtc 120  
ggcactctga ccggttattc agttgtatca gcttgtgtga tcacactaag atggaatgac 180  
aaaggaacta gtcgtcgctc ccttggaagt atgtcaattt ggcaagaggg tgttctaagt 240  
cttgtcatag ttgctctttg tggttttata gtgggacttt gctatcgctt taactatgct 300  
atagccttta ttggtgttagc ttttgtgata gctgttgctg ccagtttcgc tctccagttt 360  
cgtcaggctc atgtggatcc acctggcttt tcttgtcctg gggtagcggt ggttcccatt 420  
atttctgttt tcttcaacat ggtcctgttt gctcagctac atgaagaagc gtggtataga 480  
tttgcattc ttagttctcat cgtgtgggga gttTatgccg gctatggtca gtacaatgct 540  
gttccttcca gtcagaaca ctctactatt ggttaccatg gcgttccttc tgaagccgca 600  
tgagctatgt tcatccccgg agttcttcga acatactgta cggtagcaac atacaccatg 660  
gtcaccgaag tttgaacctg ttgctttttt cttgatgttt tgcacagtgc atactcttgt 720  
agttacgctt agtactccta tatgtagaca gtgaatttcg cagcctgtgt tgtgccacc 780  
acaccattcg tcaggaagct tgcc

(2) INFORMATION FOR SEQ ID NO:4046:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 200 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..200  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579356  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4046:

Phe Ala Glu Val His Pro Thr Arg His Thr Pro Val Gln Ser Gln Ile  
1 5 10 15

00000000-00000000

Trp Val Gly Cys Val Ala Ala Val Met Ala Gly Leu Phe Asn Val Arg  
20 25 30  
Val Leu Ser His Ile Leu Ser Val Gly Thr Leu Thr Gly Tyr Ser Val  
35 40 45  
Val Ser Ala Cys Val Ile Thr Leu Arg Trp Asn Asp Lys Gly Thr Ser  
50 55 60  
Arg Arg Ser Leu Gly Ser Met Ser Ile Trp Gln Glu Gly Val Leu Ser  
65 70 75 80  
Leu Val Ile Val Ala Leu Cys Gly Phe Ile Val Gly Leu Cys Tyr Arg  
85 90 95  
Phe Asn Tyr Ala Ile Ala Phe Met Val Val Ala Phe Val Ile Ala Val  
100 105 110  
Ala Ala Ser Phe Ala Leu Gln Phe Arg Gln Val Tyr Val Asp Pro Pro  
115 120 125  
Gly Phe Ser Cys Pro Gly Val Pro Leu Val Pro Ile Ile Ser Val Phe  
130 135 140  
Phe Asn Met Val Leu Phe Ala Gln Leu His Glu Glu Ala Trp Tyr Arg  
145 150 155 160  
Phe Val Ile Leu Ser Leu Ile Ala Val Gly Val Tyr Ala Gly Tyr Gly  
165 170 175  
Gln Tyr Asn Ala Val Pro Ser Ser Ser Glu His Ser Thr Ile Gly Tyr  
180 185 190  
His Gly Val Pro Ser Glu Ala Ala  
195 200

(2) INFORMATION FOR SEQ ID NO:4047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4047:

Met Ala Gly Leu Phe Asn Val Arg Val Leu Ser His Ile Leu Ser Val  
1 5 10 15  
Gly Thr Leu Thr Gly Tyr Ser Val Val Ser Ala Cys Val Ile Thr Leu  
20 25 30  
Arg Trp Asn Asp Lys Gly Thr Ser Arg Arg Ser Leu Gly Ser Met Ser  
35 40 45  
Ile Trp Gln Glu Gly Val Leu Ser Leu Val Ile Val Ala Leu Cys Gly  
50 55 60  
Phe Ile Val Gly Leu Cys Tyr Arg Phe Asn Tyr Ala Ile Ala Phe Met  
65 70 75 80  
Val Val Ala Phe Val Ile Ala Val Ala Ala Ser Phe Ala Leu Gln Phe  
85 90 95  
Arg Gln Val Tyr Val Asp Pro Pro Gly Phe Ser Cys Pro Gly Val Pro  
100 105 110  
Leu Val Pro Ile Ile Ser Val Phe Phe Asn Met Val Leu Phe Ala Gln  
115 120 125  
Leu His Glu Glu Ala Trp Tyr Arg Phe Val Ile Leu Ser Leu Ile Ala  
130 135 140  
Val Gly Val Tyr Ala Gly Tyr Gly Gln Tyr Asn Ala Val Pro Ser Ser  
145 150 155 160  
Ser Glu His Ser Thr Ile Gly Tyr His Gly Val Pro Ser Glu Ala Ala  
165 170 175

(2) INFORMATION FOR SEQ ID NO:4048:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 130 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..130  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579358  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4048:  
Met Ser Ile Trp Gln Glu Gly Val Leu Ser Leu Val Ile Val Ala Leu  
1                  5                  10                  15  
Cys Gly Phe Ile Val Gly Leu Cys Tyr Arg Phe Asn Tyr Ala Ile Ala  
                  20                  25                  30  
Phe Met Val Val Ala Phe Val Ile Ala Val Ala Ala Ser Phe Ala Leu  
                  35                  40                  45  
Gln Phe Arg Gln Val Tyr Val Asp Pro Pro Gly Phe Ser Cys Pro Gly  
50                  55                  60  
Val Pro Leu Val Pro Ile Ile Ser Val Phe Phe Asn Met Val Leu Phe  
65                  70                  75                  80  
Ala Gln Leu His Glu Glu Ala Trp Tyr Arg Phe Val Ile Leu Ser Leu  
                  85                  90                  95  
Ile Ala Val Gly Val Tyr Ala Gly Tyr Gly Gln Tyr Asn Ala Val Pro  
                  100                 105                 110  
Ser Ser Ser Glu His Ser Thr Ile Gly Tyr His Gly Val Pro Ser Glu  
                 115                 120                 125  
Ala Ala  
130

(2) INFORMATION FOR SEQ ID NO:4049:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 650 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..650  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579359  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4049:  
attatatttat cgggtgctoga gggttcagggtt tcacgcagkc ggcgagagct ggcagccatg 60  
aagarggggga gcccattggtc gctgcggtctg ctaatttgct gcgcggcaat ggtggccatc 120  
gcgcttctcc cccaacaagg aggccaggcc gcttggttctg tgccgacgcc ggttccagct 180  
ccggcaccgc ccggtctctc cgcgacgaac acgaacgact cctccgctgc tcctcggcca 240  
gccaagccca gcgcattccc acccccattg tacggtggtg tcacccccgg cagtctccag 300  
ccacacgagt gcggcgggcg gtgcgcgggg cggtgctcgg cgacggcgta ccagaagccg 360  
tgccctcttct tctgcgcgaa gtvCtgcgcg gcgtgctgt gcgtgcgcgc gggcacctac 420  
ggcaacaaga acacctgccc ctgctacaac aactggaaga ccaagcgggg aggccccaag 480  
tgcccctagt agccctccct ctoggtctac ttgatgagat cttctgttca aaaaatcaaa 540  
aggtaagaat ctgtttaacc atcttttagat ttcacaaata aaacagggtt caatttatct 600  
ttgtagttaa acgcttgcaa ctcatgtgtg aatctcatcc aatattagt

(2) INFORMATION FOR SEQ ID NO:4050:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 162 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1579360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4050:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ile | Leu | Ser | Val | Leu | Glu | Val | Gln | Val | Ser | Arg | Xaa | Arg | Arg | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Ala | Ala | Met | Lys | Xaa | Gly | Ser | Pro | Trp | Ser | Leu | Arg | Leu | Leu | Ile |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Cys | Ala | Ala | Met | Val | Ala | Ile | Ala | Leu | Leu | Pro | Gln | Gln | Gly | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Ala | Ala | Cys | Phe | Val | Pro | Thr | Pro | Gly | Pro | Ala | Pro | Ala | Pro | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Ser | Ser | Ala | Thr | Asn | Thr | Asn | Asp | Ser | Ser | Ala | Ala | Pro | Arg | Pro |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Lys | Pro | Ser | Ala | Phe | Pro | Pro | Pro | Met | Tyr | Gly | Gly | Val | Thr | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Ser | Leu | Gln | Pro | His | Glu | Cys | Gly | Gly | Arg | Cys | Ala | Gly | Arg | Cys |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Ala | Thr | Ala | Tyr | Gln | Lys | Pro | Cys | Leu | Phe | Phe | Cys | Arg | Lys | Xaa |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Cys | Ala | Ala | Cys | Leu | Cys | Val | Pro | Pro | Gly | Thr | Tyr | Gly | Asn | Lys | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Cys | Pro | Cys | Tyr | Asn | Asn | Trp | Lys | Thr | Lys | Arg | Gly | Gly | Pro | Lys |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Cys | Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:4051:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1579361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4051:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Phe | Ile | Gly | Ala | Arg | Gly | Ser | Gly | Phe | Thr | Gln | Xaa | Ala | Arg | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gly | Ser | His | Glu | Xaa | Gly | Glu | Pro | Met | Val | Ala | Ala | Ala | Ala | Asn | Leu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Arg | Gly | Asn | Gly | Gly | His | Arg | Ala | Ser | Pro | Pro | Thr | Arg | Arg | Pro |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Gly | Arg | Leu | Phe | Arg | Ala | Asp | Ala | Gly | Ser | Ser | Ser | Gly | Thr | Ala | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Leu | Arg | Asp | Glu | His | Glu | Arg | Leu | Leu | Arg | Cys | Ser | Ser | Ala | Ser |
| 65  |     |     | 70  |     |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Gln | Ala | Gln | Arg | Ile | Pro | Thr | Pro | Asn | Val | Arg | Trp | Cys | His | Pro | Arg |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gln | Ser | Pro | Ala | Thr | Arg | Val | Arg | Arg | Pro | Val | Arg | Gly | Ala | Val | Leu |
|     | 100 |     |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Asp | Gly | Val | Pro | Glu | Ala | Val | Pro | Leu | Leu | Leu | Pro | Gln | Xaa | Leu |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Arg | Gly | Val | Pro | Val | Arg | Ala | Ala | Gly | His | Leu | Arg | Gln | Gln | Glu | His |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Pro | Leu | Leu | Gln | Gln | Leu | Glu | Asp | Gln | Ala | Gly | Arg | Pro | Gln | Val |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Pro | Leu | Val | Ala | Leu | Pro | Leu | Gly | Leu | Leu | Asp | Glu | Ile | Phe | Cys | Ser |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Lys | Asn | Gln | Lys | Val | Arg | Ile | Cys | Leu | Thr | Ile | Phe | Arg | Phe | His | Lys |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

(2) INFORMATION FOR SEQ ID NO:4052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..168
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4052:

Met Val Ala Ala Ala Asn Leu Leu Arg Gly Asn Gly Gly His Arg  
1 5 10 15  
Ala Ser Pro Pro Thr Arg Arg Pro Gly Arg Leu Phe Arg Ala Asp Ala  
20 25 30  
Gly Ser Ser Ser Gly Thr Ala Arg Leu Leu Arg Asp Glu His Glu Arg  
35 40 45  
Leu Leu Arg Cys Ser Ser Ala Ser Gln Ala Gln Arg Ile Pro Thr Pro  
50 55 60  
Asn Val Arg Trp Cys His Pro Arg Gln Ser Pro Ala Thr Arg Val Arg  
65 70 75 80  
Arg Pro Val Arg Gly Ala Val Leu Gly Asp Gly Val Pro Glu Ala Val  
85 90 95  
Pro Leu Leu Leu Pro Gln Xaa Leu Arg Gly Val Pro Val Arg Ala Ala  
100 105 110  
Gly His Leu Arg Gln Gln Glu His Leu Pro Leu Leu Gln Leu Glu  
115 120 125  
Asp Gln Ala Gly Arg Pro Gln Val Pro Leu Val Ala Leu Pro Leu Gly  
130 135 140  
Leu Leu Asp Glu Ile Phe Cys Ser Lys Asn Gln Lys Val Arg Ile Cys  
145 150 155 160  
Leu Thr Ile Phe Arg Phe His Lys  
165

(2) INFORMATION FOR SEQ ID NO:4053:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..570
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4053:

ggacgcattt attaagrcr cctccgcaa ccgcactctg cccgccgaaa gcgtcgctcg 60  
gccacctcgc actcgcgcgc gcctcaaaga tgcacaggca gctcagcctc tccgccagcm 120  
cgaagcagca gcagccgcct cctgamggca ccarcaccgg angcggcgac gcggcgggcga 180  
aggcgatggc ggcgggcgag gacgagtcgt cggcctcgca ctccagctcc aaggccagca 240  
gggggtggtc ggcgagggac gagagggcc a tccacctegt cccgctgctc accttctct 300  
gcttctctct gctcttctct tgctcccacg acccgctccc cgccgatatg toagCttcg 360  
ctggaggcgg cggcgaggga ggaggagcga gatctgggaa ccggagggtta aggatgcttt 420  
agtgtgcgta ttacctacc attggagtat tattatcgcg atgcggatgt tgtacttgct 480  
cagcagtaac caagtatggg accaaagtat gtcaccatac aaaacactct tgctgtggta 540  
atactaccaa cctacatcag catgttctct

(2) INFORMATION FOR SEQ ID NO:4054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..139
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1579367
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4054:

Thr His Leu Leu Ser Xaa Pro Pro Pro Thr Ala Leu Cys Pro Pro Lys  
1 5 10 15  
Ala Ser Ser Gly His Leu Ala Leu Ala Arg Ala Ser Lys Met His Arg  
20 25 30  
Gln Leu Ser Leu Ser Ala Ser Xaa Lys Gln Gln Gln Pro Pro Pro Xaa  
35 40 45  
Gly Thr Xaa Thr Gly Xaa Gly Asp Ala Ala Ala Lys Ala Met Ala Ala  
50 55 60  
Ala Glu Asp Glu Ser Ser Ala Ser His Ser Ser Lys Ala Ser Arg  
65 70 75 80  
Gly Trp Ser Ala Arg Asp Glu Arg Ala Ile His Leu Val Pro Leu Leu  
85 90 95  
Thr Phe Leu Cys Phe Leu Leu Leu Phe Leu Cys Ser His Asp Pro Ser  
100 105 110  
Pro Ala Asp Met Ser Ser Phe Ala Gly Gly Gly Gly Gly Gly Gly Gly  
115 120 125  
Ala Arg Ser Gly Asn Arg Arg Leu Arg Met Leu  
130 135

(2) INFORMATION FOR SEQ ID NO:4055:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 110 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..110
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1579368
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4055:

Met His Arg Gln Leu Ser Leu Ser Ala Ser Xaa Lys Gln Gln Gln Pro  
1 5 10 15  
Pro Pro Xaa Gly Thr Xaa Thr Gly Xaa Gly Asp Ala Ala Ala Lys Ala  
20 25 30  
Met Ala Ala Ala Glu Asp Glu Ser Ser Ala Ser His Ser Ser Ser Lys  
35 40 45  
Ala Ser Arg Gly Trp Ser Ala Arg Asp Glu Arg Ala Ile His Leu Val  
50 55 60  
Pro Leu Leu Thr Phe Leu Cys Phe Leu Leu Leu Phe Leu Cys Ser His  
65 70 75 80  
Asp Pro Ser Pro Ala Asp Met Ser Ser Phe Ala Gly Gly Gly Gly Gly  
85 90 95  
Gly Gly Gly Ala Arg Ser Gly Asn Arg Arg Leu Arg Met Leu  
100 105 110

(2) INFORMATION FOR SEQ ID NO:4056:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 78 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..78  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4056:

```
Met Ala Ala Ala Glu Asp Glu Ser Ser Ala Ser His Ser Ser Ser Lys
1 5 10 15
Ala Ser Arg Gly Trp Ser Ala Arg Asp Glu Arg Ala Ile His Leu Val
20 25 30
Pro Leu Leu Thr Phe Leu Cys Phe Leu Leu Leu Phe Leu Cys Ser His
35 40 45
Asp Pro Ser Pro Ala Asp Met Ser Ser Phe Ala Gly Gly Gly Gly Gly
50 55 60
Gly Gly Gly Ala Arg Ser Gly Asn Arg Arg Leu Arg Met Leu
65 70 75
```

(2) INFORMATION FOR SEQ ID NO:4057:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 618 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..618  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4057:

```
agcaatsccc aacagcgcca ctgtccagtg cgcgcgtsaa gcttgcttag stagccgcca 60
tggcctccct cgccgcgcgc tccgtgaagc ccgtggccat caagggtctc gccggcagct 120
ctatctccgg aaggaagctc gccgtcgcca gGccgtcggc ccgctccatc cgcaggcccc 180
gcgcagcCgc cgtggtggcc aagtacggcg acaagagcgt ctacttcgac ctgcagcaca 240
tcggcaacac caccggacag tgggacctct acggctctga cgcgcctcgc ccctacaacc 300
cgctacagag caagttcttc gagacgttcg cggctccgtt caccaagaga ggtctgctgc 360
tcaagttcct gctgctgggc ggccggtcac ttctggccta cgtcagcgcg tcggcgtcac 420
cggacctcct gccgatcaag aaggacctc aggagccgcc gcagcctggc ccgcgcggca 480
agatctaagc tcagctactc catttgcatg gtctagtagt agcttgcttt gtactstagg 540
gccggtcgat ccgtcgcaat cgtcatggat catctctcta tcttggtgtt acgctgttca 600
taatttggtg tattegcc
```

(2) INFORMATION FOR SEQ ID NO:4058:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..92  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4058:

```
Ala Xaa Pro Asn Ser Ala Thr Val Gln Cys Ala Arg Xaa Ala Cys Leu
1 5 10 15
Xaa Ser Arg His Gly Leu Pro Arg Arg Arg Leu Arg Glu Ala Arg Gly
20 25 30
His Gln Gly Ser Arg Arg Gln Leu Tyr Leu Arg Lys Glu Ala Arg Arg
35 40 45
Arg Gln Ala Val Gly Pro Leu His Pro Gln Ala Pro Arg Ser Arg Arg
50 55 60
Gly Gly Gln Val Arg Arg Gln Glu Arg Leu Leu Arg Pro Arg Arg His
65 70 75 80
Arg Gln His His Arg Thr Val Gly Pro Leu Arg Leu
85 90
```

(2) INFORMATION FOR SEQ ID NO:4059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4059:

Met Ala Ser Leu Ala Ala Val Ser Val Lys Pro Val Ala Ile Lys Gly  
1 5 10 15  
Leu Ala Gly Ser Ser Ile Ser Gly Arg Lys Leu Ala Val Ala Arg Pro  
20 25 30  
Ser Ala Arg Ser Ile Arg Arg Pro Arg Ala Ala Ala Val Val Ala Lys  
35 40 45  
Tyr Gly Asp Lys Ser Val Tyr Phe Asp Leu Asp Asp Ile Gly Asn Thr  
50 55 60  
Thr Gly Gln Trp Asp Leu Tyr Gly Ser Asp Ala Pro Ser Pro Tyr Asn  
65 70 75 80  
Pro Leu Gln Ser Lys Phe Phe Glu Thr Phe Ala Ala Pro Phe Thr Lys  
85 90 95  
Arg Gly Leu Leu Leu Lys Phe Leu Leu Leu Gly Gly Gly Ser Leu Leu  
100 105 110  
Ala Tyr Val Ser Ala Ser Ala Ser Pro Asp Leu Leu Pro Ile Lys Lys  
115 120 125  
Gly Pro Gln Glu Pro Pro Gln Pro Gly Pro Arg Gly Lys Ile  
130 135 140

(2) INFORMATION FOR SEQ ID NO:4060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..771
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4060:

atcacaaattc acagcgctca agttctcgcg cccagagcca aattttttctc cactcaatca 60  
ctgcagccat gnacgccagc ngascggtag caaggcgaag aagggggcgg ctgggcgcaa 120  
ggctggcggc cccaggaaga agtcggtgtc gcggtccgtc aaggccgggc tgcagttccc 180  
cgtcggccgg atcgggcgct acctcaagaa gggccggtac gcgcagcgCG tgggcaccgg 240  
cgcccccggt tatctcgccg ccgtgtttga gtacctcgcc gccgaggtgc tggagctggc 300  
cggcaacgcg gcgaaggaca acaagaagac gcgcacgtc ccgcgccacg tgctcctggc 360  
gatccgcaac gacgttgagc tcggcaagct gctggctggc gtcaccatcg cgcacggcgg 420  
tgtcctcccc aacatcaacc cggttctcct gcccaagaag gtggcggaga aggcgtctag 480  
cggcggcagc aaggagagca agtccccctaa gaaggccgcc aagtccccaa agaaggcagc 540  
caagtccccg aagaaggctt agaaattagt cactccacta gcgctctgct gtagcatgtt 600  
cgtgtttaga tctgtggatg ttatgtgttc cggcctaatt tcctctttgc cttgtggctt 660  
ctgatattgt catcgcatg tttgcggtg tgtgtttcct tggtctgatt ttgcaattca 720  
tcattctgtt gaatgaactt actatcgga aatgaagcat aataacgatg c

(2) INFORMATION FOR SEQ ID NO:4061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear



- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..186  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579399  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4061:

Ser Gln Phe Thr Ala Leu Lys Phe Ser Arg Pro Glu Pro Asn Phe Ser  
1                  5                  10                  15  
Pro Leu Asn His Cys Ser His Xaa Arg Gln Xaa Xaa Gly Ser Lys Ala  
                  20                  25                  30  
Lys Lys Gly Ala Ala Gly Arg Lys Ala Gly Gly Pro Arg Lys Lys Ser  
                  35                  40                  45  
Val Ser Arg Ser Val Lys Ala Gly Leu Gln Phe Pro Val Gly Arg Ile  
50                  55                  60  
Gly Arg Tyr Leu Lys Lys Gly Arg Tyr Ala Gln Arg Val Gly Thr Gly  
65                  70                  75                  80  
Ala Pro Val Tyr Leu Ala Ala Val Leu Glu Tyr Leu Ala Ala Glu Val  
                  85                  90                  95  
Leu Glu Leu Ala Gly Asn Ala Ala Lys Asp Asn Lys Lys Thr Arg Ile  
                  100                  105                  110  
Val Pro Arg His Val Leu Leu Ala Ile Arg Asn Asp Val Glu Leu Gly  
                  115                  120                  125  
Lys Leu Leu Ala Gly Val Thr Ile Ala His Gly Gly Val Leu Pro Asn  
130                  135                  140  
Ile Asn Pro Val Leu Leu Pro Lys Lys Val Ala Glu Lys Ala Ser Ser  
145                  150                  155                  160  
Gly Gly Ser Lys Glu Ser Lys Ser Pro Lys Lys Ala Ala Lys Ser Pro  
                  165                  170                  175  
Lys Lys Ala Ala Lys Ser Pro Lys Lys Ala  
                  180                  185

(2) INFORMATION FOR SEQ ID NO:4062:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 188 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..188  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579400  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4062:

His Asn Ser Gln Arg Ser Ser Ser Arg Ala Gln Ser Gln Ile Phe Leu  
1                  5                  10                  15  
His Ser Ile Thr Ala Ala Met Xaa Ala Ser Xaa Xaa Val Ala Arg Arg  
                  20                  25                  30  
Arg Arg Gly Arg Leu Gly Ala Arg Leu Ala Ala Pro Gly Arg Ser Arg  
                  35                  40                  45  
Cys Arg Gly Pro Ser Arg Pro Gly Cys Ser Ser Pro Ser Ala Gly Ser  
50                  55                  60  
Gly Ala Thr Ser Arg Arg Ala Gly Thr Arg Ser Ala Trp Ala Pro Ala  
65                  70                  75                  80  
Pro Pro Ser Ile Ser Pro Pro Cys Leu Ser Thr Ser Pro Pro Arg Cys  
                  85                  90                  95  
Trp Ser Trp Pro Ala Thr Arg Arg Arg Thr Thr Arg Arg Arg Ala Ser  
                  100                  105                  110  
Ser Arg Ala Thr Cys Ser Trp Arg Ser Ala Thr Thr Leu Ser Ser Ala  
                  115                  120                  125  
Ser Cys Trp Leu Ala Ser Pro Ser Arg Thr Ala Val Ser Ser Pro Thr  
130                  135                  140  
Ser Thr Arg Phe Ser Cys Pro Arg Arg Trp Arg Arg Arg Arg Leu Ala

(2) INFORMATION FOR SEO ID NO:4063:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1579401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4063:

(2) INFORMATION FOR SEO ID NO:4064:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 782 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..782

(D) OTHER INFORMATION: / Ceres Seq. ID 1579402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4064:

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| asattcagcc | cacaagcaca | taacaacata | gcaccccccc  | tagggtttca  | caacatatgt | 60  |
| accctctcgc | gcaaacactc | ctcttttcgc | rcmgcctccc  | ctcccgccca  | cttgctccgc | 120 |
| cggcgcggcc | accgcgcgcg | caccgcagca | gccagtcagc  | agatcgtaac  | catggcggat | 180 |
| tctaaggccg | ctgcgcgcgt | gacctccgc  | acgcgcaagt  | tcatgaccaa  | cgccttctc  | 240 |
| tcgcgcaagc | agttcgtgct | cgaGgtcatc | caccccgcc   | gccccaacgt  | ctccaaggcg | 300 |
| gaGbtcaagg | agaggctggc | gaagatctac | gaggtgaagg  | acccaaactg  | catcttcgtc | 360 |
| ttcaagtttc | ggaccaactt | cggagcgccg | aagtccaccg  | gtctcggtct  | catctacgac | 420 |
| aaccttgagg | ccgccaagaa | gttcgagccc | aagtaccgcc  | tctatcaggaa | cggccttgct | 480 |
| accaaggtag | agaagtcacg | aaagcagatg | aaggaacgta  | agracagggc  | gaagaaaatc | 540 |
| cgtggtgtga | agaagacaaa | agcgggagat | gccaaagaaga | agtaaggggag | gaagttactt | 600 |

gccttgccat ttctcatctt aggccttggg ttgtttaggg tgggctcctt ccggcaatgc 660  
tgaatgtgtt tagttagaag tagagaagat tttgccaatc acccattacg ttgagtttct 720  
cgttgcacct tctgttcagt tttgaggcac tttgtcagac acaagaatat atatacctgg 780  
tc

(2) INFORMATION FOR SEQ ID NO:4065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..194
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4065:

Xaa Phe Ser Pro Gln Ala His Asn Asn Ile Ala Pro Pro Leu Gly Phe  
1 5 10 15  
His Asn Ile Cys Thr Leu Ser Arg Lys His Ser Ser Phe Arg Xaa Ala  
20 25 30  
Ser Pro Pro Ala His Leu Leu Arg Arg Arg Gly His Arg Arg Arg Thr  
35 40 45  
Ala Ala Ala Ser Gln Gln Ile Val Thr Met Ala Asp Ser Lys Ala Ala  
50 55 60  
Ala Ala Val Thr Leu Arg Thr Arg Lys Phe Met Thr Asn Arg Leu Leu  
65 70 75 80  
Ser Arg Lys Gln Phe Val Leu Glu Val Ile His Pro Gly Arg Pro Asn  
85 90 95  
Val Ser Lys Ala Glu Xaa Lys Glu Arg Leu Ala Lys Ile Tyr Glu Val  
100 105 110  
Lys Asp Pro Asn Cys Ile Phe Val Phe Lys Phe Arg Thr Asn Phe Gly  
115 120 125  
Gly Gly Lys Ser Thr Gly Phe Gly Leu Ile Tyr Asp Asn Leu Glu Ala  
130 135 140  
Ala Lys Lys Phe Glu Pro Lys Tyr Arg Leu Ile Arg Asn Gly Leu Ala  
145 150 155 160  
Thr Lys Val Glu Lys Ser Arg Lys Gln Met Lys Glu Arg Lys Xaa Arg  
165 170 175  
Ala Lys Lys Ile Arg Gly Val Lys Lys Thr Lys Ala Gly Asp Ala Lys  
180 185 190  
Lys Lys

(2) INFORMATION FOR SEQ ID NO:4066:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..137
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4066:

Met Ala Asp Ser Lys Ala Ala Ala Val Thr Leu Arg Thr Arg Lys  
1 5 10 15  
Phe Met Thr Asn Arg Leu Leu Ser Arg Lys Gln Phe Val Leu Glu Val  
20 25 30  
Ile His Pro Gly Arg Pro Asn Val Ser Lys Ala Glu Xaa Lys Glu Arg  
35 40 45  
Leu Ala Lys Ile Tyr Glu Val Lys Asp Pro Asn Cys Ile Phe Val Phe

50 55 60  
Lys Phe Arg Thr Asn Phe Gly Gly Lys Ser Thr Gly Phe Gly Leu  
65 70 75 80  
Ile Tyr Asp Asn Leu Glu Ala Ala Lys Lys Phe Glu Pro Lys Tyr Arg  
85 90 95  
Leu Ile Arg Asn Gly Leu Ala Thr Lys Val Glu Lys Ser Arg Lys Gln  
100 105 110  
Met Lys Glu Arg Lys Xaa Arg Ala Lys Lys Ile Arg Gly Val Lys Lys  
115 120 125  
Thr Lys Ala Gly Asp Ala Lys Lys Lys  
130 135

(2) INFORMATION FOR SEQ ID NO:4067:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4067:

Met Thr Asn Arg Leu Leu Ser Arg Lys Gln Phe Val Leu Glu Val Ile  
1 5 10 15  
His Pro Gly Arg Pro Asn Val Ser Lys Ala Glu Xaa Lys Glu Arg Leu  
20 25 30  
Ala Lys Ile Tyr Glu Val Lys Asp Pro Asn Cys Ile Phe Val Phe Lys  
35 40 45  
Phe Arg Thr Asn Phe Gly Gly Gly Lys Ser Thr Gly Phe Gly Leu Ile  
50 55 60  
Tyr Asp Asn Leu Glu Ala Ala Lys Lys Phe Glu Pro Lys Tyr Arg Leu  
65 70 75 80  
Ile Arg Asn Gly Leu Ala Thr Lys Val Glu Lys Ser Arg Lys Gln Met  
85 90 95  
Lys Glu Arg Lys Xaa Arg Ala Lys Lys Ile Arg Gly Val Lys Lys Thr  
100 105 110  
Lys Ala Gly Asp Ala Lys Lys Lys  
115 120

(2) INFORMATION FOR SEQ ID NO:4068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 650 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..650
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4068:

attcacgctc cacgttccat atggcttccct gcaggatggc actcctcctt ggcttgcctgc 60  
tgctagtagt aGcttcgccc gcgatcgctg atgacgactc cggatatctac taccagctgg 120  
ctcttatgtg gccaggagca tactgcgagc agaccagcgc tgggtgctgc aaGccgacca 180  
ccggcgtctc ccggrcgccg gacttctaca taacgggctt caccgtcctt aacgcgacca 240  
ccgacgctgc agtgacggga tgcagcaaca aagttcctta cgaccctaac ctgattaccg 300  
gcacccaagg cctgaatcag tactggagca acatcagggtg ccccagcaac aacgggcaga 360  
gcagctggaa gaacgcctgg aagaaggccg gcgcctgatc ttgctccaga ggggtgtgttt 420  
gggaattggg agggggaaaa aaagaggaaa ttgctgcata gagtcagacg gtgtatcagc 480  
ttgtacgcca tcaatcaagt gctgtaaaca tgccctgggaa ataattgggg acctggattt 540  
gaataagatt tgagttgttg ggggcgagac tgctacatta ggccttggtc gggttattcct 600

aataccttcg gtgcaataaaa ggaaatcatc ttgcgcgtga ccgagcgtgc

(2) INFORMATION FOR SEQ ID NO:4069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1579407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4069:

Ser Pro Ser Thr Phe His Met Ala Ser Cys Arg Met Ala Leu Leu Leu  
1 5 10 15  
Gly Leu Leu Leu Leu Val Val Ala Ser Pro Ala Ile Ala Asp Asp Asp  
20 25 30  
Ser Gly Ile Tyr Tyr Gln Leu Ala Leu Met Trp Pro Gly Ala Tyr Cys  
35 40 45  
Glu Gln Thr Ser Ala Gly Cys Cys Lys Pro Thr Thr Gly Val Ser Pro  
50 55 60  
Xaa Arg Asp Phe Tyr Ile Thr Gly Phe Thr Val Leu Asn Ala Thr Thr  
65 70 75 80  
Asp Ala Ala Val Thr Gly Cys Ser Asn Lys Val Pro Tyr Asp Pro Asn  
85 90 95  
Leu Ile Thr Gly Ile Gln Gly Leu Asn Gln Tyr Trp Ser Asn Ile Arg  
100 105 110  
Cys Pro Ser Asn Asn Gly Gln Ser Ser Trp Lys Asn Ala Trp Lys Lys  
115 120 125  
Ala Gly Ala  
130

(2) INFORMATION FOR SEQ ID NO:4070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1579408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4070:

Met Ala Ser Cys Arg Met Ala Leu Leu Leu Gly Leu Leu Leu Val  
1 5 10 15  
Val Ala Ser Pro Ala Ile Ala Asp Asp Asp Ser Gly Ile Tyr Tyr Gln  
20 25 30  
Leu Ala Leu Met Trp Pro Gly Ala Tyr Cys Glu Gln Thr Ser Ala Gly  
35 40 45  
Cys Cys Lys Pro Thr Thr Gly Val Ser Pro Xaa Arg Asp Phe Tyr Ile  
50 55 60  
Thr Gly Phe Thr Val Leu Asn Ala Thr Thr Asp Ala Ala Val Thr Gly  
65 70 75 80  
Cys Ser Asn Lys Val Pro Tyr Asp Pro Asn Leu Ile Thr Gly Ile Gln  
85 90 95  
Gly Leu Asn Gln Tyr Trp Ser Asn Ile Arg Cys Pro Ser Asn Asn Gly  
100 105 110  
Gln Ser Ser Trp Lys Asn Ala Trp Lys Lys Ala Gly Ala  
115 120 125

(2) INFORMATION FOR SEQ ID NO:4071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..120
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1579409
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4071:

Met Ala Leu Leu Gly Leu Leu Leu Val Val Ala Ser Pro Ala  
1 5 10 15  
Ile Ala Asp Asp Asp Ser Gly Ile Tyr Tyr Gln Leu Ala Leu Met Trp  
20 25 30  
Pro Gly Ala Tyr Cys Glu Gln Thr Ser Ala Gly Cys Cys Lys Pro Thr  
35 40 45  
Thr Gly Val Ser Pro Xaa Arg Asp Phe Tyr Ile Thr Gly Phe Thr Val  
50 55 60  
Leu Asn Ala Thr Thr Asp Ala Ala Val Thr Gly Cys Ser Asn Lys Val  
65 70 75 80  
Pro Tyr Asp Pro Asn Leu Ile Thr Gly Ile Gln Gly Leu Asn Gln Tyr  
85 90 95  
Trp Ser Asn Ile Arg Cys Pro Ser Asn Asn Gly Gln Ser Ser Trp Lys  
100 105 110  
Asn Ala Trp Lys Lys Ala Gly Ala  
115 120

- (2) INFORMATION FOR SEQ ID NO:4072:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 635 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..635
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1579440

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4072:

atttatattt atttattgct gccgcgtcca cgcgtccgtcc ccaaacccta ccgcagtcgc 60  
cgccaccgtc tccccctctg atccaatcca atggcgcgcc tccacctcgt ggccgtggca 120  
atgggcttgc tcttggcctt gacgacggcg caggcaccgg gcgcgtccac gatgcccgCg 180  
cccatggcgC agntccggcg acctcggcgc ctccctcgtcc cgcgccatcc ccgaccaga 240  
agaccgctcc agctccggcg cccaatgcca cggtaccgcg ccccgccctcG ccgccggcgc 300  
cgagctctat cgggcagacg ccgaccgagg cgccgtcctc ccctccgccg ccagcgccg 360  
cgtccagcgt tgccctccgcc ttgtacgtgg Nccgccgcta tggcgGctgt cgtgtttttc 420  
ttctgaggtc ggtactcggc gccgatggat ccgccgccta tggatggta cggtcgggtg 480  
tggatttgac acgatggctc ccCgctaccg ctggtcgagt ttgcttatta ggatactagt 540  
agttaattaa tagttgggtt gatcagatca gatctagcgt ttttgttgag tggggatatt 600  
atttcttcta cggatctgca cactagggtt atgtc

- (2) INFORMATION FOR SEQ ID NO:4073:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 178 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..178
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1579441
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4073:

Leu Tyr Leu Phe Ile Ala Ala Ala Ser Thr Val Arg Pro Gln Thr Leu  
1 5 10 15  
Pro Gln Ser Pro Pro Pro Ser Pro Leu Leu Ile Gln Ser Asn Gly Ala  
20 25 30  
Pro Pro Pro Arg Gly Arg Gly Asn Gly Leu Ala Leu Gly Leu Asp Asp  
35 40 45  
Gly Ala Gly Thr Gly Arg Val His Asp Ala Arg Ala His Gly Ala Xaa  
50 55 60  
Pro Ala Thr Ser Ala Pro Pro Arg Pro Ala Pro Ser Pro Thr Gln Lys  
65 70 75 80  
Thr Ala Pro Ala Pro Ala Pro Asn Ala Thr Val Pro Ala Pro Ala Ser  
85 90 95  
Pro Pro Ala Pro Ser Ser Ile Gly Gln Thr Pro Thr Glu Ala Pro Ser  
100 105 110  
Ser Pro Pro Pro Pro Ser Ala Ala Ser Ser Val Ala Ser Ala Leu Tyr  
115 120 125  
Val Xaa Arg Arg Tyr Gly Gly Cys Arg Val Phe Leu Leu Arg Ser Val  
130 135 140  
Leu Gly Ala Asp Gly Ser Ala Ala Tyr Gly Met Val Arg Cys Gly Val  
145 150 155 160  
Asp Leu Thr Arg Trp Leu Pro Ala Thr Ala Gly Arg Val Cys Leu Leu  
165 170 175  
Gly Tyr

(2) INFORMATION FOR SEQ ID NO:4074:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1579442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4074:

Met Ala Arg Leu His Leu Val Ala Val Ala Met Gly Leu Leu Leu Ala  
1 5 10 15  
Leu Thr Thr Ala Gln Ala Pro Gly Ala Ser Thr Met Pro Ala Pro Met  
20 25 30  
Ala Gln Xaa Arg Arg Pro Arg Arg Leu Leu Val Pro Arg His Pro Arg  
35 40 45  
Pro Arg Arg Pro Leu Gln Leu Arg Arg Pro Met Pro Arg Tyr Pro Pro  
50 55 60  
Pro Pro Arg Arg Arg Arg Ala Leu Ser Gly Arg Arg Arg Pro Arg  
65 70 75 80  
Arg Arg Pro Pro Leu Arg Arg Pro Ala Pro Arg Pro Ala Leu Pro Pro  
85 90 95  
Pro Cys Thr Trp Xaa Ala Ala Met Ala Ala Val Val Phe Phe Phe  
100 105 110

(2) INFORMATION FOR SEQ ID NO:4075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1579443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4075:

Met Gly Leu Leu Leu Ala Leu Thr Thr Ala Gln Ala Pro Gly Ala Ser  
1 5 10 15  
Thr Met Pro Ala Pro Met Ala Gln Xaa Arg Arg Pro Arg Arg Leu Leu  
20 25 30  
Val Pro Arg His Pro Arg Pro Arg Arg Pro Leu Gln Leu Arg Arg Pro  
35 40 45  
Met Pro Arg Tyr Pro Pro Pro Pro Arg Arg Arg Arg Arg Ala Leu Ser  
50 55 60  
Gly Arg Arg Arg Pro Arg Arg Arg Pro Pro Leu Arg Arg Pro Ala Pro  
65 70 75 80  
Arg Pro Ala Leu Pro Pro Pro Cys Thr Trp Xaa Ala Ala Met Ala Ala  
85 90 95  
Val Val Phe Phe Phe  
100

(2) INFORMATION FOR SEQ ID NO:4076:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..780
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4076:

actcagccca ctacctttca gatttttctt catctgccgc cgcctgcacc caacaagcct 60  
ctcgacgcta gtcattggcgc cttccaacgg cgccgcscgg tcgacgagac cgtcgccgcc 120  
accgactccg tgcaggagcc tcccagaag atctccaaga tctctcccct gctcaagggtg 180  
aagaagctct ccgagaaggc cgtgctgccg tcccgcggct ccgctctcgc cgccggctac 240  
gacctctcga gcgcgagga gatggtggtg ccggcgcggtg gcaaggcgct cgtgccgacc 300  
gacctcagcg tcgccatccc gcacggaacc tacgcgCgca tcgcGCCcag gtcgggggtg 360  
gcgctgaagc actccatcga cgtggggcgc ggcgtgatcg acgcggacta ccgaggcccc 420  
gtcggcgta tctctttcaa ccaactccgac gccgacttcg ccgtgaagcc cggcgacagg 480  
atcgcgcaga tgatcatcga ggtgatcgcg acgcccagag tcgcggaggt ggaggacctc 540  
gacgccaccg tccgtggggg cggagggttc ggggtccaccg gcgtctgaag ggattcgggtg 600  
tctaggtag gatggcgatg caagccttgg tgtcttttgt tggctctaag aaatcgtgat 660  
gttcaccatc actatcctgc tatcgataat tagtattgag attagtagct aggttgcgta 720  
gttagctcga tgcacgtact attgtcgaga actcgctatt ctgtgatgtt gaaaatgtct 780

(2) INFORMATION FOR SEQ ID NO:4077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..195
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4077:

Thr Gln Pro Thr Thr Phe Gln Ile Phe Pro His Leu Pro Pro Pro Ala  
1 5 10 15  
Pro Asn Lys Pro Leu Asp Ala Ser His Gly Arg Phe Gln Arg Arg Arg  
20 25 30  
Xaa Val Asp Glu Thr Val Ala Ala Thr Asp Ser Val Gln Glu Pro Pro  
35 40 45  
Gln Lys Ile Ser Lys Ile Ser Pro Leu Leu Lys Val Lys Lys Leu Ser  
50 55 60



Glu Lys Ala Val Leu Pro Ser Arg Gly Ser Ala Leu Ala Ala Gly Tyr  
65 70 75 80  
Asp Leu Ser Ser Ala Glu Glu Met Val Val Pro Ala Arg Gly Lys Ala  
85 90 95  
Leu Val Pro Thr Asp Leu Ser Val Ala Ile Pro His Gly Thr Tyr Ala  
100 105 110  
Arg Ile Ala Pro Arg Ser Gly Leu Ala Leu Lys His Ser Ile Asp Val  
115 120 125  
Gly Ala Gly Val Ile Asp Ala Asp Tyr Arg Gly Pro Val Gly Val Ile  
130 135 140  
Leu Phe Asn His Ser Asp Ala Asp Phe Ala Val Lys Pro Gly Asp Arg  
145 150 155 160  
Ile Ala Gln Met Ile Ile Glu Val Ile Ala Thr Pro Glu Val Ala Glu  
165 170 175  
Val Glu Asp Leu Asp Ala Thr Val Arg Gly Asp Gly Gly Phe Gly Ser  
180 185 190  
Thr Gly Val  
195

(2) INFORMATION FOR SEQ ID NO:4078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4078:

Met Val Val Pro Ala Arg Gly Lys Ala Leu Val Pro Thr Asp Leu Ser  
1 5 10 15  
Val Ala Ile Pro His Gly Thr Tyr Ala Arg Ile Ala Pro Arg Ser Gly  
20 25 30  
Leu Ala Leu Lys His Ser Ile Asp Val Gly Ala Gly Val Ile Asp Ala  
35 40 45  
Asp Tyr Arg Gly Pro Val Gly Val Ile Leu Phe Asn His Ser Asp Ala  
50 55 60  
Asp Phe Ala Val Lys Pro Gly Asp Arg Ile Ala Gln Met Ile Ile Glu  
65 70 75 80  
Val Ile Ala Thr Pro Glu Val Ala Glu Val Glu Asp Leu Asp Ala Thr  
85 90 95  
Val Arg Gly Asp Gly Gly Phe Gly Ser Thr Gly Val  
100 105

(2) INFORMATION FOR SEQ ID NO:4079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..469
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4079:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atccgttgct catctacca gaagcgaaGc cggaggaggg aggaaggaga tcgcgagcag   | 60  |
| ccggagccgg aggcCgagag gatgaagacg ttcgaccggt ggccggtctt cttccgccgg  | 120 |
| gagtggaaagc gcaactggcc cttcctcacg gggttcgcca tcaccggctt catcatcacc | 180 |
| aagatgacgg ccaacttcac cgaggaggac ctcaagaact ccaagtctgt ccaggaacac  | 240 |
| aagaagcgct gaccaaccgg gagtcgtccg aatcgctctgc ggatgaaaaa ttagccccct | 300 |

atttatcttg tctttttttt tatctagatg cgtgcactct attgtaataa tgtaataaga 360  
ggcaattgga ttgatccaac agcaaccggc ttctgatttt gaTcygcttc gctgacataa 420  
tatgtgcctt ttttctggat gttggattgc atctaactct gttgaattg

(2) INFORMATION FOR SEQ ID NO:4080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4080:

Ile Arg Cys Ser Ser His Gln Lys Arg Ser Arg Arg Arg Glu Glu Gly  
1 5 10 15  
Asp Arg Glu Gln Pro Glu Pro Glu Ala Glu Arg Met Lys Thr Phe Asp  
20 25 30  
Pro Trp Pro Val Phe Phe Arg Arg Glu Trp Lys Arg Asn Trp Pro Phe  
35 40 45  
Leu Thr Gly Phe Ala Ile Thr Gly Phe Ile Ile Thr Lys Met Thr Ala  
50 55 60  
Asn Phe Thr Glu Glu Asp Leu Lys Asn Ser Lys Phe Val Gln Glu His  
65 70 75 80  
Lys Lys Arg

(2) INFORMATION FOR SEQ ID NO:4081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4081:

Pro Leu Leu Ile Ser Pro Glu Ala Lys Pro Glu Glu Gly Gly Arg Arg  
1 5 10 15  
Ser Arg Ala Ala Gly Ala Gly Gly Arg Glu Asp Glu Asp Val Arg Pro  
20 25 30  
Val Ala Gly Leu Leu Pro Pro Gly Val Glu Ala Gln Leu Ala Leu Pro  
35 40 45  
His Gly Val Arg His His Arg Leu His His His Gln Asp Asp Gly Gln  
50 55 60  
Leu His Arg Gly Gly Pro Gln Glu Leu Gln Val Arg Pro Gly Thr Gln  
65 70 75 80  
Glu Ala Leu Thr Asn Arg Glu Ser Ser Glu Ser Pro Ala Asp Glu Lys  
85 90 95  
Leu Ala Pro Tyr Leu Ser Cys Leu Phe Tyr Leu Asp Ala Cys Thr  
100 105 110  
Leu Leu

(2) INFORMATION FOR SEQ ID NO:4082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..741

(D) OTHER INFORMATION: / Ceres Seq. ID 1579457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4082:

```
ccttcttccc ccactgtcgc cgtcctcgt ctccactct ctccactttg ctgcttcttc 60
tcccttatta atgctcgtgg gctcctatga tccgccctcc gccgcgggtt tcttgatcca 120
tccccggccc aaggaagcgg accccggcga aactcctga cagattcgcc cCgtccgccg 180
ctccctcgat tcggtccCTt ccccgtcagc ggcaggtgtt taggGacctc tgcagcatag 240
catctggtcc gtccctggag atgtccggcg tacaggagca gttcgagatc aagttccggG 300
ctgccggacg gcaccgacat cggaccNcag gcggttcccg ccgrcgcca ccgtcgccac 360
gctcaaggag accatcatcg cccagtggcc cgatgatggt gaaggctctg cagcgcaagc 420
cggcgatgta tactggcggc ggcggcggcg gcgagcaaag cgggaggagc agctggtgag 480
gagattgaga ctgtggtggt gcgtggcgtg tactgttcat cgttcagaca gatgacttgc 540
tggccCatgc tgtgggctca ggaactgctt cttoacagtg gcgatgttct gatctgtaat 600
gcacgaagca cgatactatt tgttgtatat gtatgtatgt gtaactacag ataagattag 660
gaacggtgtg aaagaataaa gaaaccgatg gaataagtga tttgggaaca atctcagaat 720
caatttatgc agtcctttag g
```

(2) INFORMATION FOR SEQ ID NO:4083:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..52

(D) OTHER INFORMATION: / Ceres Seq. ID 1579458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4083:

```
Leu Leu Pro Pro Leu Ser Pro Leu Leu Val Phe His Ser Leu His Phe
1 5 10 15
Ala Ala Ser Ser Pro Leu Leu Met Leu Val Gly Ser Tyr Asp Pro Pro
20 25 30
Ser Ala Ala Gly Phe Leu Ile His Pro Arg Pro Lys Glu Ala Asp Pro
35 40 45
Gly Glu His Ser
50
```

(2) INFORMATION FOR SEQ ID NO:4084:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1579459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4084:

```
Met Ser Gly Val Gln Glu Gln Phe Glu Ile Lys Phe Arg Ala Ala Gly
1 5 10 15
Arg His Arg His Arg Thr Xaa Gly Gly Ser Arg Xaa Arg Pro Pro Ser
20 25 30
Pro Arg Ser Arg Arg Pro Ser Ser Pro Ser Gly Pro Met Met Val Lys
35 40 45
Ala Leu Gln Arg Lys Pro Ala Met Tyr Thr Gly Gly Gly Gly Gly Gly
50 55 60
Glu Gln Ser Gly Arg Ser Ser Trp
65 70
```

(2) INFORMATION FOR SEQ ID NO:4085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4085:

Met Thr Cys Trp Pro Met Leu Trp Ala Gln Glu Leu Leu Leu His Ser  
1                   5                   10                   15  
Gly Asp Val Leu Ile Cys Asn Ala Arg Ser Thr Ile Leu Phe Val Val  
                  20                   25                   30  
Tyr Val Cys Met Cys Asn Tyr Arg  
                  35                   40

(2) INFORMATION FOR SEQ ID NO:4086:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 629 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..629
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4086:

aaaaagaggt gtccatggtg ctcaagctca gccaaagcaaa taagacgact tgttttcattg           60  
attcttgaag agatcgagct tcttttgcac cacaaggtcg aggatgtctt gcaactgcgg           120  
atcaagctgc ggctgcggct caagctgcaa gtgcggcaag aagtaccctg acctggagga           180  
gacgagcacc gccgcgcagg ccaccgctgt cctcggcgtg gcccgcgaga agaaggccgc           240  
gcccagttc gtcgaggccg cggcggagtc cggcggaggcc gcccAcgAcc tgcggctgcg           300  
gtagcaGctg caagtgcgac ccctgcaact gctgatcaca tcgatcgacg accatggata           360  
tgattattat ctatctagct tgtggtggtg gttgaacaat aataagcgag gccgagctgg           420  
ctgccataca taggtattgt gtggtgtgtg agagagagag agaaacagag ttcttcagtt           480  
tgctatctct ctctctgcat gtttggcgtc agtctttgtg ctcatgtacg tgtgtctaca           540  
tgcattgttg ttgatccgat tgcgtctgct gtaaccatat attaattggt ccacgatgat           600  
atgatttgat actatatata tatatatat

(2) INFORMATION FOR SEQ ID NO:4087:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4087:

Lys Lys Arg Cys Pro Trp Cys Ser Ser Ala Lys Gln Ile Arg Arg  
1                   5                   10                   15  
Leu Val Ser Leu Ile Leu Glu Glu Ile Glu Leu Leu Leu His His Lys  
                  20                   25                   30  
Val Glu Asp Val Leu Gln Leu Arg Ile Lys Leu Arg Leu Arg Leu Lys  
                  35                   40                   45  
Leu Gln Val Arg Gln Glu Val Pro  
                  50                   55

(2) INFORMATION FOR SEQ ID NO:4088:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4088:

```
Met Ser Cys Asn Cys Gly Ser Ser Cys Gly Cys Gly Ser Ser Cys Lys
1 5 10 15
Cys Gly Lys Lys Tyr Pro Asp Leu Glu Glu Thr Ser Thr Ala Ala Gln
 20 25 30
Ala Thr Val Val Leu Gly Val Ala Pro Glu Lys Lys Ala Ala Pro Glu
 35 40 45
Phe Val Glu Ala Ala Ala Glu Ser Gly Glu Ala Ala His Asp Leu Arg
 50 55 60
Leu Arg
65
```

(2) INFORMATION FOR SEQ ID NO:4089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..676
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4089:

```
actcctccaa accctagccc agagcagccg catcgaactc tacctgcctt tctctcgtcc 60
ctggcggcgg cggcaggatg gcggcttcta ctgcgaggac ggtgaaggat gtgaaccccc 120
acgagtttgt caaggcctac tccgcccata tcaaacgctc cggcaagatg gagcttcctg 180
agtgggttga cattgtgaag actgcgaggt tcaaggagct ccctccttat gacctgact 240
ggtactacat cagggctgca tctgtagcaa ggaagatcta cttgagacaa ggcattggtg 300
ttggtggctt ccagaagatt tatggtggcc gccagaggaa tgGctcacgc ccacctcact 360
tctgcaagag cagtggtgcc atttcacgca acatcctcca gcagctgcag gagatgggca 420
tcattgatgt cgatcccaag ggtggacggc gcatcacctc ccaggggaagg cgtgatctgg 480
accaggtggc tggaaaggggt gctggtgaag cttgagcaat ctcatatttg gtttctatga 540
tgtcatgttt gattgttgag atggctacac tttatttgca ctttgatta ggatttttgt 600
gttaagagaa ctcaaggcat tctagctatg gttcacactg tattttccct gagtacctat 660
ttatcaaaac ctattc
```

(2) INFORMATION FOR SEQ ID NO:4090:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4090:

```
Met Ala Ala Ser Thr Ala Arg Thr Val Lys Asp Val Asn Pro His Glu
1 5 10 15
Phe Val Lys Ala Tyr Ser Ala His Leu Lys Arg Ser Gly Lys Met Glu
```

20 25 30  
Leu Pro Glu Trp Val Asp Ile Val Lys Thr Ala Arg Phe Lys Glu Leu  
35 40 45  
Pro Pro Tyr Asp Pro Asp Trp Tyr Tyr Ile Arg Ala Ala Ser Val Ala  
50 55 60  
Arg Lys Ile Tyr Leu Arg Gln Gly Ile Gly Val Gly Gly Phe Gln Lys  
65 70 75 80  
Ile Tyr Gly Gly Arg Gln Arg Asn Gly Ser Arg Pro Pro His Phe Cys  
85 90 95  
Lys Ser Ser Gly Ala Ile Ser Arg Asn Ile Leu Gln Gln Leu Gln Glu  
100 105 110  
Met Gly Ile Ile Asp Val Asp Pro Lys Gly Gly Arg Arg Ile Thr Ser  
115 120 125  
Gln Gly Arg Arg Asp Leu Asp Gln Val Ala Gly Arg Val Ala Val Glu  
130 135 140  
Ala  
145

(2) INFORMATION FOR SEQ ID NO:4091:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1579473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4091:

Met Glu Leu Pro Glu Trp Val Asp Ile Val Lys Thr Ala Arg Phe Lys  
1 5 10 15  
Glu Leu Pro Pro Tyr Asp Pro Asp Trp Tyr Tyr Ile Arg Ala Ala Ser  
20 25 30  
Val Ala Arg Lys Ile Tyr Leu Arg Gln Gly Ile Gly Val Gly Gly Phe  
35 40 45  
Gln Lys Ile Tyr Gly Gly Arg Gln Arg Asn Gly Ser Arg Pro Pro His  
50 55 60  
Phe Cys Lys Ser Ser Gly Ala Ile Ser Arg Asn Ile Leu Gln Gln Leu  
65 70 75 80  
Gln Glu Met Gly Ile Ile Asp Val Asp Pro Lys Gly Gly Arg Arg Ile  
85 90 95  
Thr Ser Gln Gly Arg Arg Asp Leu Asp Gln Val Ala Gly Arg Val Ala  
100 105 110  
Val Glu Ala  
115

(2) INFORMATION FOR SEQ ID NO:4092:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1579474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4092:

Met Val Ala Ala Arg Gly Met Ala His Ala His Leu Thr Ser Ala Arg  
1 5 10 15  
Ala Val Val Pro Phe His Ala Thr Ser Ser Ser Ser Cys Arg Arg Trp  
20 25 30

Ala Ser Leu Met Ser Ile Pro Arg Val Asp Gly Ala Ser Pro Pro Arg  
35 40 45  
Glu Gly Val Ile Trp Thr Arg Trp Leu Glu Gly Leu Leu Leu Lys Leu  
50 55 60  
Glu Gln Ser His Ile Trp Phe Leu  
65 70

(2) INFORMATION FOR SEQ ID NO:4093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..321
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4093:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| aaataggaca cgccggctag tactgcgcca gccCactcca gcgctgaagg cctgcagcgc   | 60  |
| cagcgcagcg cytctctgct actgtgncgt ctgacgccgg tggggtgtga gccaactgcg   | 120 |
| agctgtgcc acccctgctg ccgcgkctga ccgccggccc cggaccgaga tggacgctcg    | 180 |
| gtgggcggtg ctgctcgcgc tgctggtcgc cagcggcggc gtccgtgtct gcgcgcgcgc   | 240 |
| tgkggccaaag ggcgccaaact ggctgggcgg gctgagccgc gcgtcgttcc ccaaggggtt | 300 |
| cgtgttcggg acggcgacgt c                                             |     |

(2) INFORMATION FOR SEQ ID NO:4094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4094:

|                                                             |  |
|-------------------------------------------------------------|--|
| Asn Arg Thr Arg Leu Val Leu Arg Gln Pro Thr Pro Ala Leu Lys |  |
| 1 5 10 15                                                   |  |
| Ala Cys Ser Ala Ser Ala Ala Xaa Leu Cys Tyr Cys Xaa Cys     |  |
| 20 25 30                                                    |  |

(2) INFORMATION FOR SEQ ID NO:4095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4095:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Asp Ala Arg Trp Ala Val Leu Leu Ala Leu Leu Val Ala Ser Gly |  |
| 1 5 10 15                                                       |  |
| Gly Val Arg Val Cys Ala Ala Ala Xaa Ala Lys Gly Ala Asn Trp Leu |  |
| 20 25 30                                                        |  |
| Gly Gly Leu Ser Arg Ala Ser Phe Pro Lys Gly Phe Val Phe Gly Thr |  |
| 35 40 45                                                        |  |
| Ala Thr                                                         |  |
| 50                                                              |  |

(2) INFORMATION FOR SEQ ID NO:4096:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4096:

(2) INFORMATION FOR SEO ID NO:4097:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4097:

(2) INFORMATION FOR SEO ID NO:4098:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4098:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | His | Pro | Ser | Pro | Phe | Pro | Pro | Pro | Arg | Arg | Arg | Glu | Thr | Pro | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Pro | Ile | His | His | His | Val | Ala | Pro | Pro | Pro | His | Pro | Ser | Pro | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ala | Gln | Gly | Tyr | Arg | Arg | Arg | Arg | Arg | Gly | Pro | Cys | Gly | Val | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Leu | Cys | Ser | Pro | Arg | Arg | Pro | Ala | Leu | Leu | Gly | Gly | Arg | Arg | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |



(2) INFORMATION FOR SEQ ID NO:4099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..67  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4099:

[illegible]

(2) INFORMATION FOR SEO ID NO:4100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 737 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..737  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4100:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| atagaaagtt | gaaaggatga | agttagagga  | tctcgttcca | ctgcgctacg | agacggcagc | 60  |
| gctgcggaac | aacaatggcg | atgatgcctc  | ctgcagcggc | gtcatccctc | gcctccactc | 120 |
| cccgcggcat | cgcgcctcgg | cctactcgca  | cggcatccct | gtgcatccgc | ttaggtgtcg | 180 |
| tgacggcgac | gctgttcgct | ggactggcgg  | cggcgtcgca | gccagtggag | cgtcacgcgg | 240 |
| cggtggtggt | cgcgatggcg | aagagggagc  | aggagctgga | ggggatccag | gccatgcaga | 300 |
| cggaacagct | ggaggaggag | gtggtagacc  | tcaaggggga | gcttttctcG | cttcgcctta | 360 |
| aGcgctcgcc | gcgccaggag | tccaagaaca  | gcgagttcgg | cgcgatgcgc | aagaggattg | 420 |
| ctcgtatggt | gactgtgaaa | agagagcggg  | aaactgaaca | aggaataaac | aagagattgt | 480 |
| ccagggagct | tgataggaaa | tggaaagcagg | gcatttgtgt | cagaccacca | ccatctctaa | 540 |
| gggagaacaa | agaggagtag | agagctgcaa  | aagaagcaat | ctgcaaaagt | cgtttcatgc | 600 |
| aagagtgttg | caagaagggt | cctttgtgat  | tccaaacttt | atttcattgt | tacgtattcc | 660 |
| atgtttacat | tttactaagc | attgctatcc  | gaatctgaat | ttcagtcggt | agtctcttct | 720 |
| gtaaatttga | tttatct    |             |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:4101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..161  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4101:



(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1579506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4103:

Met Pro Pro Ala Ala Ala Ser Ser Leu Ala Ser Thr Pro Arg Gly Ile  
1 5 10 15  
Ala Ala Pro Pro Thr Arg Thr Ala Ser Leu Cys Ile Arg Leu Gly Val  
20 25 30  
Val Thr Ala Thr Leu Phe Ala Gly Leu Ala Ala Ala Ser Gln Pro Val  
35 40 45  
Glu Arg His Ala Ala Val Val Val Ala Met Ala Lys Arg Glu Gln Glu  
50 55 60  
Leu Glu Gly Ile Gln Ala Met Thr Thr Glu Gln Leu Glu Glu Glu Val  
65 70 75 80  
Val Asp Leu Lys Gly Glu Leu Phe Leu Leu Arg Leu Lys Arg Ser Ala  
85 90 95  
Arg Gln Glu Phe Lys Asn Ser Glu Phe Gly Arg Met Arg Lys Arg Ile  
100 105 110  
Ala Arg Met Leu Thr Val Lys Arg Glu Arg Glu Thr Glu Gln Gly Ile  
115 120 125  
Asn Lys Arg Leu Ser Arg Glu Leu Asp Arg Lys Trp Lys Gln Gly Ile  
130 135 140  
Val Val Arg Pro Pro Pro Ser Leu Arg Glu Asn Lys Glu Glu  
145 150 155

(2) INFORMATION FOR SEQ ID NO:4104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 456 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..456

(D) OTHER INFORMATION: / Ceres Seq. ID 1579543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4104:

agccgtcatc gtttcgcgctc tgcctcagcc cgccgcaagg agaggagaca tcttcgagaa 60  
gctgaaatgg ctccctaaagc tgctcctgcc aagaagggtg atgccaagac ccaggccttg 120  
aagggttgcca aggctgtgaa gtctggggca gccaagaaga agaccaagaa gatccgcacg 180  
tctgtgacat ttcaccgccc caccgacctg aagaaggcta gggaccccaa gtaccacga 240  
atcagcacta ccggaaggaa caagcttgat cagtaccaa ttctcaagta ccccttacc 300  
acagaatcag cgatgaagaa gattgaagat aacaacactc tggctctcat tgttgacctc 360  
aaggcagaca agaagaagat caaggctgcc gtcaagaaga tgtatgacat ccaggcaaaag 420  
aaggtaaca ccttgatcag gcctgatggg aagaag

(2) INFORMATION FOR SEQ ID NO:4105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1579544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4105:

Ser Arg His Arg Phe Ala Ser Ala Ser Ala Arg Arg Lys Glu Arg Arg  
1 5 10 15  
His Leu Arg Glu Ala Glu Met Ala Pro Lys Ala Ala Pro Ala Lys Lys  
20 25 30

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Gly Asp Ala Lys Thr Gln Ala Leu Lys Val Ala Lys Ala Val Lys Ser  
35 40 45  
Gly Ala Ala Lys Lys Lys Thr Lys Lys Ile Arg Thr Ser Val Thr Phe  
50 55 60  
His Arg Pro Thr Thr Leu Lys Lys Ala Arg Asp Pro Lys Tyr Pro Arg  
65 70 75 80  
Ile Ser Thr Thr Gly Arg Asn Lys Leu Asp Gln Tyr Gln Ile Leu Lys  
85 90 95  
Tyr Pro Leu Thr Thr Glu Ser Ala Met Lys Lys Ile Glu Asp Asn Asn  
100 105 110  
Thr Leu Val Phe Ile Val Asp Leu Lys Ala Asp Lys Lys Lys Ile Lys  
115 120 125  
Ala Ala Val Lys Lys Met Tyr Asp Ile Gln Ala Lys Lys Val Asn Thr  
130 135 140  
Leu Ile Arg Pro Asp Gly Lys Lys  
145 150

(2) INFORMATION FOR SEQ ID NO:4106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1579545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4106:

Met Ala Pro Lys Ala Ala Pro Ala Lys Lys Gly Asp Ala Lys Thr Gln  
1 5 10 15  
Ala Leu Lys Val Ala Lys Ala Val Lys Ser Gly Ala Ala Lys Lys Lys  
20 25 30  
Thr Lys Lys Ile Arg Thr Ser Val Thr Phe His Arg Pro Thr Thr Leu  
35 40 45  
Lys Lys Ala Arg Asp Pro Lys Tyr Pro Arg Ile Ser Thr Thr Gly Arg  
50 55 60  
Asn Lys Leu Asp Gln Tyr Gln Ile Leu Lys Tyr Pro Leu Thr Thr Glu  
65 70 75 80  
Ser Ala Met Lys Lys Ile Glu Asp Asn Asn Thr Leu Val Phe Ile Val  
85 90 95  
Asp Leu Lys Ala Asp Lys Lys Lys Ile Lys Ala Ala Val Lys Lys Met  
100 105 110  
Tyr Asp Ile Gln Ala Lys Lys Val Asn Thr Leu Ile Arg Pro Asp Gly  
115 120 125  
Lys Lys  
130

(2) INFORMATION FOR SEQ ID NO:4107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 445 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..445

(D) OTHER INFORMATION: / Ceres Seq. ID 1579546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4107:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aaaaaaacc  | tactaacgc  | gtctcctctc | cagcgccgc  | cgtcgccgc  | gccctcctct | 60  |
| tgggtccgc  | gtccgtcgag | gtcatcatgg | tgagggtcag | tgtgctcaac | gatgcgtca  | 120 |
| agtccatgta | caatgcagag | aagaggggca | agaggcaggt | catgatcagg | ccgtcgtcca | 180 |



tggttcgcgc agcaccagca ccacgaggcc gccttcgcgc cgcgcgcga cgccgagctc 300  
gacgtgcgcg cgctcctccc cgacgactcc gtcgacctcc tcgacaccga cgacctcttc 360  
tacgcgcctg acgtccacca cccccacaac gccaaagccg cgctgctgcc cgggtacgac 420  
ctcgacatgc tcagggcgct gaggctcagc tccccccggg ccg

(2) INFORMATION FOR SEQ ID NO:4111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1579570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4111:

Met Ala Thr Ser Ser Leu Asn Pro Asn Ala Pro Leu Phe Ile Pro Ala  
1 5 10 15  
Ala Tyr Arg Gln Val Glu Glu Phe Ser Pro Glu Trp Tyr Glu Leu Val  
20 25 30  
Asn Thr Thr Ala Trp Phe Arg Asp His Trp Phe Arg Gln His Gln His  
35 40 45  
His Glu Ala Ala Phe Ala Ala Ala Ala Asp Ala Glu Leu Asp Val Ala  
50 55 60  
Ala Leu Leu Pro Asp Asp Ser Val Asp Leu Leu Asp Thr Asp Asp Leu  
65 70 75 80  
Phe Tyr Ala Pro Asp Val His His Pro His Asn Ala Lys Pro Ala Leu  
85 90 95  
Leu Pro Gly Tyr Asp Leu Asp Met Leu Arg Ala Leu Ser Leu Ser Ser  
100 105 110  
Pro Arg Ala  
115

(2) INFORMATION FOR SEQ ID NO:4112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1579571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4112:

Met Ser Ser Ser Thr Pro Pro Pro Gly Ser Gly Thr Thr Gly Ser Ala  
1 5 10 15  
Ser Thr Ser Thr Thr Arg Pro Pro Ser Pro Pro Pro Pro Thr Pro Ser  
20 25 30  
Ser Thr Ser Pro Arg Ser Ser Pro Thr Thr Pro Ser Thr Ser Ser Thr  
35 40 45  
Pro Thr Thr Ser Ser Thr Arg Leu Thr Ser Thr Thr Pro Thr Thr Pro  
50 55 60  
Ser Arg Arg Cys Cys Pro Gly Thr Thr Ser Thr Cys Ser Gly Arg  
65 70 75

(2) INFORMATION FOR SEQ ID NO:4113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(D) OTHER INFORMATION: / Ceres Seq. ID 1579576

|              |            |            |             |             |             |     |
|--------------|------------|------------|-------------|-------------|-------------|-----|
| aaaaaaaaacgc | ccaccacgcc | gccactcgca | accgcacacc  | agccctcgca  | accacaccacc | 60  |
| acgtccgaga   | cgtccgagat | ggagtctctc | gccgcgtacc  | tgtctgccgtg | cctgggcgcc  | 120 |
| ggcccgcccc   | ccacgctccc | gaccaaggac | gacgtgcgtc  | gcatactgag  | atccgtcagc  | 180 |
| gccgaggttg   | aggaggaccg | cctcgacctg | gtcttcgcc   | tcctagaggt  | taaggacatc  | 240 |
| gccgagctga   | tcgccaccgg | cggggagcat | ctcgccctacg | cgccgtcagg  | agccgctgct  | 300 |
| gccgtcggtt   | ccactcctgc | cgtctccgag | gtcgaggagg  | aggccacgaa  | ggaggaggat  | 360 |
| gaggacatcg   | ccctcttcaa | ctctctcgac | tgatcgtgca  | accctacgtg  | gaccgatcga  | 420 |
| tgcatacttc   | gtcctttgct | gctgccggtt | gcttggtgct  | ctgattgtac  | atttgaat    |     |

(D) OTHER INFORMATION: / Ceres Seq. ID 1579577

[illegible]

(D) OTHER INFORMATION: / Ceres Seq. ID 1579578

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asn | Ala | His | His | Ala | Ala | Thr | Arg | Asn | Arg | Thr | Pro | Ala | Leu | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | His | His | His | Val | Arg | Asp | Val | Arg | Asp | Gly | Val | Pro | Arg | Arg | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ala | Ala | Val | Pro | Gly | Arg | Arg | Pro | Gly | Pro | His | Ala | Pro | Asp | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

Gly Arg Arg Ala Ser His Pro Glu Ile Arg Gln Arg Arg Gly Gly Gly  
50 55 60  
Gly Pro Pro Arg Pro Gly Leu Arg Pro Pro Arg Gly  
65 70 75

(2) INFORMATION FOR SEQ ID NO:4116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1579579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4116:

Met Glu Phe Leu Ala Ala Tyr Leu Leu Pro Cys Leu Gly Ala Gly Pro  
1 5 10 15  
Ala Pro Thr Leu Pro Thr Lys Asp Asp Val Arg Arg Ile Leu Arg Ser  
20 25 30  
Val Ser Ala Glu Val Glu Glu Asp Arg Leu Asp Leu Val Phe Ala Leu  
35 40 45  
Leu Glu Val Lys Asp Ile Ala Glu Leu Ile Ala Thr Gly Gly Glu His  
50 55 60  
Leu Ala Tyr Ala Pro Ser Gly Ala Ala Ala Val Val Ala Thr Pro  
65 70 75 80  
Ala Ala Ala Glu Val Glu Glu Glu Ala Thr Lys Glu Glu Asp Glu Asp  
85 90 95  
Ile Ala Leu Phe Asn Leu Phe Asp  
100

(2) INFORMATION FOR SEQ ID NO:4117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..448

(D) OTHER INFORMATION: / Ceres Seq. ID 1579584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4117:

gctgtctttc ttctgctctt ccacgcgcc agtggtttga gaagctggtc ggcgctccta 60  
gatcccttcg cctctctcgc gttcgaggct aggtagccgc caccatgagc cgctcggggc 120  
agcctocgga tctcaagaag tacatggaca agaagcttca gattaagctg aatgcaaacc 180  
gtgttggttat tggcacactt cggggattcg accagttcat gaatctggtg atcgacaaca 240  
ctgtggagggt caatggaaat gacaagacag atattggaat ggtgggttatc aggggaaaca 300  
gtgttggtcat gatcgaggca ctggagccag ttgccaagtc gcagtgaatc cttatttttc 360  
agctgatata gtcgcagcat gaaaactgat gtaaagtcta tgagtgaacc ctgttggtact 420  
tgcatttgta attgaagtct gtcgcttt

(2) INFORMATION FOR SEQ ID NO:4118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1579585

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4118:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Arg | Ser | Gly | Gln | Pro | Pro | Asp | Leu | Lys | Lys | Tyr | Met | Asp | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Leu | Gln | Ile | Lys | Leu | Asn | Ala | Asn | Arg | Val | Val | Ile | Gly | Thr | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Gly | Phe | Asp | Gln | Phe | Met | Asn | Leu | Val | Ile | Asp | Asn | Thr | Val | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Asn | Gly | Asn | Asp | Lys | Thr | Asp | Ile | Gly | Met | Val | Val | Ile | Arg | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asn | Ser | Val | Val | Met | Ile | Glu | Ala | Leu | Glu | Pro | Val | Ala | Lys | Ser | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

(2) INFORMATION FOR SEQ ID NO:4119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4119:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Lys | Lys | Leu | Gln | Ile | Lys | Leu | Asn | Ala | Asn | Arg | Val | Val | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Thr | Leu | Arg | Gly | Phe | Asp | Gln | Phe | Met | Asn | Leu | Val | Ile | Asp | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Val | Glu | Val | Asn | Gly | Asn | Asp | Lys | Thr | Asp | Ile | Gly | Met | Val | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Arg | Gly | Asn | Ser | Val | Val | Met | Ile | Glu | Ala | Leu | Glu | Pro | Val | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Lys | Ser | Gln |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:4120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4120:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Leu | Val | Ile | Asp | Asn | Thr | Val | Glu | Val | Asn | Gly | Asn | Asp | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Asp | Ile | Gly | Met | Val | Val | Ile | Arg | Gly | Asn | Ser | Val | Val | Met | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ala | Leu | Glu | Pro | Val | Ala | Lys | Ser | Gln |     |     |     |     |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:4121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..517

(D) OTHER INFORMATION: / Ceres Seq. ID 1579596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4121:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| ccgtgaaacc aacgcccctc tctccccgcg cagagaccc atcgcgaaatg gaagttgctc   | 60  |
| ctgcggtgaa gcaactcctc cccatggcgc agggcccca ctccccgtcc tctccacca     | 120 |
| cctcctcctc gccctcgccc tcggccgcgc cgcggtcccc gccgcccgcg cagcagcagt   | 180 |
| cgcagtcgca ggcgcccgtg ccgcgcacatc togcacaccac gcccttcccc accaccttcg | 240 |
| tgcaggccga cacggccagc ttcaaggagg tgcgtccagag gctcaccggc tccgacacgc  | 300 |
| cgccgcctgc ccagaagccc gccaaagacc acggccacca ccaccaccac cacggcggcg   | 360 |
| gcggcgctcg gcccaagaag ccggccttca agctctacga gcgccggatc ggcaagaaca   | 420 |
| acctcaagat gatcgcgccg ctggcggggc cgtcgccgcg gaaggcggcg ccggagggtc   | 480 |
| tgctgcccag cgtgctcgac ttccctttcn ctggcgc                            |     |

(2) INFORMATION FOR SEQ ID NO:4122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..172

(D) OTHER INFORMATION: / Ceres Seq. ID 1579597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4122:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | Glu | Thr | Asn | Ala | Pro | Leu | Ser | Pro | Arg | Thr | Arg | Pro | Ile | Ala | Asn |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Gly | Ser | Cys | Ser | Cys | Gly | Glu | Ala | Thr | Pro | Pro | His | Gly | Ala | Gly | Pro |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |
| Gln | Leu | Pro | Val | Leu | Leu | His | His | Leu | Leu | Leu | Ala | Leu | Ala | Leu | Gly |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Arg | Ala | Val | Pro | Ala | Ala | Ala | Pro | Ala | Ala | Val | Ala | Val | Ala | Gly |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Ala | Arg | Ala | Ala | His | His | Arg | His | His | Ala | Leu | Pro | His | His | Leu | Arg |  |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |  |
| Ala | Gly | Arg | His | Gly | Gln | Leu | Gln | Gly | Gly | Arg | Pro | Glu | Ala | His | Arg |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Leu | Arg | His | Ala | Ala | Ala | Cys | Pro | Glu | Ala | Arg | Gln | Asp | Pro | Arg | Pro |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Pro | Pro | Pro | Pro | Pro | Arg | Arg | Arg | Arg | Arg | Arg | Ala | Gln | Glu | Ala | Gly |  |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |  |
| Leu | Gln | Ala | Leu | Arg | Ala | Pro | Asp | Arg | Gln | Glu | Gln | Pro | Gln | Asp | Asp |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |  |
| Arg | Ala | Ala | Gly | Gly | Ala | Val | Ala | Ala | Glu | Gly | Ala | Gly | Gly | Ala |     |  |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Val | Ala | Gln | Arg | Ala | Arg | Leu | Pro | Phe | Xaa | Trp | Arg |     |     |     |     |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:4123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1579598

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4123:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Lys | Pro | Thr | Pro | Leu | Ser | Pro | Arg | Ala | Arg | Asp | Pro | Ser | Arg | Met |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |

Glu Val Ala Pro Ala Val Lys Gln Leu Leu Pro Met Ala Gln Gly Pro  
20 25 30  
Asn Ser Pro Ser Ser Ser Thr Thr Ser Ser Ser Pro Ser Pro Ser Ala  
35 40 45  
Ala Ala Pro Ser Pro Pro Pro Arg Gln Gln Gln Ser Gln Ser Gln Ala  
50 55 60  
Pro Val Pro Arg Ile Ile Asp Thr Thr Pro Phe Pro Thr Thr Phe Val  
65 70 75 80  
Gln Ala Asp Thr Ala Ser Phe Lys Glu Val Val Gln Arg Leu Thr Gly  
85 90 95  
Ser Asp Thr Pro Pro Pro Ala Gln Lys Pro Ala Lys Thr His Gly His  
100 105 110  
His His His His His Gly Gly Gly Gly Val Gly Pro Lys Lys Pro Ala  
115 120 125  
Phe Lys Leu Tyr Glu Arg Arg Ile Gly Lys Asn Asn Leu Lys Met Ile  
130 135 140  
Ala Pro Leu Ala Gly Pro Ser Pro Arg Lys Ala Ala Pro Glu Val Leu  
145 150 155 160  
Ser Pro Ser Val Leu Asp Phe Pro Phe Xaa Gly  
165 170

(2) INFORMATION FOR SEQ ID NO:4124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4124:

Met Glu Val Ala Pro Ala Val Lys Gln Leu Leu Pro Met Ala Gln Gly  
1 5 10 15  
Pro Asn Ser Pro Ser Ser Ser Thr Thr Ser Ser Ser Pro Ser Pro Ser  
20 25 30  
Ala Ala Ala Pro Ser Pro Pro Pro Arg Gln Gln Gln Ser Gln Ser Gln  
35 40 45  
Ala Pro Val Pro Arg Ile Ile Asp Thr Thr Pro Phe Pro Thr Thr Phe  
50 55 60  
Val Gln Ala Asp Thr Ala Ser Phe Lys Glu Val Val Gln Arg Leu Thr  
65 70 75 80  
Gly Ser Asp Thr Pro Pro Pro Ala Gln Lys Pro Ala Lys Thr His Gly  
85 90 95  
His His His His His Gly Gly Gly Gly Val Gly Pro Lys Lys Pro  
100 105 110  
Ala Phe Lys Leu Tyr Glu Arg Arg Ile Gly Lys Asn Asn Leu Lys Met  
115 120 125  
Ile Ala Pro Leu Ala Gly Pro Ser Pro Arg Lys Ala Ala Pro Glu Val  
130 135 140  
Leu Ser Pro Ser Val Leu Asp Phe Pro Phe Xaa Gly  
145 150 155

(2) INFORMATION FOR SEQ ID NO:4125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

00000000-00000000

(B) LOCATION: 1..487

(D) OTHER INFORMATION: / Ceres Seq. ID 1579610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4125:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| attccgagtc tactattgta cctctccgtg gggcgcatcc gccatttgtg ccaattctag | 60  |
| catcagcgtc cgatcgacca ggagtgtgaa gtaggtgtgg gagatcaagg gcacgagcga | 120 |
| cccggccaag tttagtgtgg attttaaaat caagttcctt acagttggtg gaaagaaact | 180 |
| aaagttgaca atatgggata ccgctggcca ggagaggttt aggacaataa ctagttctta | 240 |
| ctacagaggt gctcagggaa ttattttagt atatgatgtc acaaagagag agagtttctc | 300 |
| aaatttggct gatgtttgga ctaaggaaat agaagcaaac tcaacaaaca aagactgcat | 360 |
| aaaaatgctt gttggaaaca aagttgacaa ggatgatgaa agaatggtca cagaagaaga | 420 |
| aggtcttgct tttgctgaag aatctggttg tctgtttctt gagagcagtg caaaacacga | 480 |
| gaaaatg                                                           |     |

(2) INFORMATION FOR SEQ ID NO:4126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..30

(D) OTHER INFORMATION: / Ceres Seq. ID 1579611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4126:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Arg | Val | Tyr | Tyr | Cys | Thr | Ser | Pro | Trp | Gly | Arg | Ser | Ala | Ile | Cys |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Asn | Ser | Ser | Ile | Ser | Val | Arg | Ser | Thr | Arg | Ser | Val | Lys |     |     |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |

(2) INFORMATION FOR SEQ ID NO:4127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..41

(D) OTHER INFORMATION: / Ceres Seq. ID 1579612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4127:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Val | Gly | Asn | Lys | Val | Asp | Lys | Asp | Asp | Glu | Arg | Met | Val | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Glu | Glu | Gly | Leu | Ala | Phe | Ala | Glu | Glu | Ser | Gly | Cys | Leu | Phe | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ser | Ser | Ala | Lys | His | Glu | Lys | Met |     |     |     |     |     |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:4128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..31

(D) OTHER INFORMATION: / Ceres Seq. ID 1579613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4128:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Lys | Glu | Trp | Ser | Gln | Lys | Lys | Lys | Val | Leu | Leu | Leu | Leu | Lys |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Leu | Val | Val | Cys | Phe | Leu | Arg | Ala | Val | Gln | Asn | Thr | Arg | Lys |     |

20 25 30

(2) INFORMATION FOR SEQ ID NO:4129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 490 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..490

(D) OTHER INFORMATION: / Ceres Seq. ID 1579614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4129:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| agtggccgcc  | cgtgtcgtgt | agtgtgtagt | cgcagcagct | agcgcccggc | cggccagtcg | 60  |
| agtgagtcca  | tcctccatcg | ccatccaatg | gccgccaccg | cctgagcatg | agcatcctcc | 120 |
| gcgcgccgcc  | gccctgcttc | tcgtccccac | tcaggctcag | ggtcgcgggt | gccaagccgc | 180 |
| tggcgccccc  | catgcggcgc | cagctgctgc | gcgcgcaggc | cacctacaac | gtgaagctga | 240 |
| tcacgccgga  | gggggaggtg | gagctgcagg | tgcccagcga | cgtctacatc | ctggacttcg | 300 |
| ccgaggagga  | aggcatcgac | ctgcccttct | cctgccgtgc | ggggtcctgc | tcctcctgcg | 360 |
| ccggcaagggt | cgtctctggc | tcgctcgacc | agtccgacca | gagcttcctc | aacgacaacc | 420 |
| aggtcgcgca  | cggttgggtg | ctcactgcgc | tgcgtacccc | acctccgacg | tcgtcatcga | 480 |
| gacgcacaag  |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:4130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1579615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4130:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ile | Leu | Arg | Ala | Pro | Pro | Pro | Cys | Phe | Ser | Ser | Pro | Leu | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Arg | Val | Ala | Val | Ala | Lys | Pro | Leu | Ala | Ala | Pro | Met | Arg | Arg | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Leu | Arg | Ala | Gln | Ala | Thr | Tyr | Asn | Val | Lys | Leu | Ile | Thr | Pro | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Glu | Val | Glu | Leu | Gln | Val | Pro | Asp | Asp | Val | Tyr | Ile | Leu | Asp | Phe |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Glu | Glu | Glu | Gly | Ile | Asp | Leu | Pro | Phe | Ser | Cys | Arg | Ala | Gly | Ser |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Cys | Ser | Ser | Cys | Ala | Gly | Lys | Val | Val | Ser | Gly | Ser | Val | Asp | Gln | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asp | Gln | Ser | Phe | Leu | Asn | Asp | Asn | Gln | Val | Ala | Asp | Gly | Trp | Val | Leu |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Thr | Ala | Leu | Arg | Thr | Pro | Pro | Pro | Thr | Ser | Ser | Ser | Arg | Arg | Thr |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |

(2) INFORMATION FOR SEQ ID NO:4131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1579616

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4131:

```
Met Arg Arg Gln Leu Leu Arg Ala Gln Ala Thr Tyr Asn Val Lys Leu
1 5 10 15
Ile Thr Pro Glu Gly Glu Val Glu Leu Gln Val Pro Asp Asp Val Tyr
 20 25 30
Ile Leu Asp Phe Ala Glu Glu Glu Gly Ile Asp Leu Pro Phe Ser Cys
 35 40 45
Arg Ala Gly Ser Cys Ser Ser Cys Ala Gly Lys Val Val Ser Gly Ser
 50 55 60
Val Asp Gln Ser Asp Gln Ser Phe Leu Asn Asp Asn Gln Val Ala Asp
65 70 75 80
Gly Trp Val Leu Thr Ala Leu Arg Thr Pro Pro Pro Thr Ser Ser Ser
 85 90 95
Arg Arg Thr
```

(2) INFORMATION FOR SEQ ID NO:4132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..468
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4132:

```
acacaatttc accgaaatcc tccaatacc caccctacga atcttcttct cgggctcctt 60
ctgcgccatc ttctggctca agaagcgcg cctcatgccg ggcctcactt tctctaata 120
gctcatctcc cgggacgagg gcctccactg cgacttcgcc tgccctcctt atgacctct 180
tcggggcaag ctcgatgagt cccgcgtccg cgagatcggt gccgacgccg tcgacatcg 240
gcgtgagttc gtttgcgacg cgctccccgt cgcgctggtc ggaatgaacg gcgggctcat 300
gagccagtac atcgagttcg tcgcgcaccg cctgctcatg gcgctggggc acaggaagat 360
gtacaacgtc gccaacccct tcgactggat ggagctcatt tccctgcagg ccaaagacta 420
acttctttga gaagcgcgtc gggwagtacc agaagcgctc cgtaatgt
```

(2) INFORMATION FOR SEQ ID NO:4133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4133:

```
His Asn Phe Thr Glu Ile Leu Gln Tyr Pro Thr Leu Arg Ile Phe Phe
1 5 10 15
Ser Gly Ser Phe Cys Ala Ile Phe Trp Leu Lys Lys Arg Gly Leu Met
 20 25 30
Pro Gly Leu Thr Phe Ser Asn Glu Leu Ile Ser Arg Asp Glu Gly Leu
 35 40 45
His Cys Asp Phe Ala Cys Leu Leu Tyr Asp Leu Leu Arg Gly Lys Leu
50 55 60
Asp Glu Ser Arg Val Arg Glu Ile Val Ala Asp Ala Val Asp Ile Glu
65 70 75 80
Arg Glu Phe Val Cys Asp Ala Leu Pro Val Ala Leu Val Gly Met Asn
 85 90 95
Gly Gly Leu Met Ser Gln Tyr Ile Glu Phe Val Ala Asp Arg Leu Leu
 100 105 110
```

Met Ala Leu Gly His Arg Lys Met Tyr Asn Val Ala Asn Pro Phe Asp  
115 120 125

Trp Met Glu Leu Ile Ser Leu Gln Ala Lys Asp  
130 135

(2) INFORMATION FOR SEQ ID NO:4134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1579620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4134:

Thr Ile Ser Pro Lys Ser Ser Asn Thr Pro Pro Tyr Glu Ser Ser Ser  
1 5 10 15  
Arg Ala Pro Ser Ala Pro Ser Ser Gly Ser Arg Ser Ala Ala Ser Cys  
20 25 30  
Arg Ala Ser Leu Ser Leu Met Ser Ser Ser Pro Gly Thr Arg Ala Ser  
35 40 45  
Thr Ala Thr Ser Pro Ala Ser Phe Met Thr Ser Phe Gly Ala Ser Ser  
50 55 60  
Met Ser Pro Ala Ser Ala Arg Ser Leu Pro Thr Pro Ser Thr Ser Ser  
65 70 75 80  
Val Ser Ser Phe Ala Thr Arg Ser Pro Ser Arg Trp Ser Glu  
85 90

(2) INFORMATION FOR SEQ ID NO:4135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1579621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4135:

Met Pro Gly Leu Thr Phe Ser Asn Glu Leu Ile Ser Arg Asp Glu Gly  
1 5 10 15  
Leu His Cys Asp Phe Ala Cys Leu Leu Tyr Asp Leu Leu Arg Gly Lys  
20 25 30  
Leu Asp Glu Ser Arg Val Arg Glu Ile Val Ala Asp Ala Val Asp Ile  
35 40 45  
Glu Arg Glu Phe Val Cys Asp Ala Leu Pro Val Ala Leu Val Gly Met  
50 55 60  
Asn Gly Gly Leu Met Ser Gln Tyr Ile Glu Phe Val Ala Asp Arg Leu  
65 70 75 80  
Leu Met Ala Leu Gly His Arg Lys Met Tyr Asn Val Ala Asn Pro Phe  
85 90 95  
Asp Trp Met Glu Leu Ile Ser Leu Gln Ala Lys Asp  
100 105

(2) INFORMATION FOR SEQ ID NO:4136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..445

(D) OTHER INFORMATION: / Ceres Seq. ID 1579629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4136:

|             |            |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|------------|-----|
| aaggccagtc  | tgagtgtg   | cg         | ttcgattcgc | ttgtgctgca | gctaggggtt | agagggtttc | 60  |
| tgggcgcgga  | gcgaggagcg | gcggcggcta | tggctgcggc | ggaggaggag | atcgcggtga |            | 120 |
| aggagccgct  | ggatctgata | cgcctcagcc | tgcacgagcg | catctacgtc | aagctccgat |            | 180 |
| ccgaccgcga  | gctgcgcggc | aagctccatg | cgtatgatca | acatttaa   | ac         | atgatacttg | 240 |
| gagatgttga  | agaggtcgtg | acaactgttg | agatagatga | tgaacatat  | gaagaaattg |            | 300 |
| tgcgcgataa  | tctttgcaga | ccacgaaacg | cactatcccc | tttctttttg | tccgaggtga |            | 360 |
| tggtgtcata  | ttggtttctc | cacccttcg  | tacggcayga | astttgaagt | tagatcatgc |            | 420 |
| tggttggttaa | ttatgataac | tggtg      |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:4137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1579630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4137:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Gln | Ser | Glu | Cys | Ala | Phe | Asp | Ser | Leu | Val | Leu | Gln | Leu | Gly | Phe |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Gly | Phe | Leu | Gly | Ala | Glu | Arg | Glu | Ala | Ala | Ala | Ala | Met | Ala | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Glu | Glu | Glu | Ile | Ala | Val | Lys | Glu | Pro | Leu | Asp | Leu | Ile | Arg | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Leu | Asp | Glu | Arg | Ile | Tyr | Val | Lys | Leu | Arg | Ser | Asp | Arg | Glu | Leu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Gly | Lys | Leu | His | Ala | Tyr | Asp | Gln | His | Leu | Asn | Met | Ile | Leu | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asp | Val | Glu | Glu | Val | Thr | Thr | Val | Glu | Ile | Asp | Asp | Glu | Thr | Tyr |     |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Glu | Ile | Val | Arg | Asp | Asn | Leu | Cys | Arg | Pro | Arg | Asn | Ala | Leu | Ser |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Pro | Phe | Phe | Leu | Ser | Glu | Val | Met | Val | Ser | Tyr | Trp | Phe | Leu | His | Pro |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Phe | Val | Arg | Xaa | Glu | Xaa |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 130 |

(2) INFORMATION FOR SEQ ID NO:4138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1579631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4138:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Ala | Glu | Glu | Glu | Ile | Ala | Val | Lys | Glu | Pro | Leu | Asp | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Arg | Leu | Ser | Leu | Asp | Glu | Arg | Ile | Tyr | Val | Lys | Leu | Arg | Ser | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Glu | Leu | Arg | Gly | Lys | Leu | His | Ala | Tyr | Asp | Gln | His | Leu | Asn | Met |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |



Ile Leu Gly Asp Val Glu Glu Val Val Thr Thr Val Glu Ile Asp Asp  
50 55 60  
Glu Thr Tyr Glu Glu Ile Val Arg Asp Asn Leu Cys Arg Pro Arg Asn  
65 70 75 80  
Ala Leu Ser Pro Phe Phe Leu Ser Glu Val Met Val Ser Tyr Trp Phe  
85 90 95  
Leu His Pro Phe Val Arg Xaa Glu Xaa  
100 105

(2) INFORMATION FOR SEQ ID NO:4139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..408
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4139:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atataaaagc tgccctgcgc acctagcacc agccctgccca ctccactcct accccacaca | 60  |
| gaagcggcgg cggcggagca aasgcaggcg aaggcgaggg tgtgagggaa ggagcaccag  | 120 |
| ccatggtgca cgtcaacttc taccgcaact atggtaagac gttcaagaaa ccaaggcgtc  | 180 |
| cttatgagaa ggagcgtctt gatgctgaac tgaagctggc cggtgagtat gggctgaggt  | 240 |
| gcaagcgtga gctttggagg gtccagtatg cactgagcag gatccgtaat gctgcaaggc  | 300 |
| acttgctcac ccttgacgag aagaaccccc gtcgtatctt tgagggtgag gcgcttcttc  | 360 |
| gccgcatgaa ccgctatggg ctgcttgctg agggtcagaa caagcttg               |     |

(2) INFORMATION FOR SEQ ID NO:4140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4140:

Tyr Lys Ser Cys Pro Arg Asp Leu Ala Pro Ala Leu Pro Leu His Ser  
1 5 10 15  
Tyr Pro Thr Gln Lys Arg Arg Arg Arg Ser Lys Xaa Arg Arg Arg Arg  
20 25 30  
Gly Cys Glu Gly Arg Ser Thr Ser His Gly Ala Arg Gln Leu Leu Pro  
35 40 45  
Gln Leu Trp  
50

(2) INFORMATION FOR SEQ ID NO:4141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4141:

Met Val His Val Asn Phe Tyr Arg Asn Tyr Gly Lys Thr Phe Lys Lys  
1 5 10 15

(2) INFORMATION FOR SEO ID NO:4142:

(A) LENGTH: 467 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1579635

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| cgaaaaaatcc | atcgagctgc | cgcgcgcg   | cagttaagct | cacacatcag  | ctagctcacc  | 60  |
| ttggacggcc  | gaccaggta  | gttgcgagc  | atggcgggat | acaaagcgtc  | gggcggcacg  | 120 |
| gcgctcggcg  | tgttcctggc | tgttgccgcg | ctcctcgccg | cggcggcgat  | ggcgggtggac | 180 |
| gacgagcaca  | tgtaccactg | gaagtgtctc | aactcgtgca | cggggaagtg  | ccgcgacgag  | 240 |
| gacgcctttg  | acgacggcca | ccgttcgggg | gattcgaaag | tctcttcogt  | cgtctctggc  | 300 |
| ggcaagtgcg  | acaacagggt | cctcagcgag | tgcttcgagg | acctgccggc  | catctgctac  | 360 |
| caccagtgca  | tcgtcagcaa | gtgcctctgc | ttcccaccct | ttagcacaaga | gaaaacgatg  | 420 |
| tqcatgaaga  | qctqctqcaa | caagtqcttc | caccacggcc | cqccagc     |             |     |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1579636

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Tyr | Lys | Ala | Ser | Gly | Gly | Thr | Ala | Leu | Gly | Val | Val | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Val | Ala | Ala | Leu | Leu | Ala | Ala | Ala | Ala | Met | Ala | Val | Asp | Asp | Glu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| His | Met | Tyr | His | Trp | Lys | Cys | Phe | Asn | Ser | Cys | Thr | Gly | Lys | Cys | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Glu | Asp | Ala | Phe | Asp | Asp | Gly | His | Arg | Ser | Gly | Asp | Ser | Asn | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Ser | Val | Val | Ser | Gly | Gly | Lys | Cys | Asn | Asn | Arg | Cys | Leu | Ser | Glu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Cys | Phe | Glu | Asp | Leu | Pro | Ala | Ile | Cys | Tyr | His | Gln | Cys | Val | Val | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Cys | Leu | Cys | Phe | Pro | Pro | Phe | Ser | Lys | Glu | Lys | Thr | Met | Cys | Met |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Lys | Ser | Cys | Cys | Asn | Lys | Cys | Phe | His | His | Gly | Pro | Pro |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4146:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| atccggtccg gacacccgag taccgacctg cttgctcacc gcgcgcaccc gccaaagcaa | 60  |
| ccaaccgcc catcgcccc gtcctgttcc ggcaggcagc cgctcccgtc cccgctcccc   | 120 |

caccccactc cccctcgcgc ggcgcgttct cagatccccc gcccggttgg caccggcacc 180  
ccggtccgaa atgcgaggag ccttgtagcg cctcggagca cggacggaat cgcgccgcat 240  
gcatcccaag cccgagggcg gcggcgacga cgacggggcc gccgcggagg tgggctcccc 300  
gcggtccggc tacttcggc agcggagcat gcacgccgcc gccgcgcccg cggatccgga 360  
ggcggcgcg cgcgcgttcc acgtcgagaa cccgccttgc tccgcggcg gggggctgcg 420  
gccagcgagt ccgtcaccaa gctggagtcg

(2) INFORMATION FOR SEQ ID NO:4147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1579644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4147:

Ile Arg Ser Gly His Pro Ser Thr Asp Leu Leu Ala His Arg Ala His  
1 5 10 15  
Pro Pro Lys Gln Pro Thr Ala Pro Ser Ser Pro Ser Cys Ser Gly Arg  
20 25 30  
Gln Pro Leu Pro Leu Pro Leu Pro His Pro Thr Pro Pro Arg Ala Ala  
35 40 45  
Arg Ser Gln Ile Pro Arg Pro Val Gly Thr Gly Thr Pro Val Arg Asn  
50 55 60  
Ala Arg Ser Leu Val Ala Pro Arg Ser Thr Asp Gly Ile Ala Pro His  
65 70 75 80  
Ala Ser Gln Ala Arg Gly Arg Arg Arg Arg Arg Arg Gly Arg Arg Gly  
85 90 95  
Gly Gly Leu Pro Ala Val Arg Leu Leu Pro Ala Ala Glu His Ala Arg  
100 105 110  
Arg Arg Arg Arg Arg Gly Ser Gly Gly Gly Ala Pro Ala Val Pro Arg  
115 120 125  
Arg Glu Pro Ala Leu Leu Arg Arg Arg Gly Ala Ala Ala Ser Glu Ser  
130 135 140  
Val Thr Lys Leu Glu Ser  
145 150

(2) INFORMATION FOR SEQ ID NO:4148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1579645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4148:

Pro Val Arg Thr Pro Glu Tyr Arg Pro Ala Cys Ser Ser Arg Ala Pro  
1 5 10 15  
Ala Lys Ala Thr Asn Arg Pro Ile Val Pro Val Leu Phe Arg Gln Ala  
20 25 30  
Ala Ala Pro Ala Pro Ala Pro Pro His Ser Pro Ser Arg Gly Ala  
35 40 45  
Phe Ser Asp Pro Pro Pro Gly Trp His Arg His Pro Gly Pro Lys Cys  
50 55 60  
Glu Glu Pro Cys Ser Ala Ser Glu His Gly Arg Asn Arg Ala Ala Cys  
65 70 75 80  
Ile Pro Ser Pro Arg Ala Ala Ala Thr Thr Thr Gly Pro Pro Arg Arg

85 90 95  
Trp Ala Pro Arg Gly Pro Ala Thr Ser Gly Ser Gly Ala Cys Thr Pro  
100 105 110  
Pro Pro Pro Pro Arg Ile Arg Arg Arg Arg Ala Gly Arg Ser Thr Ser  
115 120 125  
Arg Thr Arg Leu Ala Pro Pro Ala Gly Gly Cys Gly Gln Arg Val Arg  
130 135 140  
His Gln Ala Gly Val  
145

(2) INFORMATION FOR SEQ ID NO:4149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..475
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4149:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| cttcgacggc cacggcggcg ccgaggtggc cagctactgc cgggagaggc tccaggtgct  | 60  |
| cctgagggcag gaactgaggc tgctcagcaa ggatttgggg gagacaagcg aggccgacat | 120 |
| gaaggagcac tgggacgagc tggtcaccag gtgtttccag aggctggatg acgaagtgtc  | 180 |
| ggggcagggc agcaggctcg tcggtggcgt ccaggagaca cggccggtgg ccgccgagaa  | 240 |
| cgtcggctcc actgcggttg tcgccgtcgt gtgctcctcc catgtggtgg tcgccaaactg | 300 |
| cggggattcg cgtgttggtt tctgccgtgg aaaggagccc ttagagctgt cgattgatca  | 360 |
| taaggtgagc tttttttag ctaagctgga gctatgatgc ttatggtgtt catccgattt   | 420 |
| ggttgtttca gcctgacagg aaggatgaac gagcgaggat tgaggccctg gggggg      |     |

(2) INFORMATION FOR SEQ ID NO:4150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4150:

Phe Asp Gly His Gly Gly Ala Glu Val Ala Ser Tyr Cys Arg Glu Arg  
1 5 10 15  
Leu Gln Val Leu Leu Arg Gln Glu Leu Arg Leu Leu Ser Lys Asp Leu  
20 25 30  
Gly Glu Thr Ser Glu Ala Asp Met Lys Glu His Trp Asp Glu Leu Phe  
35 40 45  
Thr Arg Cys Phe Gln Arg Leu Asp Asp Glu Val Ser Gly Gln Ala Ser  
50 55 60  
Arg Leu Val Gly Gly Val Gln Glu Thr Arg Pro Val Ala Ala Glu Asn  
65 70 75 80  
Val Gly Ser Thr Ala Val Val Ala Val Val Cys Ser Ser His Val Val  
85 90 95  
Val Ala Asn Cys Gly Asp Ser Arg Val Val Leu Cys Arg Gly Lys Glu  
100 105 110  
Pro Leu Glu Leu Ser Ile Asp His Lys Val Ser Phe Phe Val Ala Lys  
115 120 125  
Leu Glu Leu  
130

(2) INFORMATION FOR SEQ ID NO:4151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..92  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579648  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4151:  
Met Lys Glu His Trp Asp Glu Leu Phe Thr Arg Cys Phe Gln Arg Leu  
1 5 10 15  
Asp Asp Glu Val Ser Gly Gln Ala Ser Arg Leu Val Gly Gly Val Gln  
20 25 30  
Glu Thr Arg Pro Val Ala Ala Glu Asn Val Gly Ser Thr Ala Val Val  
35 40 45  
Ala Val Val Cys Ser Ser His Val Val Val Ala Asn Cys Gly Asp Ser  
50 55 60  
Arg Val Val Leu Cys Arg Gly Lys Glu Pro Leu Glu Leu Ser Ile Asp  
65 70 75 80  
His Lys Val Ser Phe Phe Val Ala Lys Leu Glu Leu  
85 90

(2) INFORMATION FOR SEQ ID NO:4152:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 420 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..420  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4152:

|             |            |             |            |            |             |     |
|-------------|------------|-------------|------------|------------|-------------|-----|
| aaaaaaaaaca | cacggtacgc | gcttctctctc | ctcgcttgcc | gccgccgccg | ccgccgcgat  | 60  |
| ggaaaaggag  | aagctctcgt | tctccatata  | ctcctcgaag | cagcggcccc | ccaagcctcc  | 120 |
| cgcacgacct  | gcggccgcgc | cagacgacga  | tgacctccgc | tccgcgcccc | ctccggggcca | 180 |
| gcagtacgtc  | accgagttcg | atccgtccca  | aaccctagcc | gccgcctgcg | cggcgcgcgc  | 240 |
| cgtcacgcgc  | ccgctcccca | actccggcaa  | ctycctcacc | caccgcccac | gcaaaccgtc  | 300 |
| ctcgtcctcc  | acccctgagg | aggaggccgc  | cctcgccgcg | gaatccggcg | gctggggccc  | 360 |
| cgcyttcgtc  | ctcgacacct | cgaccgctcc  | cgaagacca  | tcattcaaaa | tcggctacgc  | 420 |

(2) INFORMATION FOR SEQ ID NO:4153:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 139 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..139  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4153:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Lys Lys Thr His Gly Thr Arg Phe Ser Ser Ser Leu Ala Ala Ala Ala |  |
| 1 5 10 15                                                       |  |
| Ala Ala Ala Met Glu Lys Glu Lys Leu Ser Phe Ser Ile Ser Ser Ser |  |
| 20 25 30                                                        |  |
| Lys Gln Arg Pro Pro Lys Pro Pro Ala Arg Pro Ala Ala Ala Asp     |  |
| 35 40 45                                                        |  |
| Asp Asp Asp Leu Arg Ser Ala Pro Ala Pro Gly Gln Gln Tyr Val Thr |  |

(2) INFORMATION FOR SEQ ID NO:4154:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1579702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4154:

[illegible]

(2) INFORMATION FOR SEQ ID NO:4155:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1579703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4155:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Lys | Glu | Lys | Leu | Ser | Phe | Ser | Ile | Ser | Ser | Ser | Lys | Gln | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Pro | Lys | Pro | Pro | Ala | Arg | Pro | Ala | Ala | Ala | Ala | Asp | Asp | Asp | Asp |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Arg | Ser | Ala | Pro | Ala | Pro | Gly | Gln | Gln | Tyr | Val | Thr | Glu | Phe | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Ser | Gln | Thr | Leu | Ala | Ala | Ala | Cys | Ala | Ala | Arg | Ala | Val | Ile | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Leu | Pro | Asn | Ser | Gly | Asn | Xaa | Leu | Thr | His | Arg | Pro | Arg | Lys | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Ser | Leu | Pro | Thr | Pro | Glu | Glu | Glu | Ala | Ala | Leu | Ala | Ala | Glu | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Gly | Trp | Gly | Pro | Xaa | Phe | Val | Leu | Asp | Thr | Ser | Thr | Ala | Pro | Glu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Pro | Ser | Ser | Lys | Ile | Gly | Tyr |     |     |     |     |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

- (B) LOCATION: 1..451

- (D) OTHER INFORMATION: / Ceres Seq. ID 1579709

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4156:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| atgctggaga | tgatgataat | gatgatgatg | atgatgaacc | tctctttaat  | gaagacgacg | 60  |
| acgaggagtt | agatgacctt | gagcaagggg | aggatgaacc | tmacacacaa  | catcttgtac | 120 |
| ttgcacaatt | tgataaagtg | tcaaggacca | agaatcgttg | gaagtgcacc  | ttgaaggatg | 180 |
| gaatcatgca | tttgaatggc | agggatgtcc | tttttaacaa | ggcgacagggt | gagtttgatt | 240 |
| tttgatTTTT | tggatgaaga | tgagctattt | tagaagcagc | tgtatggaca  | tatctttgtc | 300 |
| ttgacataag | gacagggagg | tgacagtgtt | cttggtgggg | tcttggcagc  | atgactgcgt | 360 |
| cgtgttttct | ttcctattga | atcttcgttc | caccctcttg | tttgtcaccg  | caactgttat | 420 |
| cgctgtaaag | aagttactgc | ttgtgctgtg | c          |             |            |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..80

- (D) OTHER INFORMATION: / Ceres Seq. ID 1579710

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4157:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gly | Asp | Asp | Asp | Asn | Asp | Asp | Asp | Asp | Asp | Glu | Pro | Pro | Leu | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Asp | Asp | Asp | Glu | Glu | Leu | Asp | Asp | Leu | Glu | Gln | Gly | Glu | Asp | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Xaa | Thr | Gln | His | Leu | Val | Leu | Ala | Gln | Phe | Asp | Lys | Val | Ser | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Lys | Asn | Arg | Trp | Lys | Cys | Thr | Leu | Lys | Asp | Gly | Ile | Met | His | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Gly | Arg | Asp | Val | Leu | Phe | Asn | Lys | Ala | Thr | Gly | Glu | Phe | Asp | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..440

- (D) OTHER INFORMATION: / Ceres Seq. ID 1579711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4158:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aggactctag | gagaactggg | acgacagcag | cggcgggcga | cggggatgag | aaccctgtac | 60  |
| tgtatttcgt | cgacctttgc | catggcgctg | togatgatga | gttctcgcgc | gggcgcggcg | 120 |
| gcggccggag | gaggagaaca | ccgcgctgag | cacgtcaccg | tggcgctcgg | tgggctgacg | 180 |
| cggccgagta | ctaggccctg | gccggggcga | gctggcccac | ggcccgggac | gccgaggccg | 240 |
| cggggacctg | ccgaagctgc | gggcggctcc | tcgtcttcgt | cggcgacggg | gcgcgcgggg | 300 |



ccggagtgcactggtggggcgctgccgcgcggcagcaggcgacgccgagcggtcgagg360  
agcggcagggcgcggggcgcgcgcgtgccacgggcaaggggaaccgcga gctggtgaga420  
cgggcgctcagcgggccc

(2) INFORMATION FOR SEQ ID NO:4159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579712

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4159:

Arg Thr Leu Gly Glu Leu Gly Arg Gln Gln Arg Arg Ala Thr Gly Met  
1 5 10 15  
Arg Thr Leu Tyr Cys Ile Ser Ser Thr Phe Ala Met Ala Ser Ser Met  
20 25 30  
Met Ser Ser Arg Ala Gly Ala Ala Ala Gly Gly Gly Glu His Arg  
35 40 45  
Arg Gln His Val Thr Val Ala Cys Gly Gly Leu Thr Arg Pro Ser Thr  
50 55 60  
Arg Pro Val Pro Gly Ala Ala Gly Pro Arg Pro Gly Thr Pro Arg Pro  
65 70 75 80  
Arg Gly Pro Ala Ala Ala Gly Gly Ser Ser Ser Ser Ser Pro Thr  
85 90 95  
Gly Arg Ala Gly Pro Glu Cys Asn Trp Trp Gly Ala Ala Ala Arg Gln  
100 105 110  
Gln Ala Thr Pro Arg Arg Ser Arg Ser Gly Arg Ala Ala Gly Ala Arg  
115 120 125  
Val Pro Thr Gly Lys Gly Asn Arg Glu Leu Val Arg Arg Ala Leu Thr  
130 135 140  
Pro Ala  
145

(2) INFORMATION FOR SEQ ID NO:4160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4160:

Asp Ser Arg Arg Thr Gly Thr Thr Ala Ala Ala Gly Asp Gly Asp Glu  
1 5 10 15  
Asn Pro Val Leu Tyr Phe Val Asp Leu Cys His Gly Val Val Asp Asp  
20 25 30  
Glu Phe Ser Arg Gly Arg Gly Gly Arg Arg Arg Arg Thr Pro Pro  
35 40 45  
Ser Ala Arg His Arg Gly Val Arg Trp Ala Asp Ala Ala Glu Tyr Gln  
50 55 60  
Ala Arg Ala Gly Arg Ser Trp Pro Thr Ala Arg Asp Ala Glu Ala Ala  
65 70 75 80  
Gly Thr Cys Cys Ser Cys Gly Arg Leu Leu Val Phe Val Ala Asp Gly  
85 90 95  
Ala Arg Gly Ala Gly Val Gln Leu Val Gly Arg Cys Arg Ala Ala Ala  
100 105 110

Gly Asp Ala Glu Ala Val Glu Glu Arg Gln Gly Arg Gly Arg Ala Arg  
115 120 125  
Ala His Gly Gln Gly Glu Pro Arg Ala Gly Glu Thr Gly Ala His Ala  
130 135 140  
Gly Pro  
145

(2) INFORMATION FOR SEQ ID NO:4161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4161:

Met Arg Thr Leu Tyr Cys Ile Ser Ser Thr Phe Ala Met Ala Ser Ser  
1 5 10 15  
Met Met Ser Ser Arg Ala Gly Ala Ala Ala Ala Gly Gly Gly Glu His  
20 25 30  
Arg Arg Gln His Val Thr Val Ala Cys Gly Gly Leu Thr Arg Pro Ser  
35 40 45  
Thr Arg Pro Val Pro Gly Ala Ala Gly Pro Arg Pro Gly Thr Pro Arg  
50 55 60  
Pro Arg Gly Pro Ala Ala Ala Gly Gly Ser Ser Ser Ser Pro  
65 70 75 80  
Thr Gly Arg Ala Gly Pro Glu Cys Asn Trp Trp Gly Ala Ala Ala Arg  
85 90 95  
Gln Gln Ala Thr Pro Arg Arg Ser Arg Ser Gly Arg Ala Ala Gly Ala  
100 105 110  
Arg Val Pro Thr Gly Lys Gly Asn Arg Glu Leu Val Arg Arg Ala Leu  
115 120 125  
Thr Pro Ala  
130

(2) INFORMATION FOR SEQ ID NO:4162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..434
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579724

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4162:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ccaattagcc ttgtttaaga ccaacagaaa ggatagcatg tttgctgacc gggtatttga  | 60  |
| cttgtttgac acgaaacaca atggaattct cgagtttgag gaatttgctc gagccctttc  | 120 |
| tgtgttccat ccgagtgcac caatcgattt caaaattgat tttgctttca aattgtatga  | 180 |
| tctcaagcaa carggtttca ttgaaaagca ggaggtcaag caaatggtgg tcgcaacact  | 240 |
| tgctgaayca ggaatgaatc tttcagatga tattattgaa ggcattattg ataagacatt  | 300 |
| tgaggaagca gwatacaaaag cacgwtggca aaattgataw ggaggattgg cgcagccttg | 360 |
| tcttgaggca tccatctctg ttaaaaaata tgaccctccc atatctccgg gatatcacca  | 420 |
| caacwtttcm aagc                                                    |     |

(2) INFORMATION FOR SEQ ID NO:4163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..111  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4163:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Leu | Ala | Leu | Phe | Lys | Thr | Asn | Arg | Lys | Asp | Ser | Met | Phe | Ala | Asp |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Val | Phe | Asp | Leu | Phe | Asp | Thr | Lys | His | Asn | Gly | Ile | Leu | Glu | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Glu | Phe | Ala | Arg | Ala | Leu | Ser | Val | Phe | His | Pro | Ser | Ala | Pro | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Phe | Lys | Ile | Asp | Phe | Ala | Phe | Lys | Leu | Tyr | Asp | Leu | Lys | Gln | Xaa |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Phe | Ile | Glu | Lys | Gln | Glu | Val | Lys | Gln | Met | Val | Val | Ala | Thr | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Glu | Xaa | Gly | Met | Asn | Leu | Ser | Asp | Asp | Ile | Ile | Glu | Gly | Ile | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Lys | Thr | Phe | Glu | Glu | Ala | Xaa | Tyr | Lys | Ala | Xaa | Trp | Gln | Asn |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:4164:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 99 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..99  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4164:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Ala | Asp | Arg | Val | Phe | Asp | Leu | Phe | Asp | Thr | Lys | His | Asn | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | Leu | Glu | Phe | Glu | Glu | Phe | Ala | Arg | Ala | Leu | Ser | Val | Phe | His | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Ser | Ala | Pro | Ile | Asp | Phe | Lys | Ile | Asp | Phe | Ala | Phe | Lys | Leu | Tyr | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Lys | Gln | Xaa | Gly | Phe | Ile | Glu | Lys | Gln | Glu | Val | Lys | Gln | Met | Val |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Ala | Thr | Leu | Ala | Glu | Xaa | Gly | Met | Asn | Leu | Ser | Asp | Asp | Ile | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Gly | Ile | Ile | Asp | Lys | Thr | Phe | Glu | Glu | Ala | Xaa | Tyr | Lys | Ala | Xaa |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Trp | Gln | Asn |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:4165:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 58 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..58  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579727

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4165:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Phe | Ser | Ser | Leu | Arg | Asn | Leu | Glu | Pro | Phe | Leu | Cys | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |

(2) INFORMATION FOR SEQ ID NO:4166:

(A) LENGTH: 516 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: sing

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (α)

(A) NAM

(B) LOCATION: 1

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:4166:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| gttcctgatt | gttgatatcc | agttttcttct | gtgagtgga  | tgcgcaggaa | gaaggatgtc | 120 |
| gtgctgcgga | ggcaactgcg | ggtgcggcgc  | cggctgcaag | tgcggcagcg | gctgcggagg | 180 |
| gtgcaagatg | taccocgaca | tggcagagca  | ggtgaccacc | accagactg  | tcatcatggg | 240 |
| tgttgacca  | tccaagggcg | ggttcgaggc  | ggccgcgcga | gctgagaatg | gcgggtgcaa | 300 |
| gtgcggcgcc | aactgcacct | gcgacccctg  | cacctgcaag | tgagacgacg | gcggcggcga | 360 |
| tgacgtgca  | gggtctgcag | gccctgatgg  | ggtcgggaag | actctttatc | tctctagcta | 420 |
| attaataaag | tctagctagt | atataatatt  | ctagcagtgt | cgtttgctgt | gttttgtycg | 480 |
| agtcagttag | acagtcagcc | gcgtgccatg  | ggccat     |            |            |     |

(2) INFORMATION FOR SEQ ID NO:4167:

(A) LENGTH: 75 amino aci

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(A) NAME

(B) LOCATION: 1..75

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:4167:

```

1 5 10 15
Gly Ser Gly Cys Gly Gly Cys Lys Met Tyr Pro Asp Met Ala Glu Gln
 20 25 30
Val Thr Thr Thr Gln Thr Val Ile Met Gly Val Ala Pro Ser Lys Gly
 35 40 45
Gly Phe Glu Ala Ala Ala Gly Ala Glu Asn Gly Gly Cys Lys Cys Gly
 50 55 60
Ala Asn Cys Thr Cys Asp Pro Cys Thr Cys Lys
65 70 75
(2) INFORMATION FOR SEQ ID NO:4168:

```

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(A) NAM

(B) LOCATION: 1..51

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:4168:

(iii)  $\mathcal{C} \cap \mathcal{K} = \emptyset$  and  $\mathcal{C} \cap \mathcal{K} = \emptyset$  and  $\mathcal{C} \cap \mathcal{K} = \emptyset$ .

Met Tyr Pro Asp Met Ala Glu Gln Val Thr Thr Thr Gln Thr Val Ile  
1 5 10 15  
Met Gly Val Ala Pro Ser Lys Gly Gly Phe Glu Ala Ala Ala Gly Ala  
20 25 30  
Glu Asn Gly Gly Cys Lys Cys Gly Ala Asn Cys Thr Cys Asp Pro Cys  
35 40 45  
Thr Cys Lys  
50

(2) INFORMATION FOR SEQ ID NO:4169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4169:

Met Ala Glu Gln Val Thr Thr Thr Gln Thr Val Ile Met Gly Val Ala  
1 5 10 15  
Pro Ser Lys Gly Gly Phe Glu Ala Ala Ala Gly Ala Glu Asn Gly Gly  
20 25 30  
Cys Lys Cys Gly Ala Asn Cys Thr Cys Asp Pro Cys Thr Cys Lys  
35 40 45

(2) INFORMATION FOR SEQ ID NO:4170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..435
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4170:

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| atctgattct | gtgatcgaga  | tcgaggccga | tcggccaggt | ttcttggtgcg | tgcgctctgc | 60  |
| tactgcatgg | cggtagctca  | ccttcttctc | caactctctg | ccggagtcaa  | tggagctagc | 120 |
| aggaacagga | tgctcattcc  | agccattctt | tcgattcttc | agcttattca  | cctcgagcgc | 180 |
| ccggggagcg | gcgggcagga  | cttctacgat | gttagcctcg | tcgacggcct  | caacgtgccg | 240 |
| gtgcgcgtgg | cgccctcggg  | cggcggtggc | gactgtcgtc | ccgcggcgtg  | cgcgggcgac | 300 |
| gtgaacgcga | tgtgccccgc  | ggacctccgc | gtcgtcgcct | cgtccggcag  | cggcggcgtc | 360 |
| gtggcgtaca | agagcgcggtg | cagcgcctac | ggcagcgcgc | gctactgctg  | caccggccag | 420 |
| tacggcacgc | cggag       |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:4171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4171:

Met Ala Val Ala His Leu Leu Leu Gln Leu Ser Ala Gly Val Asn Gly  
1 5 10 15  
Ala Ser Arg Asn Arg Met Leu Ile Pro Ala Ile Leu Ser Ile Leu Gln

20 25 30  
Leu Ile His Leu Ala Ala Pro Gly Ser Gly Gly Gln Asp Phe Tyr Asp  
35 40 45  
Val Ser Leu Val Asp Gly Phe Asn Val Pro Val Arg Val Ala Pro Ser  
50 55 60  
Gly Gly Gly Gly Asp Cys Arg Pro Ala Ala Cys Ala Gly Asp Val Asn  
65 70 75 80  
Ala Met Cys Pro Ala Asp Leu Arg Val Val Ala Ser Ser Gly Ser Gly  
85 90 95  
Gly Val Val Ala Tyr Lys Ser Ala Cys Ser Ala Tyr Gly Ser Ala Arg  
100 105 110  
Tyr Cys Cys Thr Gly Gln Tyr Gly Thr Pro Glu  
115 120

(2) INFORMATION FOR SEQ ID NO:4172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4172:

Met Glu Leu Ala Gly Thr Gly Cys Ser Phe Gln Pro Phe Phe Arg Phe  
1 5 10 15  
Phe Ser Leu Phe Thr Ser Gln Arg Arg Gly Ala Ala Gly Arg Thr Ser  
20 25 30  
Thr Met Leu Ala Ser Ser Thr Ala Ser Thr Cys Arg Cys Ala Trp Arg  
35 40 45  
Pro Arg Ala Ala Val Ala Thr Val Val Pro Arg Arg Ala Arg Ala Thr  
50 55 60

(2) INFORMATION FOR SEQ ID NO:4173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4173:

Met Leu Ile Pro Ala Ile Leu Ser Ile Leu Gln Leu Ile His Leu Ala  
1 5 10 15  
Ala Pro Gly Ser Gly Gly Gln Asp Phe Tyr Asp Val Ser Leu Val Asp  
20 25 30  
Gly Phe Asn Val Pro Val Arg Val Ala Pro Ser Gly Gly Gly Gly Asp  
35 40 45  
Cys Arg Pro Ala Ala Cys Ala Gly Asp Val Asn Ala Met Cys Pro Ala  
50 55 60  
Asp Leu Arg Val Val Ala Ser Ser Gly Ser Gly Gly Val Val Ala Tyr  
65 70 75 80  
Lys Ser Ala Cys Ser Ala Tyr Gly Ser Ala Arg Tyr Cys Cys Thr Gly  
85 90 95  
Gln Tyr Gly Thr Pro Glu  
100

(2) INFORMATION FOR SEQ ID NO:4174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..470
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4174:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| actccaagtc caagccacct ctcagctctc accagctagc tctactctcg cggcgcttcc  | 60  |
| cctcgccggt cgctgccatc gattgacatt ggtccaaccc aaccgcgcag ctagatagat  | 120 |
| ctacgtcgac cggcggccgc gagggacgct cgctcgctcg tgcgtcgaca tggcgaaatg  | 180 |
| cagcagcaag atccggtaca tcgtgtggct gcggcagacg ctgcggcggt ggcggtccc   | 240 |
| cgcgggcggt cgcgsggcgg tcccggcggg ccacgtggcg gtgtgcgtgg gcggcgcggc  | 300 |
| gcggcggttc gtggtgcggg cggcgcacct gaaccacccc gtgttcggg agctgctccg   | 360 |
| gcaggcgagg gaggagtacg gggtcccgtc gggggcctgc gcgggccccca tcgcgtcccc | 420 |
| ctgcgacgag ggcctcttcg agcacgtcct cggccacctc tctctcccgt             |     |

(2) INFORMATION FOR SEQ ID NO:4175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4175:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ala Lys Cys Ser Ser Lys Ile Arg Tyr Ile Val Trp Leu Arg Gln |  |
| 1 5 10 15                                                       |  |
| Thr Leu Arg Arg Trp Arg Ser Arg Ala Ala Ala Arg Xaa Ala Val Pro |  |
| 20 25 30                                                        |  |
| Ala Gly His Val Ala Val Cys Val Gly Gly Ala Ala Arg Arg Phe Val |  |
| 35 40 45                                                        |  |
| Val Arg Ala Ala His Leu Asn His Pro Val Phe Arg Glu Leu Leu Arg |  |
| 50 55 60                                                        |  |
| Gln Ala Glu Glu Glu Tyr Gly Phe Pro Ser Gly Ala Cys Ala Gly Pro |  |
| 65 70 75 80                                                     |  |
| Ile Ala Leu Pro Cys Asp Glu Gly Leu Phe Glu His Val Leu Gly His |  |
| 85 90 95                                                        |  |
| Leu Ser Ser Pro                                                 |  |
| 100                                                             |  |

(2) INFORMATION FOR SEQ ID NO:4176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4176:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Gln Gln Gln Asp Pro Val His Arg Val Ala Ala Ala Asp Ala Ala |  |
| 1 5 10 15                                                       |  |
| Ala Val Ala Val Pro Arg Gly Gly Ser Xaa Gly Gly Pro Gly Gly Pro |  |

|                                                                 |    |  |    |  |    |
|-----------------------------------------------------------------|----|--|----|--|----|
|                                                                 | 20 |  | 25 |  | 30 |
| Arg Gly Gly Val Arg Gly Arg Arg Gly Ala Ala Val Arg Gly Ala Gly |    |  |    |  |    |
|                                                                 | 35 |  | 40 |  | 45 |
| Gly Ala Pro Glu Pro Pro Arg Val Pro Gly Ala Ala Pro Ala Gly Gly |    |  |    |  |    |
|                                                                 | 50 |  | 55 |  | 60 |
| Gly Gly Val Arg Val Pro Val Gly Gly Leu Arg Gly Pro His Arg Ala |    |  |    |  |    |
|                                                                 | 65 |  | 70 |  | 75 |
| Pro Leu Arg Arg Gly Pro Leu Arg Ala Arg Pro Arg Pro Pro Leu Leu |    |  |    |  |    |
|                                                                 | 85 |  | 90 |  | 95 |
| Pro                                                             |    |  |    |  |    |

(2) INFORMATION FOR SEQ ID NO:4177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..471
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4177:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| ggcttggtcg cagttcgtgg cggatggcgt gttcttcgcg gagctgaatg agatgctgac   | 60  |
| ccgcgagctc gcggaggatg gctactccgg cgtcgagggtc cgcgtcaccc ccattgcgcac | 120 |
| cgagatcatc atccgtgccca cccgcactca gaacgttctc ggcgagaagg gccggaggat  | 180 |
| cagggagctg acttctgttg ttcagaagcg cttcaacttc ccggagggtg gtgttgagct   | 240 |
| ctacgcagag aaggtgaaca accgtggcct ctgcgccatt gccagggccg agtcgctccg   | 300 |
| ctacaagctt cttggtggac tagccgtgag aagggtcatgt tatggtgttc tcaggtttgt  | 360 |
| catggagagt ggtgctaagg gctgtgaggt tattgtaagt ggcaagctca gggctcagcg   | 420 |
| agctaagtct atgaagttca aggatgggta catgatttct tctggtcatb c            |     |

(2) INFORMATION FOR SEQ ID NO:4178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4178:

|                                                                 |    |
|-----------------------------------------------------------------|----|
| Ala Trp Ser Gln Phe Val Ala Asp Gly Val Phe Phe Ala Glu Leu Asn |    |
| 1                                                               | 15 |
|                                                                 |    |
| Glu Met Leu Thr Arg Glu Leu Ala Glu Asp Gly Tyr Ser Gly Val Glu |    |
|                                                                 |    |
|                                                                 |    |
| Val Arg Val Thr Pro Met Arg Thr Glu Ile Ile Ile Arg Ala Thr Arg |    |
|                                                                 |    |
|                                                                 |    |
| Thr Gln Asn Val Leu Gly Glu Lys Gly Arg Arg Ile Arg Glu Leu Thr |    |
|                                                                 |    |
|                                                                 |    |
| Ser Val Val Gln Lys Arg Phe Asn Phe Pro Glu Gly Gly Val Glu Leu |    |
|                                                                 |    |
|                                                                 |    |
| Tyr Ala Glu Lys Val Asn Asn Arg Gly Leu Cys Ala Ile Ala Gln Ala |    |
|                                                                 |    |
|                                                                 |    |
| Glu Ser Leu Arg Tyr Lys Leu Leu Gly Gly Leu Ala Val Arg Arg Ala |    |
|                                                                 |    |
|                                                                 |    |
| Cys Tyr Gly Val Leu Arg Phe Val Met Glu Ser Gly Ala Lys Gly Cys |    |
|                                                                 |    |
|                                                                 |    |
| Glu Val Ile Val Ser Gly Lys Leu Arg Ala Gln Arg Ala Lys Ser Met |    |
|                                                                 |    |
|                                                                 |    |



Lys Phe Lys Asp Gly Tyr Met Ile Ser Ser Gly His  
145 150 155

(2) INFORMATION FOR SEQ ID NO:4179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4179:

Met Leu Thr Arg Glu Leu Ala Glu Asp Gly Tyr Ser Gly Val Glu Val  
1 5 10 15  
Arg Val Thr Pro Met Arg Thr Glu Ile Ile Ile Arg Ala Thr Arg Thr  
20 25 30  
Gln Asn Val Leu Gly Glu Lys Gly Arg Arg Ile Arg Glu Leu Thr Ser  
35 40 45  
Val Val Gln Lys Arg Phe Asn Phe Pro Glu Gly Gly Val Glu Leu Tyr  
50 55 60  
Ala Glu Lys Val Asn Asn Arg Gly Leu Cys Ala Ile Ala Gln Ala Glu  
65 70 75 80  
Ser Leu Arg Tyr Lys Leu Leu Gly Gly Leu Ala Val Arg Arg Ala Cys  
85 90 95  
Tyr Gly Val Leu Arg Phe Val Met Glu Ser Gly Ala Lys Gly Cys Glu  
100 105 110  
Val Ile Val Ser Gly Lys Leu Arg Ala Gln Arg Ala Lys Ser Met Lys  
115 120 125  
Phe Lys Asp Gly Tyr Met Ile Ser Ser Gly His  
130 135

(2) INFORMATION FOR SEQ ID NO:4180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4180:

Met Arg Thr Glu Ile Ile Arg Ala Thr Arg Thr Gln Asn Val Leu  
1 5 10 15  
Gly Glu Lys Gly Arg Arg Ile Arg Glu Leu Thr Ser Val Val Gln Lys  
20 25 30  
Arg Phe Asn Phe Pro Glu Gly Gly Val Glu Leu Tyr Ala Glu Lys Val  
35 40 45  
Asn Asn Arg Gly Leu Cys Ala Ile Ala Gln Ala Glu Ser Leu Arg Tyr  
50 55 60  
Lys Leu Leu Gly Gly Leu Ala Val Arg Arg Ala Cys Tyr Gly Val Leu  
65 70 75 80  
Arg Phe Val Met Glu Ser Gly Ala Lys Gly Cys Glu Val Ile Val Ser  
85 90 95  
Gly Lys Leu Arg Ala Gln Arg Ala Lys Ser Met Lys Phe Lys Asp Gly  
100 105 110  
Tyr Met Ile Ser Ser Gly His  
115

(2) INFORMATION FOR SEQ ID NO:4181:

00000000-00000000

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 529 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..529  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4181:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| agggagagac cctttccatc caagctagcc aaaccctagc caccgtcggg tccaatctgc  | 60  |
| caacatctcg tccgctgggt ggtggctcgg cctcggcggc atggcctcgt ccgcctacgc  | 120 |
| ttgggacgcc gcgaggagg cgacatcga cgcctccgca tcgcaggagg agctcatcgt    | 180 |
| ccgcgcccgc ttcattctccc gtgacaatga ggaggagggg gagggggagg gggaggggga | 240 |
| ggaggaggag gaggaggagg tcgagggtgt cagcacgccg cctctcacgc atcaggaccc  | 300 |
| gcagagtccg ggggaagaag tcatcgccat gtgctccatc ccttcacccc agcctgaccc  | 360 |
| caagcctcct cccgctccyg ctccctcccc tcctcgggac agtaagagtc gccgtccgga  | 420 |
| gcgggtcaaa ttgaagccgc ggaagaaggt ctgcaagagg aaagagtgtc tgcaatgagg  | 480 |
| aaggtgagaa gagccaaaca agatcaggtc tccgactccg aagccgcag              |     |

(2) INFORMATION FOR SEQ ID NO:4182:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 143 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..143  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4182:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Glu | Thr | Leu | Ser | Ile | Gln | Ala | Ser | Gln | Thr | Leu | Ala | Thr | Val | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Asn | Leu | Pro | Thr | Ser | Arg | Pro | Leu | Val | Gly | Gly | Ser | Ala | Ser | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Trp | Pro | Arg | Pro | Pro | Thr | Leu | Gly | Thr | Pro | Arg | Arg | Arg | Thr |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Thr | Pro | Pro | His | Arg | Arg | Arg | Ser | Ser | Ser | Ser | Ala | Pro | Ala | Ser |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Pro | Val | Thr | Met | Arg | Arg | Arg | Gly | Arg | Gly | Arg | Gly | Arg | Gly | Arg |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Arg | Arg | Arg | Arg | Arg | Ser | Arg | Cys | Ser | Ala | Arg | Arg | Leu | Ser | Arg |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Arg | Thr | Arg | Arg | Val | Arg | Gly | Lys | Lys | Ser | Ser | Pro | Cys | Ala | Pro |
|     |     |     |     |     | 100 |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Pro | Ser | Pro | Ser | Leu | Thr | Pro | Arg | Leu | Leu | Pro | Leu | Xaa | Leu | Pro |
|     |     |     |     |     | 115 |     |     | 120 |     |     |     | 125 |     |     |     |
| Pro | Leu | Pro | Arg | Thr | Val | Arg | Val | Ala | Val | Arg | Ser | Gly | Ser | Asn |     |
|     |     |     |     |     | 130 |     |     | 135 |     |     |     | 140 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:4183:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 125 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..125  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4183:

Met Ala Ser Ser Ala Tyr Ala Trp Asp Ala Ala Glu Glu Ala Asp Ile  
1 5 10 15  
Asp Ala Ser Ala Ser Gln Glu Glu Leu Ile Val Arg Ala Arg Phe Ile  
20 25 30  
Ser Arg Asp Asn Glu Glu Glu Gly Glu Gly Glu Gly Glu Glu Glu  
35 40 45  
Glu Glu Glu Glu Glu Val Glu Val Phe Ser Thr Pro Pro Leu Thr His  
50 55 60  
Gln Asp Pro Gln Ser Pro Gly Glu Glu Val Ile Ala Met Cys Ser Ile  
65 70 75 80  
Pro Phe Thr Gln Pro Asp Pro Thr Pro Pro Pro Ala Xaa Ala Pro Ser  
85 90 95  
Pro Pro Ser Asp Ser Lys Ser Arg Arg Pro Glu Arg Val Lys Leu Lys  
100 105 110  
Pro Arg Lys Lys Val Cys Lys Arg Lys Glu Cys Leu Gln  
115 120 125

(2) INFORMATION FOR SEQ ID NO:4184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4184:

Met Arg Arg Arg Gly Arg Gly Arg Gly Arg Arg Arg Arg Arg  
1 5 10 15  
Arg Arg Ser Arg Cys Ser Ala Arg Arg Leu Ser Arg Ile Arg Thr Arg  
20 25 30  
Arg Val Arg Gly Lys Lys Ser Ser Pro Cys Ala Pro Ser Pro Ser Pro  
35 40 45  
Ser Leu Thr Pro Arg Leu Leu Pro Leu Xaa Leu Pro Pro Leu Pro Arg  
50 55 60  
Thr Val Arg Val Ala Val Arg Ser Gly Ser Asn  
65 70 75

(2) INFORMATION FOR SEQ ID NO:4185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..437
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4185:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aaggtccaga agcccagaac cagacgagca cggacggatc tcccccaacg cgcgtgcgtc | 60  |
| cgcaactagc gtctgcccgc ggcgccttct tccgcacccc ccgacgcggc aaggagcccc | 120 |
| ccgccatgag ggtccaccgc gccccgcgga agcgcaccat cgccgtgcaa cgtgcgcc   | 180 |
| ccgcggcggc gggcgcgctc ggcgggaaga agctgcgccg cctgccgcac atattcgaca | 240 |
| aggtgctgga gctcccgctc gcggccgacg cggacgtgtc cgtcgaggag gacgcggcgg | 300 |
| cgctgcgggt cgtcgccgc gccgacgagt tctccctcgc gggcgcccgc gcgcacgccg  | 360 |
| tcgagatcca cccaggggtc accaaggtcg tcgtccgcgg cctctcctcc tctccctcg  | 420 |
| gcggcgatgg cgacgac                                                |     |

(2) INFORMATION FOR SEQ ID NO:4186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..145
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1579829
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4186:

Arg Ser Arg Ser Pro Glu Pro Asp Glu His Gly Arg Ile Ser Pro Asn  
1 5 10 15  
Ala Arg Ala Ser Ala Thr Ser Val Cys Arg Arg Arg Leu Leu Pro His  
20 25 30  
Pro Pro Thr Arg Gln Gly Ala Pro Arg His Glu Gly Pro Pro Gly Pro  
35 40 45  
Ala Glu Ala His His Arg Arg Ala Thr Leu Arg Leu Arg Gly Gly Gly  
50 55 60  
Arg Ala Arg Arg Glu Glu Ala Ala Pro Pro Ala His Ile Arg Gln  
65 70 75 80  
Gly Ala Gly Ala Pro Val Arg Gly Arg Arg Gly Arg Val Arg Arg Gly  
85 90 95  
Gly Arg Gly Gly Ala Ala Val Arg Arg Arg Arg Arg Arg Val Leu Pro  
100 105 110  
Arg Gly Arg Pro Arg Ala Arg Arg Arg Asp Pro Pro Arg Gly His Gln  
115 120 125  
Gly Arg Arg Pro Arg Pro Leu Leu Leu Pro Arg Arg Arg Trp Arg  
130 135 140  
Arg  
145

- (2) INFORMATION FOR SEQ ID NO:4187:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 145 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..145
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1579830
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4187:

Gly Pro Glu Ala Gln Asn Gln Thr Ser Thr Asp Gly Ser Pro Pro Thr  
1 5 10 15  
Arg Val Arg Pro Gln Leu Ala Ser Ala Ala Gly Ala Phe Phe Arg Thr  
20 25 30  
Pro Arg Arg Gly Lys Glu Pro Pro Ala Met Arg Val His Pro Ala Pro  
35 40 45  
Arg Lys Arg Thr Ile Ala Val Gln Arg Cys Ala Ser Ala Ala Ala Gly  
50 55 60  
Ala Leu Gly Gly Lys Lys Leu Arg Arg Leu Pro His Ile Phe Asp Lys  
65 70 75 80  
Val Leu Glu Leu Pro Phe Ala Ala Asp Ala Asp Val Ser Val Glu Glu  
85 90 95  
Asp Ala Ala Ala Leu Arg Phe Val Ala Ala Ala Asp Glu Phe Ser Leu  
100 105 110  
Ala Gly Ala Arg Ala His Ala Val Glu Ile His Pro Gly Val Thr Lys  
115 120 125  
Val Val Val Arg Gly Leu Ser Ser Ser Ser Leu Gly Gly Asp Gly Asp  
130 135 140  
Asp

002104-15553500

145

(2) INFORMATION FOR SEQ ID NO:4188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4188:

Met Arg Val His Pro Ala Pro Arg Lys Arg Thr Ile Ala Val Gln Arg  
1 5 10 15  
Cys Ala Ser Ala Ala Ala Gly Ala Leu Gly Gly Lys Lys Leu Arg Arg  
20 25 30  
Leu Pro His Ile Phe Asp Lys Val Leu Glu Leu Pro Phe Ala Ala Asp  
35 40 45  
Ala Asp Val Ser Val Glu Glu Asp Ala Ala Ala Leu Arg Phe Val Ala  
50 55 60  
Ala Ala Asp Glu Phe Ser Leu Ala Gly Ala Arg Ala His Ala Val Glu  
65 70 75 80  
Ile His Pro Gly Val Thr Lys Val Val Val Arg Gly Leu Ser Ser Ser  
85 90 95  
Ser Leu Gly Gly Asp Gly Asp Asp  
100

(2) INFORMATION FOR SEQ ID NO:4189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..425
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4189:

attcctcttc cagctccagc tatttccacc gcacattgtc cacgtctgcc attggcccat 60  
tgccggttcc tctcgtcaag ccctagctcc aaccaaccg tttccatggg agccatacga 120  
gttgcaagcc ttctactcct cgtggggta atctggctgt cgcgggcgat gttcggcgcg 180  
gaggccgccg gcacgacggt gttcacgctg cacaacaact gacccacac ggtctggccg 240  
gccacactgt ccgggaacag cgcggcggcc gtcggggcg ggggcttcga gctgtcgccc 300  
ggcgccaccg tctcgttccc ggcgccggcg ggctggtcgg gccgcctgtg ggcgcgcacg 360  
ggctgcgtcg cgtcgtcgtc gtccccgcc ggccgcctct cgtgcgcacg ggcgactgca 420  
gcggc

(2) INFORMATION FOR SEQ ID NO:4190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4190:

Ile Pro Leu Pro Ala Pro Ala Ile Ser Thr Ala His Cys Pro Arg Leu  
1 5 10 15

Pro Leu Ala His Cys Arg Phe Leu Ser Ser Ser Pro Ser Ser Asn Gln  
20 25 30  
Pro Val Ser Met Gly Ala Ile Arg Val Ala Ser Leu Leu Leu Leu Ala  
35 40 45  
Gly Val Ile Trp Leu Ser Arg Ala Met Phe Gly Ala Glu Ala Ala Gly  
50 55 60  
Thr Thr Val Phe Thr Leu His Asn Asn Cys Thr His Thr Val Trp Pro  
65 70 75 80  
Ala Thr Leu Ser Gly Asn Ser Ala Ala Val Gly Gly Gly Gly Phe  
85 90 95  
Glu Leu Ser Pro Gly Ala Thr Val Ser Phe Pro Ala Pro Ala Gly Trp  
100 105 110  
Ser Gly Arg Leu Trp Ala Arg Thr Gly Cys Val Ala Ser Ser Ser Ser  
115 120 125  
Pro Ala Gly Arg Leu Ser Cys Ala Arg Ala Thr Ala Ala  
130 135 140

(2) INFORMATION FOR SEQ ID NO:4191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1579838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4191:

Met Gly Ala Ile Arg Val Ala Ser Leu Leu Leu Ala Gly Val Ile  
1 5 10 15  
Trp Leu Ser Arg Ala Met Phe Gly Ala Glu Ala Ala Gly Thr Thr Val  
20 25 30  
Phe Thr Leu His Asn Asn Cys Thr His Thr Val Trp Pro Ala Thr Leu  
35 40 45  
Ser Gly Asn Ser Ala Ala Val Gly Gly Gly Gly Phe Glu Leu Ser  
50 55 60  
Pro Gly Ala Thr Val Ser Phe Pro Ala Pro Ala Gly Trp Ser Gly Arg  
65 70 75 80  
Leu Trp Ala Arg Thr Gly Cys Val Ala Ser Ser Ser Ser Pro Ala Gly  
85 90 95  
Arg Leu Ser Cys Ala Arg Ala Thr Ala Ala  
100 105

(2) INFORMATION FOR SEQ ID NO:4192:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 aminoacids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1579839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4192:

Met Phe Gly Ala Glu Ala Ala Gly Thr Thr Val Phe Thr Leu His Asn  
1 5 10 15  
Asn Cys Thr His Thr Val Trp Pro Ala Thr Leu Ser Gly Asn Ser Ala  
20 25 30  
Ala Ala Val Gly Gly Gly Gly Phe Glu Leu Ser Pro Gly Ala Thr Val  
35 40 45  
Ser Phe Pro Ala Pro Ala Gly Trp Ser Gly Arg Leu Trp Ala Arg Thr

50 55 60  
Gly Cys Val Ala Ser Ser Ser Ser Pro Ala Gly Arg Leu Ser Cys Ala  
65 70 75 80  
Arg Ala Thr Ala Ala  
85

(2) INFORMATION FOR SEQ ID NO:4193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..406
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4193:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aacaaatagt agccatggcg atgatggcgt tggctattgg gtccgatcag atatctactc | 60  |
| aagctaggag ggacagtatc attagtggac tgaacaacct ttcaagcaat gtcagcgaag | 120 |
| ttctcaagct agatgctgga atgaaggagc tcgcctcttc gctgatcgac tcagagtgcg | 180 |
| tcctcgtgtt cggaaggggt tacaactacg ccaccgcgct ggagggcgcc ctgaaggtca | 240 |
| aggaggtggc gctgatgcac agcgaaggca tgctcgtctg cgagatgaag cacggaccgc | 300 |
| tggccctcgt ggacgagaac ctccccatca ttgtcattgc gactcgcgac gcgtgcttca | 360 |
| gcaagcagca gtcggtgatc cagcagctcc tctcgcgtag ggggcg                |     |

(2) INFORMATION FOR SEQ ID NO:4194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4194:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Gln Ile Val Ala Met Ala Met Met Ala Leu Ala Ile Gly Ser Asp Gln |  |
| 1 5 10 15                                                       |  |
| Ile Ser Thr Gln Ala Arg Arg Asp Ser Ile Ile Ser Gly Leu Asn Asn |  |
| 20 25 30                                                        |  |
| Leu Ser Ser Asn Val Ser Glu Val Leu Lys Leu Asp Ala Gly Met Lys |  |
| 35 40 45                                                        |  |
| Glu Leu Ala Ser Ser Leu Ile Asp Ser Glu Ser Leu Leu Val Phe Gly |  |
| 50 55 60                                                        |  |
| Arg Gly Tyr Asn Tyr Ala Thr Ala Leu Glu Gly Ala Leu Lys Val Lys |  |
| 65 70 75 80                                                     |  |
| Glu Val Ala Leu Met His Ser Glu Gly Met Leu Ala Gly Glu Met Lys |  |
| 85 90 95                                                        |  |
| His Gly Pro Leu Ala Leu Val Asp Glu Asn Leu Pro Ile Ile Val Ile |  |
| 100 105 110                                                     |  |
| Ala Thr Arg Asp Ala Cys Phe Ser Lys Gln Gln Ser Val Ile Gln Gln |  |
| 115 120 125                                                     |  |
| Leu Leu Ser Arg Arg Gly                                         |  |
| 130                                                             |  |

(2) INFORMATION FOR SEQ ID NO:4195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1579867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4195:

Met Ala Met Met Ala Leu Ala Ile Gly Ser Asp Gln Ile Ser Thr Gln  
1 5 10 15  
Ala Arg Arg Asp Ser Ile Ile Ser Gly Leu Asn Asn Leu Ser Ser Asn  
20 25 30  
Val Ser Glu Val Leu Lys Leu Asp Ala Gly Met Lys Glu Leu Ala Ser  
35 40 45  
Ser Leu Ile Asp Ser Glu Ser Leu Leu Val Phe Gly Arg Gly Tyr Asn  
50 55 60  
Tyr Ala Thr Ala Leu Glu Gly Ala Leu Lys Val Lys Glu Val Ala Leu  
65 70 75 80  
Met His Ser Glu Gly Met Leu Ala Gly Glu Met Lys His Gly Pro Leu  
85 90 95  
Ala Leu Val Asp Glu Asn Leu Pro Ile Ile Val Ile Ala Thr Arg Asp  
100 105 110  
Ala Cys Phe Ser Lys Gln Gln Ser Val Ile Gln Gln Leu Leu Ser Arg  
115 120 125  
Arg Gly  
130

(2) INFORMATION FOR SEQ ID NO:4196:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1579868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4196:

Met Met Ala Leu Ala Ile Gly Ser Asp Gln Ile Ser Thr Gln Ala Arg  
1 5 10 15  
Arg Asp Ser Ile Ile Ser Gly Leu Asn Asn Leu Ser Ser Asn Val Ser  
20 25 30  
Glu Val Leu Lys Leu Asp Ala Gly Met Lys Glu Leu Ala Ser Ser Leu  
35 40 45  
Ile Asp Ser Glu Ser Leu Leu Val Phe Gly Arg Gly Tyr Asn Tyr Ala  
50 55 60  
Thr Ala Leu Glu Gly Ala Leu Lys Val Lys Glu Val Ala Leu Met His  
65 70 75 80  
Ser Glu Gly Met Leu Ala Gly Glu Met Lys His Gly Pro Leu Ala Leu  
85 90 95  
Val Asp Glu Asn Leu Pro Ile Ile Val Ile Ala Thr Arg Asp Ala Cys  
100 105 110  
Phe Ser Lys Gln Gln Ser Val Ile Gln Gln Leu Leu Ser Arg Arg Gly  
115 120 125

(2) INFORMATION FOR SEQ ID NO:4197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

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(A) NAME/KEY: -

(B) LOCATION: 1..489

(D) OTHER INFORMATION: / Ceres Seq. ID 1579873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4197:

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| aaggccaggg  | atgacgaagg | acaagagaag | aaaaagccaa  | agaagaaaaa | agatccgaat | 60  |
| gctccgaaac  | gagccatgac | cccgttcacg | tattttctcaa | tggctgagcg | aggaaacatg | 120 |
| aagagcagca  | acccagatgt | gcctacgact | gagatcgcaa  | agaagcttgg | ggagatgtgg | 180 |
| caaaagatgt  | caggcgaaga | gaaacagcct | tacatccagc  | aggcccaggt | cgacaagaaa | 240 |
| cgttatgaaa  | aagaatccgc | tgtctatcgc | ggtgaagcta  | cagtcgatgt | ggattctggg | 300 |
| aacgagtcctg | actagagatc | caagctcttg | ggctggcatg  | gtggcacggg | atgaaagtct | 360 |
| agtgccatgt  | gtgctattgt | tatgtcagca | actgttgcca  | acaacattgc | tgacagtaaa | 420 |
| gagagtttct  | ctcgacgct  | acctctgcag | ggcaaaaagaa | tgtacgagtg | tagtctagtg | 480 |
| attttgtgt   |            |            |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:4198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1579874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4198:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ala | Arg | Asp | Asp | Glu | Gly | Gln | Glu | Lys | Lys | Lys | Pro | Lys | Lys | Lys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Lys | Asp | Pro | Asn | Ala | Pro | Lys | Arg | Ala | Met | Thr | Pro | Phe | Met | Tyr | Phe |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ser | Met | Ala | Glu | Arg | Gly | Asn | Met | Lys | Ser | Ser | Asn | Pro | Asp | Leu | Pro |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Thr | Thr | Glu | Ile | Ala | Lys | Lys | Leu | Gly | Glu | Met | Trp | Gln | Lys | Met | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gly | Glu | Glu | Lys | Gln | Pro | Tyr | Ile | Gln | Gln | Ala | Gln | Val | Asp | Lys | Lys |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Tyr | Glu | Lys | Glu | Ser | Ala | Val | Tyr | Arg | Gly | Glu | Ala | Thr | Val | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Asp | Ser | Gly | Asn | Glu | Ser | Asp |     |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:4199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1579875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4199:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Pro | Phe | Met | Tyr | Phe | Ser | Met | Ala | Glu | Arg | Gly | Asn | Met | Lys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Ser | Asn | Pro | Asp | Leu | Pro | Thr | Thr | Glu | Ile | Ala | Lys | Lys | Leu | Gly |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Glu | Met | Trp | Gln | Lys | Met | Ser | Gly | Glu | Glu | Lys | Gln | Pro | Tyr | Ile | Gln |
|     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |     |
| Gln | Ala | Gln | Val | Asp | Lys | Lys | Arg | Tyr | Glu | Lys | Glu | Ser | Ala | Val | Tyr |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Arg | Gly | Glu | Ala | Thr | Val | Asp | Val | Asp | Ser | Gly | Asn | Glu | Ser | Asp |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:4200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4200:

```
Met Lys Lys Asn Pro Leu Ser Ile Ala Val Lys Leu Gln Ser Met Trp
1 5 10 15
Ile Leu Gly Thr Ser Leu Thr Arg Asp Pro Ser Ser Trp Ala Gly Met
 20 25 30
Val Ala Arg Asp Glu Ser Leu Val Pro Cys Val Leu Leu Leu Cys Gln
 35 40 45
Gln Leu Leu Pro Thr Thr Leu Leu Thr Val Lys Arg Val Ser Leu Ala
 50 55 60
Ala Tyr Leu Cys Arg Ala Lys Glu Cys Thr Ser Val Val
65 70 75
```

(2) INFORMATION FOR SEQ ID NO:4201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..356
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4201:

```
attattagga agaacactgt tttgtctccg gcccgctcgca gcccactgc cgtgcgcgcc 60
accctgccgg cgcacccggc cccgccagcg cgttcgaggc cgacgcgcgc cgccacctgc 120
cgcgtcaacg tccggccatt cctgccccct caccattctg ccgcctccac cgcagcagcc 180
gcggcgatgc gaccgcgcatc ctctctctcc cgcttctcgg ccacaacatc tccgtctcgc 240
tgccgacctg aacaacgagg cacactccat tggtggccat gcttgatctc ctcatcctgc 300
tgcagtgctg ccgtggaagg gaggccagtg cggaacaac ccagactgcg agcgcc
```

(2) INFORMATION FOR SEQ ID NO:4202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4202:

```
Ile Ile Arg Lys Asn Thr Val Leu Ser Pro Ala Arg Arg Ser Pro Thr
1 5 10 15
Ala Val Arg Ala Thr Leu Pro Ala His Pro Ala Pro Pro Ala Arg Ser
 20 25 30
Arg Pro Thr Arg Ala Ala Thr Cys Arg Val Thr Leu Arg Pro Phe Leu
 35 40 45
Pro Pro His His Ser Ala Ala Ser Thr Ala Ala Ala Ala Met Arg
 50 55 60
Pro Ala Ser Ser Ser Ser Arg Phe Ser Ala Thr Thr Ser Pro Ser Arg
```

(2) INFORMATION FOR SEO ID NO:4203:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1579879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4203:

|          |     |     |     |          |     |     |     |           |           |     |     |     |     |           |     |
|----------|-----|-----|-----|----------|-----|-----|-----|-----------|-----------|-----|-----|-----|-----|-----------|-----|
| Leu<br>1 | Leu | Gly | Arg | Thr<br>5 | Leu | Phe | Cys | Leu       | Arg<br>10 | Pro | Val | Ala | Ala | Pro<br>15 | Leu |
| Pro      | Cys | Ala | Pro | Pro      | Cys | Arg | Arg | Thr<br>25 | Arg       | Pro | Arg | Gln | Arg | Val       | Arg |
| Gly      | Arg | Ala | Pro | Pro      | Pro | Ala | Ala | Ser       | Arg       | Ser | Gly | His | Ser | Cys       |     |
| Pro      | Leu | Thr | Ile | Leu      | Pro | Pro | Pro | Pro       | Gln       | Gln | Pro | Arg | Arg | Cys       | Asp |
| Pro      | His | Pro | Pro | Pro      | Pro | Ala | Ser | Arg       | Pro       | Gln | His | Leu | Arg | Leu       | Ala |
| Ala      | Asp | Leu | Asn | Asn      | Glu | Ala | His | Ser       | Ile       | Val | Gly | His | Ala |           |     |

(2) INFORMATION FOR SEQ ID NO:4204:

(A) LENGTH: 476 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..476

(D) OTHER INFORMATION: / Ceres Seq. ID 1579904

(xi) SEQUENCE DESCRIPTION: SEO ID NO:4204:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| taattgtcat | tgtgcaacg  | aactttctg   | agtcgctaga | taaagcccta | gtcagacctg | 60  |
| ggcgttttga | ccgtcatatt | gttgttccca  | accagatgt  | tgaaggtcga | cgccaaattc | 120 |
| tagaatgcc  | atatgtcaa  | gatcttgaaa  | ggtgatgatg | tggacttaat | gatcattgct | 180 |
| agaggaacac | cgggattctc | tgggtgcagac | cttgctaact | tggtaaatgt | tgctgctctt | 240 |
| aaggctgcc  | tggatggtgc | aaaagotgtc  | acaatggatg | atcttgagta | tgcaaaggac | 300 |
| cgaatcatga | tgggtagtga | gcggaagtgc  | gcagttatct | ctgacgaatg | caggaagctg | 360 |
| acagcatacc | atgagggagg | gcattgccct  | gttgcaatcc | acacgaagg  | agctcaccct | 420 |
| gtccacaagq | ctaccatcgt | acctaggggg  | atggccctag | gaatggtggc | ccaact     |     |

(2) INFORMATION FOR SEQ ID NO:4205:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4205:

(2) INFORMATION FOR SEQ ID NO:4206:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1579906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4206:

(2) INFORMATION FOR SEQ ID NO:4207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1579907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4207:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Gly | Ala | Lys | Ala | Val | Thr | Met | Asp | Asp | Leu | Glu | Tyr | Ala | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Arg | Ile | Met | Met | Gly | Ser | Glu | Arg | Lys | Ser | Ala | Val | Ile | Ser | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Cys | Arg | Lys | Leu | Thr | Ala | Tyr | His | Glu | Gly | Gly | His | Ala | Leu | Val |

(2) INFORMATION FOR SEQ ID NO:4208:

(A) LENGTH: 439 base pairs

(C) STRANDEDNESS: sing

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

(A) NAME/KEY: -

(B) LOCATION: 1..439

(D) OTHER INFORMATION: / Ceres Seq. ID 1579911

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| aaaccgattt | cccccttttt | tctttatttt  | cttcgtctct | ttcgtctcga | ctcgcgcgcc | 60  |
| agtcacctca | aatcccttcg | atccaatctc  | caaacyctag | gcaatccaac | atcaaagtat | 120 |
| tagctgcccc | cttcgtcaaa | cgcgcggcggc | gcggccatgg | cccacgcgcg | cgcgcgcggg | 180 |
| aaggcgaagg | tgacgcgcga | cctggcggtg  | gacggcgagg | gcacgcgcac | gctcaaccgc | 240 |
| actgtgctgc | agcgccctcg | cccggcgcgt  | gaggatatct | tcataccgcg | ggctcacgct | 300 |
| acgctgtacg | actttgacac | cgatgtcaac  | cagtggagac | ggaaggacgt | ggaggggtcg | 360 |
| ctcttcgctg | tcaagagcaa | tgctcaacct  | agattccagt | tcatggtcac | gaaccgcagg | 420 |
| aatacagata | atctaagttg |             |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:4209:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1579912

[illegible]

(2) INFORMATION FOR SEO ID NO:4210:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1579913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4210:

Met Ala His Gly Gly Gly Ala Gly Lys Ala Lys Val Thr Pro Asn Leu  
1 5 10 15  
Ala Val Asp Gly Glu Gly Thr Arg Thr Leu Asn Arg Thr Val Leu Gln  
20 25 30  
Arg Leu Asp Pro Ala Val Glu Asp Ile Leu Ile Thr Ala Ala His Val  
35 40 45  
Thr Leu Tyr Asp Phe Asp Thr Asp Val Asn Gln Trp Arg Arg Lys Asp  
50 55 60  
Val Glu Gly Ser Leu Phe Val Val Lys Arg Asn Ala Gln Pro Arg Phe  
65 70 75 80  
Gln Phe Met Val Met Asn Arg Arg Asn Thr Asp Asn Leu Val  
85 90

(2) INFORMATION FOR SEQ ID NO:4211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..496
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4211:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aaggccctct gtctgtgtgc gagcgcaaga gaaagggagt cagagagaga gagagagga   | 60  |
| ggagaccttg cagaggagcg aagcaagcaa ggtgggaaag aagcagcagc aaggcgcgcg  | 120 |
| ggctgccgga aggggaacat gctccctcct catctcacag agaatggcgc ggtgatgatt  | 180 |
| cagtttggcc atcagatgcc tgattacgac tccccggcta cccagtcaac cagtgaacg   | 240 |
| agccatcaag aagcgtcttg aatgagcgaa gggagcctca acgagcataa taatgacat   | 300 |
| tcaggcaacc ttgatgggta ctogaagagt gacgaaaaca agatgatgtc agcgttatcc  | 360 |
| ctgggcaatc cggaaacagc ttacgcacat aatccgaagc ctgaccgtac tcagtccttc  | 420 |
| gccatatcat acccatatgc cgatccatac tacggtggcg cgggtggcagc agcttatggc | 480 |
| ccgcatgcta tcatgc                                                  |     |

(2) INFORMATION FOR SEQ ID NO:4212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4212:

Lys Ala Leu Cys Leu Cys Ala Ser Ala Arg Glu Arg Glu Ser Glu Arg  
1 5 10 15  
Glu Arg Glu Gly Gly Asp Leu Ala Glu Glu Arg Ser Lys Gln Gly Gly  
20 25 30  
Lys Glu Ala Ala Ala Arg Ala Ala Gly Cys Arg Lys Gly Asn Met Leu  
35 40 45  
Pro Pro His Leu Thr Glu Asn Gly Ala Val Met Ile Gln Phe Gly His  
50 55 60  
Gln Met Pro Asp Tyr Asp Ser Pro Ala Thr Gln Ser Thr Ser Glu Thr  
65 70 75 80  
Ser His Gln Glu Ala Ser Gly Met Ser Glu Gly Ser Leu Asn Glu His  
85 90 95  
Asn Asn Asp His Ser Gly Asn Leu Asp Gly Tyr Ser Lys Ser Asp Glu  
100 105 110  
Asn Lys Met Met Ser Ala Leu Ser Leu Gly Asn Pro Glu Thr Ala Tyr  
115 120 125

000000-000000

Ala His Asn Pro Lys Pro Asp Arg Thr Gln Ser Phe Ala Ile Ser Tyr  
130 135 140  
Pro Tyr Ala Asp Pro Tyr Tyr Gly Gly Ala Val Ala Ala Ala Tyr Gly  
145 150 155 160  
Pro His Ala Ile Met  
165

(2) INFORMATION FOR SEQ ID NO:4213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1579924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4213:

Met Leu Pro Pro His Leu Thr Glu Asn Gly Ala Val Met Ile Gln Phe  
1 5 10 15  
Gly His Gln Met Pro Asp Tyr Asp Ser Pro Ala Thr Gln Ser Thr Ser  
20 25 30  
Glu Thr Ser His Gln Glu Ala Ser Gly Met Ser Glu Gly Ser Leu Asn  
35 40 45  
Glu His Asn Asn Asp His Ser Gly Asn Leu Asp Gly Tyr Ser Lys Ser  
50 55 60  
Asp Glu Asn Lys Met Met Ser Ala Leu Ser Leu Gly Asn Pro Glu Thr  
65 70 75 80  
Ala Tyr Ala His Asn Pro Lys Pro Asp Arg Thr Gln Ser Phe Ala Ile  
85 90 95  
Ser Tyr Pro Tyr Ala Asp Pro Tyr Tyr Gly Gly Ala Val Ala Ala Ala  
100 105 110  
Tyr Gly Pro His Ala Ile Met  
115

(2) INFORMATION FOR SEQ ID NO:4214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1579925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4214:

Met Ile Gln Phe Gly His Gln Met Pro Asp Tyr Asp Ser Pro Ala Thr  
1 5 10 15  
Gln Ser Thr Ser Glu Thr Ser His Gln Glu Ala Ser Gly Met Ser Glu  
20 25 30  
Gly Ser Leu Asn Glu His Asn Asn Asp His Ser Gly Asn Leu Asp Gly  
35 40 45  
Tyr Ser Lys Ser Asp Glu Asn Lys Met Met Ser Ala Leu Ser Leu Gly  
50 55 60  
Asn Pro Glu Thr Ala Tyr Ala His Asn Pro Lys Pro Asp Arg Thr Gln  
65 70 75 80  
Ser Phe Ala Ile Ser Tyr Pro Tyr Ala Asp Pro Tyr Tyr Gly Gly Ala  
85 90 95  
Val Ala Ala Ala Tyr Gly Pro His Ala Ile Met  
100 105

(2) INFORMATION FOR SEQ ID NO:4215:

00000000-00000000

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 436 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..436  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4215:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| agcagggcgt tgggcgagtg agtgagtcag tgaggctggg atagcagcag cagtgcgcgcg | 60  |
| cactcaactt ctcttcttgc cgtgcggtgt gcgcggcgcg gggaggcacc gcacggccgc  | 120 |
| aagcaatgcc ggcgcggcag aggacgcgca gcagcgagga gctcaaggcg gaggacttcg  | 180 |
| tcgactcggt gctcaacttc ggcggcgagg aggaggatgg ggaagaggag aagcaggagg  | 240 |
| ccggcgggga cggccagccg gcggcggagt tcaagtccaa gaacctggag gccgagcgga  | 300 |
| agcggcgcgg caagctcaac cgcaacatcc tcgcgctcag ggccgtgggt ccgaacatca  | 360 |
| ccaagatgag caaggagtcc accctctcgg acgctatcga cctcatcaag aagctccaga  | 420 |
| accaggtcct tgagct                                                  |     |

(2) INFORMATION FOR SEQ ID NO:4216:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 103 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..103  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4216:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Arg | Arg | Gln | Arg | Thr | Arg | Ser | Ser | Glu | Glu | Leu | Lys | Ala | Glu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asp | Phe | Val | Asp | Ser | Val | Leu | Asn | Phe | Gly | Gly | Glu | Glu | Glu | Asp | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Glu | Glu | Glu | Lys | Gln | Glu | Ala | Gly | Asp | Gly | Gln | Pro | Ala | Ala | Glu |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Lys | Ser | Lys | Asn | Leu | Glu | Ala | Glu | Arg | Lys | Arg | Arg | Gly | Lys | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Asn | Arg | Asn | Ile | Leu | Ala | Leu | Arg | Ala | Val | Val | Pro | Asn | Ile | Thr | Lys |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Met | Ser | Lys | Glu | Ser | Thr | Leu | Ser | Asp | Ala | Ile | Asp | Leu | Ile | Lys | Lys |
|     |     |     |     |     |     |     |     | 85  |     |     | 90  |     |     | 95  |     |
| Leu | Gln | Asn | Gln | Val | Leu | Glu |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:4217:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 278 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..278  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4217:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ctaataaacc gtgcccctcc gtcccaaccg tccgccgcct ccctcccttt ccgctccgcc | 60  |
| aagaccctcc tcctcaccac actcaccag cccccctcga gcccagaagc accgcgcgca  | 120 |
| ccatgcggcc accgagaggg gcgcggcgcg gcggcggttc ggccgagggt gaggccgagg | 180 |
| cggcggcggt ggccggttcg gcggcgaggg ccgtggtggc cggttcggcg gcgggttcgc | 240 |



cgacgagggc cgcgccgcag aggttcgtcg aggtgtcg

(2) INFORMATION FOR SEQ ID NO:4218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1579932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4218:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Asn | Arg | Ala | Pro | Pro | Ser | Gln | Pro | Ser | Ala | Ala | Ser | Leu | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Arg | Ser | Ala | Lys | Thr | Leu | Leu | Leu | Thr | Pro | Leu | Thr | Gln | Leu | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ser | Pro | Glu | Ala | Pro | Arg | Ala | Pro | Cys | Gly | His | Arg | Glu | Gly | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Ala | Ala | Ala | Val | Arg | Arg | Arg | Trp | Arg | Pro | Arg | Arg | Arg | Arg | Trp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Val | Arg | Arg | Arg | Arg | Pro | Trp | Trp | Pro | Val | Arg | Arg | Arg | Val | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Arg | Gly | Pro | Ala | Arg | Arg | Gly | Ser | Ser | Arg | Cys |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:4219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1579933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4219:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Lys | Pro | Cys | Pro | Ser | Val | Pro | Thr | Val | Arg | Arg | Leu | Pro | Pro | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Leu | Arg | Gln | Asp | Pro | Pro | Pro | His | Pro | Thr | His | Pro | Ala | Pro | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Pro | Arg | Ser | Thr | Ala | Arg | Thr | Met | Arg | Pro | Pro | Arg | Gly | Arg | Gly |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Gly | Gly | Gly | Gly | Ser | Ala | Glu | Val | Glu | Ala | Glu | Ala | Ala | Ala | Val | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Ser | Ala | Ala | Glu | Ala | Val | Val | Ala | Gly | Ser | Ala | Ala | Gly | Ser | Ala |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Thr | Arg | Ala | Arg | Pro | Gln | Arg | Phe | Val | Glu | Val | Ser |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:4220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52

(D) OTHER INFORMATION: / Ceres Seq. ID 1579934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4220:

Met Arg Pro Pro Arg Gly Arg Gly Gly Gly Gly Gly Ser Ala Glu Val  
1 5 10 15  
Glu Ala Glu Ala Ala Val Ala Gly Ser Ala Ala Glu Ala Val Val  
20 25 30  
Ala Gly Ser Ala Ala Gly Ser Ala Thr Arg Ala Arg Pro Gln Arg Phe  
35 40 45  
Val Glu Val Ser  
50

(2) INFORMATION FOR SEQ ID NO:4221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..459
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4221:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aaaacgctga tcggagcaac gaagcccgcga gccatgccga cggcgacggc cacggcagct | 60  |
| cctcgccaag cggcgctctt cctgcccctg ctgctgctcc tgctcggcct ccacgccacg  | 120 |
| tccgcgcgcg ccgcgcgcgc gggcgctgcc gtggacgcg agctcacgtc caccaagcgc   | 180 |
| tccccggtcc cgaagaagcc cagcgtgaag ccgcccggcc ccggcgccgc gagcccgacc  | 240 |
| ttcccggtct tcggcatccc cgggatgggc gggttcggca tccccgggat gggcgccggc  | 300 |
| gggtggggcg ggcgctacgg cgggcccgcc ggcggtacg ccgcgcggcg cgtggtggcg   | 360 |
| cccacgctga cgtgctccga gaagggggcc tgctacagga agaaggtcac ctgccccaa   | 420 |
| aagtgtttct cctcgtagag cggcgcgcca aggggtacg                         |     |

(2) INFORMATION FOR SEQ ID NO:4222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4222:

Lys Thr Leu Ile Gly Ala Thr Lys Pro Ala Ala Met Pro Thr Ala Thr  
1 5 10 15  
Ala Thr Ala Ala Pro Arg His Ala Ala Leu Phe Leu Pro Leu Leu Leu  
20 25 30  
Leu Leu Leu Gly Leu His Ala Thr Ser Ala Ala Ala Ala Arg Ala Gly  
35 40 45  
Val Ala Val Asp Ala Glu Leu Thr Ser Thr Lys Pro Ser Pro Val Pro  
50 55 60  
Lys Lys Pro Ser Val Lys Pro Pro Gly Pro Gly Ala Ala Ser Pro Thr  
65 70 75 80  
Phe Pro Gly Phe Gly Ile Pro Gly Met Gly Gly Phe Gly Ile Pro Gly  
85 90 95  
Met Gly Ala Gly Gly Trp Gly Gly Gly Tyr Gly Gly Pro Ala Gly Gly  
100 105 110  
Tyr Ala Arg Gly Gly Val Val Ala Pro Thr Val Thr Cys Ser Glu Lys  
115 120 125  
Gly Pro Cys Tyr Arg Lys Lys Val Thr Cys Pro Lys Lys Cys Phe Ser  
130 135 140  
Ser Tyr Ser Gly Ala Ala Arg Gly Thr  
145 150

(2) INFORMATION FOR SEQ ID NO:4223:

2025 RELEASE UNDER E.O. 14176

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 152 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..152  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579955  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4223:

Asn Ala Asp Arg Ser Asn Glu Ala Arg Ser His Ala Asp Gly Asp Gly  
1                  5                  10                  15  
His Gly Ser Ser Ser Pro Arg Gly Ala Leu Pro Ala Pro Ala Ala Ala  
                  20                  25                  30  
Pro Ala Arg Pro Pro Arg His Val Arg Arg Arg Arg Ala Arg Gly Arg  
                  35                  40                  45  
Arg Arg Gly Arg Arg Ala His Val His Gln Ala Val Pro Gly Pro Glu  
50                  55                  60  
Glu Ala Gln Arg Glu Ala Ala Arg Pro Arg Arg Glu Pro Asp Leu  
65                  70                  75                  80  
Pro Gly Leu Arg His Pro Arg Asp Gly Arg Val Arg His Pro Arg Asp  
                  85                  90                  95  
Gly Arg Arg Arg Val Gly Arg Arg Leu Arg Arg Ala Arg Arg Arg Val  
                  100                 105                 110  
Arg Pro Arg Arg Arg Gly Gly Ala His Arg Asp Val Leu Arg Glu Gly  
                 115                 120                 125  
Ala Leu Leu Gln Glu Glu Gly His Leu Pro Gln Glu Val Leu Leu Leu  
130                 135                 140  
Val Gln Arg Arg Gly Lys Gly Tyr  
145                 150

(2) INFORMATION FOR SEQ ID NO:4224:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 142 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..142  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579956  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4224:

Met Pro Thr Ala Thr Ala Thr Ala Ala Pro Arg His Ala Ala Leu Phe  
1                  5                  10                  15  
Leu Pro Leu Leu Leu Leu Leu Gly Leu His Ala Thr Ser Ala Ala  
                  20                  25                  30  
Ala Ala Arg Ala Gly Val Ala Val Asp Ala Glu Leu Thr Ser Thr Lys  
                  35                  40                  45  
Pro Ser Pro Val Pro Lys Lys Pro Ser Val Lys Pro Pro Gly Pro Gly  
50                  55                  60  
Ala Ala Ser Pro Thr Phe Pro Gly Phe Gly Ile Pro Gly Met Gly Gly  
65                  70                  75                  80  
Phe Gly Ile Pro Gly Met Gly Ala Gly Gly Trp Gly Gly Gly Tyr Gly  
                  85                  90                  95  
Gly Pro Ala Gly Gly Tyr Ala Arg Gly Gly Val Val Ala Pro Thr Val  
                 100                 105                 110  
Thr Cys Ser Glu Lys Gly Pro Cys Tyr Arg Lys Lys Val Thr Cys Pro  
115                 120                 125  
Lys Lys Cys Phe Ser Ser Tyr Ser Gly Ala Ala Arg Gly Thr  
130                 135                 140

|                     |                     |                     |                     |                     |                     |     |
|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|-----|
| t t t t a g c a c c | a c c t c t c a t g | a c t a y n a c a t | t t c t t t c g g g | a a a g t a g a a a | a a a a t c t a t t | 60  |
| a c c c a t g a g g | c c a t g a t a c t | t t c c a c t t g g | a c g a a g c g a a | a t t g t t a a t t | c o t c o c t t c c | 120 |
| a g t a t a t a g c | t o g t c t c g t c | a c a c t c g g a g | c t c g t a a c a a | a g t c a t c a c t | c a t c a c a t g a | 180 |
| g c t t g c t t g t | g a c t g c c a g c | t t t g c c c a g t | g t t c a t c g c c | c a t g g a a g a g | c g g g c a c t g t | 240 |
| t c c c g g t g t c | c g a t t c c a g c | a c c a c c t g c a | g c a g c t c t g g | c t g t a c c g g c | c c c a a c t c c c | 300 |
| c t g t c t c g t c | g t c g c a g t a t | t t g g a c g a c a | c c a g c g a c g g | c g c c g g c a g c | t c g a g c a g c c | 360 |
| g g a a g c g g c c | g c g c g g g a g   | c t a a g c a t c   | c a a c g t a c c g | c g g c g t g c g c | a t g c g t g c g t | 420 |
| g g g g c a a g t g | g g t g t c c g a g | a t c c g g a g c   | c c c g c a a g a a | g t c g c g c a t c | t g g c t g g g c a | 480 |
| c c t t c a c a c c | t c c c c m q a q a | t g g c g c g c g   | c g c g c a t g a c | g t c g             |                     |     |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4226:

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4227:

Met Glu Glu Arg Ala Leu Phe Pro Val Ser Asp Ser Ser Thr Thr Cys  
1 5 10 15  
Ser Ser Ser Gly Cys Thr Gly Pro Asn Ser Pro Val Ser Ser Ser Gln  
20 25 30  
Tyr Leu Asp Asp Thr Ser Asp Gly Ala Gly Ser Ser Ser Ser Arg Lys  
35 40 45  
Arg Pro Arg Arg Glu Leu Lys His Pro Thr Tyr Arg Gly Val Arg Met  
50 55 60  
Arg Ala Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Arg Lys Lys  
65 70 75 80  
Ser Arg Ile Trp Leu Gly Thr Phe Asp Thr Pro Xaa Arg Trp Pro Arg  
85 90 95  
Ala Arg Met Thr Ser  
100

(2) INFORMATION FOR SEQ ID NO:4228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..513
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4228:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| acttcacccc tctcaatctc gtcctacact ctctcccacc ttcaacttcac ctgctctctc | 60  |
| tggttctcgag ctagctcaca tcagggggag gaagaggaac cagcacctgc ctcgccatgt | 120 |
| cgctctccat ggtgtccaag aacgcgccgc cgccggccgg gtacggcgac ggcgaaggca  | 180 |
| gcgtgctcga ggccgcgccg gtgacgagct gcctgtacct gcgccccggg gcggggggcg  | 240 |
| tggacagggg cgccgtgctg cgccgcatcc gccaccggag gcgccacgac cgctccacg   | 300 |
| acacgctgcg ctccatggtg caggcgccgc cgcggtcggc tgagccggac ggcattggacg | 360 |
| gcgcagaacg gcacctcccg tggccgctcg acgacgcctt ctcggcgcct tagcttttgt  | 420 |
| aatatagaat tagtctcttg tgcagattaa gsaaatgcac atggaacatg gtccagttcg  | 480 |
| cctctctcttg tgtagactgt gaataacaga tgc                              |     |

(2) INFORMATION FOR SEQ ID NO:4229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4229:

Leu His Pro Ser Gln Ser Arg Ser Ser Leu Ser Pro Thr Phe Thr Ser  
1 5 10 15  
Pro Ala Leu Ser Val Leu Glu Leu Ala His Ile Arg Gly Arg Lys Arg  
20 25 30  
Asn Gln His Leu Pro Arg His Val Val Leu His Gly Val Gln Glu Arg  
35 40 45  
Ala Ala Ala Gly Arg Val Arg Arg Arg Arg Gln Arg Arg Arg Gly  
50 55 60  
Arg Ala Gly Asp Glu Leu Pro Val Pro Ala Pro Arg Gly Gly Gly Ala  
65 70 75 80  
Gly Gln Gly Arg Arg Ala Ala Pro His Pro Pro Pro Glu Ala Pro Arg  
85 90 95  
Pro Pro Pro Arg His Ala Ala Leu His Gly Ala Gly Ala Ala Val  
100 105 110

(2) INFORMATION FOR SEQ ID NO:4230:

- (ii) MOLECULE TYPE: peptide

- (A) NAME/KEY: peptide

- (D) OTHER INFORMATION: / Ceres Seq. ID 1579977

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4230:

Ala Pro

- (2) INFORMATION FOR SEQ ID NO:4231:

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..94

- (D) OTHER INFORMATION: / Ceres Seq. ID 1579978

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4231:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ser | Lys | Asn | Ala | Pro | Pro | Pro | Ala | Gly | Tyr | Gly | Asp | Gly | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ser | Val | Val | Glu | Ala | Ala | Pro | Val | Thr | Ser | Cys | Leu | Tyr | Leu | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Gly | Ala | Gly | Ala | Leu | Asp | Arg | Asp | Ala | Val | Leu | Arg | Arg | Ile | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Arg | Arg | Arg | His | Asp | Arg | Leu | His | Asp | Thr | Leu | Arg | Ser | Met | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Ala | Pro | Pro | Arg | Ser | Ala | Glu | Pro | Asp | Gly | Met | Asp | Gly | Ala | Glu |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | His | Leu | Pro | Trp | Pro | Leu | Asp | Asp | Ala | Phe | Ser | Ala | Pro |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:4232:

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..481

(D) OTHER INFORMATION: / Ceres Seq. ID 1579979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4232:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ctctccacgc | ccgcgcaccg | ccgctccgcc | actccacct  | tctactcacc | gccgccaccg | 60  |
| ctcggctccg | cccgtgcgca | gcgccagcga | ccaagccccg | ccgccgctcc | ctcgtcctcg | 120 |
| tccgcgcctc | cagctcggac | cctccgcagc | agcagctcaa | cctctccgtg | ctccgcttca | 180 |
| ccctcgggat | tccggggctg | gacgaatcgt | acctcccccg | gtggataggc | ctcggtttcg | 240 |
| gcgcgctcgt | cgtgctcaac | cacctcctct | ctgcgtcccc | gacgcccgcg | cagctcaggt | 300 |
| ccgaggctgt | ggggctgtgc | ctggccgcgt | tctcggcgac | gctgccgttc | ctggggaggt | 360 |
| tccttgaggg | cgctgatgct | gccagccgag | tgccgttgcc | cgaggggagc | atccaagtat | 420 |
| tcgtcatgtc | tgagaacctg | tcagctgtgc | agaaggagga | catggcgtgg | gcgtcgtacg | 480 |
| t          |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:4233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1579980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4233:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Pro | Arg | Pro | Arg | Thr | Ala | Ala | Pro | Pro | Leu | Pro | Pro | Ser | Thr | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Arg | His | Arg | Ser | Ala | Pro | Pro | Val | Arg | Ser | Ala | Ser | Asp | Gln | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Pro | Pro | Leu | Pro | Arg | Pro | Arg | Pro | Arg | Leu | Gln | Leu | Gly | Pro | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Ala | Ala | Ala | Ala | Gln | Pro | Leu | Arg | Ala | Pro | Leu | His | Pro | Arg | Asp | Ser |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Gly | Ala | Gly | Arg | Ile | Val | Pro | Pro | Pro | Val | Asp | Arg | Pro | Arg | Phe | Arg |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Ala | Arg | Arg | Ala | Gln | Pro | Pro | Pro | Leu | Cys | Val | Pro | Asp | Ala | Arg |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Ala | Gln | Val | Arg | Gly | Cys | Gly | Ala | Val | Pro | Gly | Arg | Val | Leu | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Ala | Ala | Val | Pro | Gly | Glu | Val | Pro |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:4234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1579981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4234:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | His | Ala | Arg | Ala | Pro | Pro | Leu | Arg | His | Ser | His | Leu | Leu | Leu | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ala | Thr | Ala | Arg | Leu | Arg | Pro | Cys | Ala | Ala | Pro | Ala | Thr | Lys | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Arg | Arg | Ser | Leu | Val | Leu | Val | Arg | Ala | Ser | Ser | Ser | Asp | Pro | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Gln | Gln | Leu | Asn | Leu | Ser | Val | Leu | Arg | Phe | Thr | Leu | Gly | Ile | Pro |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Gly | Leu | Asp | Glu | Ser | Tyr | Leu | Pro | Arg | Trp | Ile | Gly | Leu | Gly | Phe | Gly |

(2) INFORMATION FOR SEQ ID NO:4235:

|             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| cagagagttta | tggagttaat | gttgtagttg | caatcaacaa | atttgcataca | gatactgagg | 60  |
| cagaaatgaa  | ggcagtgac  | agtgcagcta | tggctgctgg | tgcttttgac  | gctgttgtct | 120 |
| gcacacacca  | tgccatggg  | ggtaaaggag | cggttgagct | tggacttgct  | gttcaacgag | 180 |
| catgcgaaag  | ccaggcagaa | cctctgaagt | ttttgtatcc | cttggaatct  | agcataaagg | 240 |
| agaagattga  | gtcaattgct | aagttctatg | gtgctagtgg | cgttgaatat  | tccgagcagg | 300 |
| ctgagaagca  | gattgagatg | tacaccaagc | aagggttctc | cagcctcccc  | atttgcattg | 360 |
| cgaagaccca  | gtactcgttc | tcacatgtcc | cgtccatgaa | gggcgccccg  | accggtcttg | 420 |
| ttctgccgat  | aagagacgtg | agggccagca | tcggcgctgg | gttcatctac  | ccgctcgtgg | 480 |
| gc          |            |            |            |             |            |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Tyr | Gly | Val | Asn | Val | Val | Val | Ala | Ile | Asn | Lys | Phe | Ala | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Thr | Glu | Ala | Glu | Met | Lys | Ala | Val | His | Ser | Ala | Ala | Met | Ala | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ala | Phe | Asp | Ala | Val | Val | Cys | Thr | His | His | Ala | His | Gly | Gly | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Ala | Val | Glu | Leu | Gly | Leu | Ala | Val | Gln | Arg | Ala | Cys | Glu | Ser | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Glu | Pro | Leu | Lys | Phe | Leu | Tyr | Pro | Leu | Glu | Ser | Ser | Ile | Lys | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Ile | Glu | Ser | Ile | Ala | Lys | Phe | Tyr | Gly | Ala | Ser | Gly | Val | Glu | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Glu | Gln | Ala | Glu | Lys | Gln | Ile | Glu | Met | Tyr | Thr | Lys | Gln | Gly | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Ser | Leu | Pro | Ile | Cys | Met | Ala | Lys | Thr | Gln | Tyr | Ser | Phe | Ser | His |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Pro | Ser | Met | Lys | Gly | Ala | Pro | Thr | Gly | Phe | Val | Leu | Pro | Ile | Arg |



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 130                                                             | 135 | 140 |
| Asp Val Arg Ala Ser Ile Gly Ala Gly Phe Ile Tyr Pro Leu Val Gly |     |     |
| 145                                                             | 150 | 155 |
|                                                                 |     | 160 |

(2) INFORMATION FOR SEQ ID NO:4237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4237:

Met Lys Ala Val His Ser Ala Ala Met Ala Ala Gly Ala Phe Asp Ala  
1 5 10 15  
Val Val Cys Thr His His Ala His Gly Gly Lys Gly Ala Val Glu Leu  
20 25 30  
Gly Leu Ala Val Gln Arg Ala Cys Glu Ser Gln Ala Glu Pro Leu Lys  
35 40 45  
Phe Leu Tyr Pro Leu Glu Ser Ser Ile Lys Glu Lys Ile Glu Ser Ile  
50 55 60  
Ala Lys Phe Tyr Gly Ala Ser Gly Val Glu Tyr Ser Glu Gln Ala Glu  
65 70 75 80  
Lys Gln Ile Glu Met Tyr Thr Lys Gln Gly Phe Ser Ser Leu Pro Ile  
85 90 95  
Cys Met Ala Lys Thr Gln Tyr Ser Phe Ser His Val Pro Ser Met Lys  
100 105 110  
Gly Ala Pro Thr Gly Phe Val Leu Pro Ile Arg Asp Val Arg Ala Ser  
115 120 125  
Ile Gly Ala Gly Phe Ile Tyr Pro Leu Val Gly  
130 135

(2) INFORMATION FOR SEQ ID NO:4238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4238:

Met Ala Ala Gly Ala Phe Asp Ala Val Val Cys Thr His His Ala His  
1 5 10 15  
Gly Gly Lys Gly Ala Val Glu Leu Gly Leu Ala Val Gln Arg Ala Cys  
20 25 30  
Glu Ser Gln Ala Glu Pro Leu Lys Phe Leu Tyr Pro Leu Glu Ser Ser  
35 40 45  
Ile Lys Glu Lys Ile Glu Ser Ile Ala Lys Phe Tyr Gly Ala Ser Gly  
50 55 60  
Val Glu Tyr Ser Glu Gln Ala Glu Lys Gln Ile Glu Met Tyr Thr Lys  
65 70 75 80  
Gln Gly Phe Ser Ser Leu Pro Ile Cys Met Ala Lys Thr Gln Tyr Ser  
85 90 95  
Phe Ser His Val Pro Ser Met Lys Gly Ala Pro Thr Gly Phe Val Leu  
100 105 110

Pro Ile Arg Asp Val Arg Ala Ser Ile Gly Ala Gly Phe Ile Tyr Pro  
115 120 125  
Leu Val Gly  
130

(2) INFORMATION FOR SEQ ID NO:4239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..433
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4239:

|             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| acaatttgat  | tttgaccgct | cgctgcctg  | gcgcctcct  | agtcgtaatc  | ccgccccgcc | 60  |
| gcctccccct  | ctccggcctt | ctccgctccg | cgcgggcgcc | atgtcgggtga | cgctgcacac | 120 |
| gaacctgggc  | gacatcaagt | gcgaggtgtt | ctgcgaccag | gtgccgcgca  | cgcgcgagaa | 180 |
| cttctctggcg | ctctgcgcca | gcggctacta | cgacggcacc | gtgttccacc  | gcaacatcaa | 240 |
| gggcttcatg  | gtccagggcg | gcgacccac  | cggcaccggc | aaggcggggt  | cgtccatctg | 300 |
| gggcgccaag  | ttcgcgacg  | agttgaggga | gtcgtcaag  | cacaacgcgc  | gcgggatcat | 360 |
| gtcgatggcc  | aacagcgggc | ccaacaccaa | cggcagccag | ttcttcatca  | cctacgcca  | 420 |
| gcagccgcac  | ctc        |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:4240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4240:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Phe | Asp | Phe | Asp | Pro | Ser | Pro | Ala | Trp | Pro | Pro | Pro | Ser | Arg | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ala | Pro | Pro | Pro | Pro | Pro | Leu | Arg | Pro | Ser | Pro | Leu | Arg | Ala | Gly |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Met | Ser | Val | Thr | Leu | His | Thr | Asn | Leu | Gly | Asp | Ile | Lys | Cys | Glu |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Phe | Cys | Asp | Gln | Val | Pro | Arg | Thr | Ala | Glu | Asn | Phe | Leu | Ala | Leu |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Cys | Gly | Ser | Gly | Tyr | Tyr | Asp | Gly | Thr | Val | Phe | His | Arg | Asn | Ile | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Phe | Met | Val | Gln | Gly | Gly | Asp | Pro | Thr | Gly | Thr | Gly | Lys | Gly | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Ser | Ile | Trp | Gly | Ala | Lys | Phe | Ala | Asp | Glu | Leu | Arg | Glu | Ser | Leu |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | His | Asn | Ala | Arg | Gly | Ile | Met | Ser | Met | Ala | Asn | Ser | Gly | Pro | Asn |
|     |     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Asn | Gly | Ser | Gln | Phe | Phe | Ile | Thr | Tyr | Ala | Lys | Gln | Pro | His | Leu |
|     |     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:4241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Val | Thr | Leu | His | Thr | Asn | Leu | Gly | Asp | Ile | Lys | Cys | Glu | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Cys | Asp | Gln | Val | Pro | Arg | Thr | Ala | Glu | Asn | Phe | Leu | Ala | Leu | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ser | Gly | Tyr | Tyr | Asp | Gly | Thr | Val | Phe | His | Arg | Asn | Ile | Lys | Gly |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Phe | Met | Val | Gln | Gly | Gly | Asp | Pro | Thr | Gly | Thr | Gly | Lys | Gly | Gly | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Ile | Trp | Gly | Ala | Lys | Phe | Ala | Asp | Glu | Leu | Arg | Glu | Ser | Leu | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| His | Asn | Ala | Arg | Gly | Ile | Met | Ser | Met | Ala | Asn | Ser | Gly | Pro | Asn | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Gly | Ser | Gln | Phe | Phe | Ile | Thr | Tyr | Ala | Lys | Gln | Pro | His | Leu |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

(i) SEQUENCE CHARACTERISTICS:

(A) NAME/KEY: -  
(B) LOCATION: 1..291  
(D) OTHER INFORMATION: / Ceres Seq. ID 1580028

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| acctggccgc | caccttcctt | ctacctcgtc | cccctgcttc | cctgaccgag | cagcgcccag | 60  |
| gcaaccgcat | agcacgcgt  | gacctgacc  | gccaggagcc | cgaccgycg  | aagccccacc | 120 |
| gccaggagcg | cagccgcgc  | acccgaccg  | aagccgccc  | cgtccttgca | cacgacgcgc | 180 |
| caccgaggac | cgagccacc  | actcgaccg  | gacccagct  | accgtcgcca | cgtcgcgcca | 240 |
| gqccgagccc | tqcatccgcg | ccgagcgacc | gcgccaggaa | cccgacccc  | g          |     |

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1580029

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ala | Ala | Thr | Phe | Leu | Leu | Pro | Arg | Pro | Pro | Ala | Ser | Leu | Thr | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Arg | Pro | Gly | Asn | Arg | Ile | Ala | Pro | Arg | Asp | Pro | Asp | Arg | Gln | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Asp | Arg | Pro | Lys | Pro | His | Arg | Gln | Asp | Ala | Ser | Arg | Ala | Thr | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Glu | Ala | Ala | Arg | Val | Pro | Ala | His | Asp | Ala | Pro | Pro | Arg | Thr | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Arg | Thr | Arg | Pro | Arg | Pro | Arg | Leu | Pro | Ser | Pro | Arg | Arg | Ala | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Ser | Pro | Ala | Ser | Ala | Pro | Ser | Asp | Arg | Ala | Arg | Asn | Pro | Thr | Pro |

85

90

95

(2) INFORMATION FOR SEQ ID NO:4244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..302
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4244:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| attttttccc ttgcgcatga cgccgcccgc gccgcctccg tgcctgcct gctcctcac    | 60  |
| cctcctctctc ctgcgcccgc cggcgccgcy accggccggc gccatctgcg tcccgcgcaa | 120 |
| tcccgggtggc cacagcaagc caggagcgcc ggccaagccc gcgccaccga aactaaagcc | 180 |
| cctcacgccc gggcgccgcy cgccgcccga gccgacgccc atggccccgc gcgccgacat  | 240 |
| cgtgcggagc ctgtgcctga agaccgacta ccccgacctg tgcattgctg ccatcgcgaa  | 300 |

gc

(2) INFORMATION FOR SEQ ID NO:4245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4245:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ile Ser Ser Leu Arg His Asp Ala Ala Ala Ala Ser Val Pro Arg     |  |
| 1 5 10 15                                                       |  |
| Leu Pro Pro His Pro Pro Pro Pro Arg Arg Arg Gly Gly Xaa Thr Gly |  |
| 20 25 30                                                        |  |
| Arg Arg His Leu Arg Pro Ala Gln Ser Arg Trp Pro Gln Gln Ala Arg |  |
| 35 40 45                                                        |  |
| Ser Ala Gly Gln Ala Arg Ala Thr Glu Thr Lys Ala Pro His Ala Arg |  |
| 50 55 60                                                        |  |
| Gly Ala Gly Ala Ala Glu Ala Asp Ala Asp Gly Pro Gly Arg Arg His |  |
| 65 70 75 80                                                     |  |
| Arg Ala Glu Pro Val Pro Glu Asp Arg Leu Pro Arg Pro Val His Val |  |
| 85 90 95                                                        |  |
| Gly His Arg Glu                                                 |  |
| 100                                                             |  |

(2) INFORMATION FOR SEQ ID NO:4246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4246:

|                                                             |  |
|-------------------------------------------------------------|--|
| Phe Leu Pro Phe Ala Met Thr Pro Pro Pro Pro Pro Cys Leu Ala |  |
| 1 5 10 15                                                   |  |

Cys Leu Leu Thr Leu Leu Leu Leu Ala Ala Ala Ala Xaa Pro Ala  
20 25 30  
Gly Ala Ile Cys Val Pro Arg Asn Pro Gly Gly His Ser Lys Pro Gly  
35 40 45  
Ala Pro Ala Lys Pro Ala Pro Pro Lys Leu Lys Pro Leu Thr Pro Ala  
50 55 60  
Ala Pro Ala Pro Pro Lys Pro Thr Pro Met Ala Pro Gly Ala Asp Ile  
65 70 75 80  
Val Arg Ser Leu Cys Leu Lys Thr Asp Tyr Pro Asp Leu Cys Met Ser  
85 90 95  
Ala Ile Ala Lys  
100

(2) INFORMATION FOR SEQ ID NO:4247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4247:

Met Thr Pro Pro Pro Pro Pro Pro Cys Leu Ala Cys Leu Leu Thr Leu  
1 5 10 15  
Leu Leu Leu Ala Ala Ala Ala Ala Xaa Pro Ala Gly Ala Ile Cys Val  
20 25 30  
Pro Arg Asn Pro Gly Gly His Ser Lys Pro Gly Ala Pro Ala Lys Pro  
35 40 45  
Ala Pro Pro Lys Leu Lys Pro Leu Thr Pro Ala Ala Pro Ala Pro Pro  
50 55 60  
Lys Pro Thr Pro Met Ala Pro Gly Ala Asp Ile Val Arg Ser Leu Cys  
65 70 75 80  
Leu Lys Thr Asp Tyr Pro Asp Leu Cys Met Ser Ala Ile Ala Lys  
85 90 95

(2) INFORMATION FOR SEQ ID NO:4248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..416
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4248:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| cgcgccctcct | ctcgccctcg | ctccgcgcgc | gccgcgcgcg | cgccgcatca | agcaccgcgc | 60  |
| ccgccgtcgc  | ctgaggtaga | caccaatccg | ccgccatggg | gcgtatgcac | agccgcggga | 120 |
| agggtatctc  | atcgctggcg | ctgccgtaca | agaggacgcc | tcctcccttg | tcaagatcct | 180 |
| ccgcatcctc  | aaggcccatg | ggctggcacc | agaaatcccc | gaggacctgt | acttcctcat | 240 |
| caagaaggcg  | gtggcgataa | ggaagcacct | tgagaggaac | aggaaggaca | aagactctaa | 300 |
| attcaggctc  | attcttgtgg | agagcaggat | ccaccgcctt | gcccgtact  | acaagcgcac | 360 |
| aaagaagctt  | ccaccacac  | ggaagtatga | gtcaaccaca | gcgagcactc | tggtgg     |     |

(2) INFORMATION FOR SEQ ID NO:4249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..90  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1580052  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4249:

Arg Ala Ser Ser Arg Pro Arg Ser Ala Ala Ala Ala Ala Pro Pro His  
1                    5                    10                    15  
Gln Ala Pro Ala Pro Pro Ser Pro Glu Val Asp Thr Asn Pro Pro Pro  
                    20                    25                    30  
Trp Gly Val Cys Thr Ala Ala Gly Arg Val Ser His Arg Arg Arg Cys  
                    35                    40                    45  
Arg Thr Arg Gly Arg Leu Leu Pro Cys Gln Asp Pro Pro His Pro Gln  
50                    55                    60  
Gly Pro Trp Ala Gly Thr Arg Asn Pro Arg Gly Pro Val Leu Pro His  
65                    70                    75                    80  
Gln Glu Gly Gly Gly Asp Lys Glu Ala Pro  
                    85                    90

(2) INFORMATION FOR SEQ ID NO:4250:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 54 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..54  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1580053  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4250:

Met Gly Arg Met His Ser Arg Gly Lys Gly Ile Ser Ser Ser Ala Leu  
1                    5                    10                    15  
Pro Tyr Lys Arg Thr Pro Pro Pro Leu Ser Arg Ser Ser Ala Ser Ser  
                    20                    25                    30  
Arg Pro Met Gly Trp His Gln Lys Ser Pro Arg Thr Cys Thr Ser Ser  
35                    40                    45  
Ser Arg Arg Arg Trp Arg  
50

(2) INFORMATION FOR SEQ ID NO:4251:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 51 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..51  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1580054  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4251:

Met His Ser Arg Gly Lys Gly Ile Ser Ser Ser Ala Leu Pro Tyr Lys  
1                    5                    10                    15  
Arg Thr Pro Pro Pro Leu Ser Arg Ser Ser Ala Ser Ser Arg Pro Met  
                    20                    25                    30  
Gly Trp His Gln Lys Ser Pro Arg Thr Cys Thr Ser Ser Ser Arg Arg  
35                    40                    45  
Arg Trp Arg  
50

(2) INFORMATION FOR SEQ ID NO:4252:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 290 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..290
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1580058
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4252:

```
atatatagat tatagagagg caaacaacc tcgcccactc caacacgtga caccgcgcgc 60
cgcgctcccg ccgcacgccc ccactctctc accgccaccg ccgagatggc cgctgctcc 120
cacctgcgcg ccgcgggtgg ctcttccctt gccgcgcgcg cagtgggtcg ttccccggcg 180
cattctcagc ccgcgcgcgc ctctgcgcgc ctccggtcga cgctgcgttt ctgcagcgcc 240
ggcctgtcgg ttaagggaag cagggcgact ttcccgtagg tcgcccgcgc
```

(2) INFORMATION FOR SEQ ID NO:4253:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..96
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1580059
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4253:

```
Tyr Ile Asp Tyr Arg Glu Ala Asn Lys Pro Arg Pro Leu Gln His Val
1 5 10 15
Thr Pro Arg Gly Ala Pro Pro Pro His Ala Pro Thr Leu Ser Pro Pro
20 25 30
Pro Pro Arg Trp Pro Pro Ala Pro Thr Ser Pro Pro Arg Val Ala Leu
35 40 45
Pro Leu Pro Pro Pro Gln Trp Phe Val Pro Arg Arg Ile Pro Gln Pro
50 55 60
Pro Pro Pro Ser Arg Ala Ser Gly Arg Arg Cys Val Ser Arg Ala Pro
65 70 75 80
Ala Cys Arg Leu Arg Glu Ala Gly Arg Leu Ser Arg Gly Ser Pro Pro
85 90 95
```

(2) INFORMATION FOR SEQ ID NO:4254:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 61 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..61
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1580060
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4254:

```
Met Ala Ala Cys Ser His Leu Ala Ala Gly Gly Ser Ser Pro Ala
1 5 10 15
Ala Ala Ala Val Val Arg Ser Pro Ala His Ser Ser Ala Ala Ala Ala
20 25 30
Phe Ala Arg Leu Arg Ser Thr Leu Arg Phe Ser Ser Ala Gly Leu Ser
35 40 45
Val Lys Gly Ser Arg Ala Thr Phe Pro Trp Val Ala Ala
50 55 60
```

(2) INFORMATION FOR SEQ ID NO:4255:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4255:

(2) INFORMATION FOR SEQ ID NO:4256:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4256:

(2) INFORMATION FOR SEO ID NO:4257:

```

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..107

```



(D) OTHER INFORMATION: / Ceres Seq. ID 1580063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4257:

Met Glu Ser Pro Asp Gln Ala Ala Ala Ala Arg Gln Asp  
1 5 10 15  
Lys Glu Gln Arg Asp Tyr Arg Leu Ile Ala Lys Ala Val Asp Glu Ala  
20 25 30  
Tyr Arg Ala Val Glu Cys Asp Gly Gly Gly Tyr Pro Phe Gly Ala Val  
35 40 45  
Val Val His Gly Gly Gly Asp Asp Glu Val Val Ser Ser Ser His Asn  
50 55 60  
Ser Val Arg Lys Asp Ala Asp Pro Ser Ala His Ala Glu Val Thr Ala  
65 70 75 80  
Ile Arg Gln Ala Cys Lys Lys Leu Gly Lys Thr Ser Leu Ala Gly Cys  
85 90 95  
Glu Ile Tyr Thr Ser Cys Glu Pro Cys Arg Cys  
100 105

(2) INFORMATION FOR SEQ ID NO:4258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..242
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4258:

tcacgacgtg cgcctctggg acctggacgc cgarggggtc gcgacgtgct gctcgccctac 60  
gcggarccgc tkcggcaact cggggarcac cctgcgggtgc agtatgttca ggtgtttaag 120  
aaccatgggg catctgctgg agcttcgatg cgcattcac acagccaaat gttgggaact 180  
ccctttgtcc ctccctctgt tacaactcgg cttaactgca tgaaggagat ttttgacaga 240  
tc

(2) INFORMATION FOR SEQ ID NO:4259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4259:

Ser Arg Arg Ala Pro Leu Gly Pro Gly Arg Arg Xaa Gly Arg Asp Val  
1 5 10 15  
Leu Leu Ala Tyr Ala Xaa Arg Xaa Arg Gln Leu Gly Xaa His Pro Ala  
20 25 30  
Val Gln Tyr Val Gln Val Phe Lys Asn His Gly Ala Ser Ala Gly Ala  
35 40 45  
Ser Met Ala His Ser His Ser Gln Met Leu Gly Thr Pro Phe Val Pro  
50 55 60  
Pro Ser Val Thr Thr Arg Leu Asn Cys Met Lys Glu Ile Phe Asp Arg  
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:4260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid

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- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..73
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1580070
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4260:

His Asp Val Arg Leu Trp Asp Leu Asp Ala Xaa Gly Val Ala Thr Cys  
1 5 10 15  
Cys Ser Pro Thr Arg Xaa Ala Xaa Gly Asn Ser Gly Xaa Thr Leu Arg  
20 25 30  
Cys Ser Met Phe Arg Cys Leu Arg Thr Met Gly His Leu Leu Glu Leu  
35 40 45  
Arg Trp Arg Ile His Thr Ala Lys Cys Trp Glu Leu Pro Leu Ser Leu  
50 55 60  
Pro Leu Leu Gln Leu Gly Leu Thr Ala  
65 70

(2) INFORMATION FOR SEQ ID NO:4261:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..39
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1580071
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4261:

Met Phe Arg Cys Leu Arg Thr Met Gly His Leu Leu Glu Leu Arg Trp  
1 5 10 15  
Arg Ile His Thr Ala Lys Cys Trp Glu Leu Pro Leu Ser Leu Pro Leu  
20 25 30  
Leu Gln Leu Gly Leu Thr Ala  
35

(2) INFORMATION FOR SEQ ID NO:4262:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 407 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..407
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1580072
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4262:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aaaatatata cagaacagca tcaactcttc gactgcgcca gtaacgtatt gccccgcgtg | 60  |
| tgcgttaatc tggcagtgtc ggcgcagcac aagttcgga tcaactacgg gcagatcgcg  | 120 |
| aacgacctcc cggagccggc gcaggtggcg acgctcctgc agtcgatggg cgtgaacaag | 180 |
| gtgaagctgt acgacgcgga cccccgggtg ctgacggcgt tcgccaacac gggcgtcggc | 240 |
| ttcaccatcg ccgtgggcaa cgaggacctg caggcgatgg cgccagccc ggacgcggcg  | 300 |
| cgccgttggg tggcggcgaa cgtgcagccc tacgtcccg ccacgcgcat cacctgcgtc  | 360 |
| accgtcgga acgaggtcct gtcgggcaac gacacggcg cgatggc                 |     |

(2) INFORMATION FOR SEQ ID NO:4263:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 135 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..135
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1580073
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4263:

Lys Ile Tyr Thr Glu Gln His Gln Leu Phe Asp Cys Ala Ser Asn Val  
1 5 10 15  
Leu Pro Arg Val Cys Val Asn Leu Ala Val Ser Ala Gln His Lys Phe  
20 25 30  
Gly Ile Asn Tyr Gly Gln Ile Ala Asn Asp Leu Pro Glu Pro Ala Gln  
35 40 45  
Val Ala Thr Leu Leu Gln Ser Met Gly Val Asn Lys Val Lys Leu Tyr  
50 55 60  
Asp Ala Asp Pro Arg Val Leu Thr Ala Phe Ala Asn Thr Gly Val Gly  
65 70 75 80  
Phe Thr Ile Ala Val Gly Asn Glu Asp Leu Gln Ala Met Ala Ala Ser  
85 90 95  
Pro Asp Ala Ala Arg Arg Trp Val Ala Ala Asn Val Gln Pro Tyr Val  
100 105 110  
Pro Ala Thr Arg Ile Thr Cys Val Thr Val Gly Asn Glu Val Leu Ser  
115 120 125  
Gly Asn Asp Thr Ala Ala Met  
130 135

(2) INFORMATION FOR SEQ ID NO:4264:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 80 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..80
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1580074
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4264:

Met Gly Val Asn Lys Val Lys Leu Tyr Asp Ala Asp Pro Arg Val Leu  
1 5 10 15  
Thr Ala Phe Ala Asn Thr Gly Val Gly Phe Thr Ile Ala Val Gly Asn  
20 25 30  
Glu Asp Leu Gln Ala Met Ala Ala Ser Pro Asp Ala Ala Arg Arg Trp  
35 40 45  
Val Ala Ala Asn Val Gln Pro Tyr Val Pro Ala Thr Arg Ile Thr Cys  
50 55 60  
Val Thr Val Gly Asn Glu Val Leu Ser Gly Asn Asp Thr Ala Ala Met  
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:4265:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 466 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..466
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1580088
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4265:

acctatccgc cgctcccaa tcactctgcc cccaaactcc caccgccag catccccacg

(2) INFORMATION FOR SEQ ID NO:4266:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1580089

(xi) SEQUENCE DESCRIPTION: SEO ID NO:4266:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ile | Arg | Arg | Leu | Pro | Ile | Ile | Leu | Pro | Pro | Asn | Ser | His | Pro | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ser | Pro | Arg | His | His | Thr | Ser | Ser | Arg | Arg | Val | Val | Thr | Gly | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Met | Val | Gly | Pro | Gly | Leu | Tyr | Thr | Glu | Ile | Gly | Lys | Lys | Thr | Arg |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Asp | Leu | Leu | Tyr | Lys | Asp | Tyr | Gln | Thr | Asp | His | Lys | Phe | Thr | Leu | Thr |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Thr | Tyr | Thr | Ser | Asn | Gly | Val | Ala | Val | Thr | Ala | Ser | Ser | Thr | Lys | Lys |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Asp | Leu | Ile | Leu | Gly | Glu | Ile | Gln | Ser | Gln | Ile | Lys | Asn | Lys | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Thr | Ile | Asp | Val | Lys | Ala | Asn | Ser | Glu | Ser | Asn | Ile | Ile | Thr | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Thr | Val | Asp | Glu | Ile | Ala | Thr | Pro | Gly | Leu | Lys | Thr | Ile | Leu | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Ala | Val | Pro | Asp | Gln | Arg | Ser | Gly | Lys | Gly |     |     |     |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:4267:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1580090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4267:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Gly | Pro | Gly | Leu | Tyr | Thr | Glu | Ile | Gly | Lys | Lys | Thr | Arg | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Leu | Tyr | Lys | Asp | Tyr | Gln | Thr | Asp | His | Lys | Phe | Thr | Leu | Thr | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Thr | Ser | Asn | Gly | Val | Ala | Val | Thr | Ala | Ser | Ser | Thr | Lys | Lys | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Leu | Ile | Leu | Gly | Glu | Ile | Gln | Ser | Gln | Ile | Lys | Asn | Lys | Asn | Met |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Ile | Asp | Val | Lys | Ala | Asn | Ser | Glu | Ser | Asn | Ile | Ile | Thr | Thr | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Val | Asp | Glu | Ile | Ala | Thr | Pro | Gly | Leu | Lys | Thr | Ile | Leu | Ser | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

Ala Val Pro Asp Gln Arg Ser Gly Lys Gly  
100 105

(2) INFORMATION FOR SEQ ID NO:4268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..488
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4268:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| acaagcacaa agagaggccc cgaccgcgat ggatcgtcag cgacagaccg accgtgacac  | 60  |
| agccaacaac taacacgcac gcgcgcgaga gagaaagaga gctgcccggg agagagagag  | 120 |
| agaggaaatc aaacgaaggc gacgacgtac ggagacggca tggccgatca ccaccaccac  | 180 |
| caccaccacg ggcacccgcc ggacggggccc ggcggcgcgg gggaccagct ggaggtaatc | 240 |
| aaggagcagg accggctgct gcccatcgcc aacgtcggcc gcatcatgaa gcagatcctg  | 300 |
| ccgcccaacg ccaagatctc caaggaggcc aaggagacga tgcaggagtg cgtgtccgag  | 360 |
| ttcatcagct tcgtcacggg cgaggcctcc gacaagtgcc acaaggagaa gcgcaagacc  | 420 |
| gtcaacggcg acgacgtctg ctgcgccttc ggcgcgctcg gcttcgacga ctacgtcgac  | 480 |
| cccatgcg                                                           |     |

(2) INFORMATION FOR SEQ ID NO:4269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4269:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Lys His Lys Glu Arg Pro Arg Pro Arg Trp Ile Val Ser Asp Arg Pro |  |
| 1 5 10 15                                                       |  |
| Thr Val Thr Gln Pro Thr Thr Asn Thr His Ala Arg Glu Arg Glu Arg |  |
| 20 25 30                                                        |  |
| Glu Leu Pro Gly Arg Glu Arg Glu Arg Lys Ser Asn Glu Gly Asp Asp |  |
| 35 40 45                                                        |  |
| Val Arg Arg Arg His Gly Arg Ser Pro Pro Pro Pro Pro Arg Ala     |  |
| 50 55 60                                                        |  |
| Ser Ala Gly Arg Ala Arg Arg Arg Gly Gly Pro Ala Gly Gly Asn Gln |  |
| 65 70 75 80                                                     |  |
| Gly Ala Gly Pro Ala Ala Ala His Arg Gln Arg Arg Pro His His Glu |  |
| 85 90 95                                                        |  |
| Ala Asp Pro Ala Ala Gln Arg Gln Asp Leu Gln Gly Gly Gln Gly Asp |  |
| 100 105 110                                                     |  |
| Asp Ala Gly Val Arg Val Arg Val His Gln Leu Arg His Gly Arg Gly |  |
| 115 120 125                                                     |  |
| Leu Arg Gln Val Pro Gln Gly Glu Ala Gln Asp Arg Gln Arg Arg Arg |  |
| 130 135 140                                                     |  |
| Arg Leu Leu Arg Leu Arg Arg Ala Arg Leu Arg Arg Leu Arg Arg Pro |  |
| 145 150 155 160                                                 |  |
| His Ala                                                         |  |

(2) INFORMATION FOR SEQ ID NO:4270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..109  
(D) OTHER INFORMATION: / Ceres Seq. ID 1580114  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4270:

Met Ala Asp His His His His His His His Gly His Pro Pro Asp Gly  
1 5 10 15  
Pro Gly Gly Ala Gly Asp Gln Leu Glu Val Ile Lys Glu Gln Asp Arg  
20 25 30  
Leu Leu Pro Ile Ala Asn Val Gly Arg Ile Met Lys Gln Ile Leu Pro  
35 40 45  
Pro Asn Ala Lys Ile Ser Lys Glu Ala Lys Glu Thr Met Gln Glu Cys  
50 55 60  
Val Ser Glu Phe Ile Ser Phe Val Thr Gly Glu Ala Ser Asp Lys Cys  
65 70 75 80  
His Lys Glu Lys Arg Lys Thr Val Asn Gly Asp Asp Val Cys Cys Ala  
85 90 95  
Phe Gly Ala Leu Gly Phe Asp Asp Tyr Val Asp Pro Met  
100 105

(2) INFORMATION FOR SEQ ID NO:4271:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 435 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..435  
(D) OTHER INFORMATION: / Ceres Seq. ID 1580115  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4271:

gacaagcaga gtcgcggcgg ccgaaccgcc acctcccttt gcgcctcact catcagtcac 60  
ggcgctcgctg ccgcctggac ctccggcggtg gtcggtgacc ctgagcctaa ggcaccgtgg 120  
cgggctggag atccgtgccc ccgcggagaa cttgctccca gggtagggcc gcggcgggga 180  
gcgcattgcc ctccgtctcc gcctccgcgc ctgctctctc ctctccgtca catccaattg 240  
cggcggtcgt ccgcggcgga ccacacagcc cgggcgcgcg ccgcgcggca gcagggtcgt 300  
ccgcttcctg cggagcaggt gggcgcggt ggcgcgggca cctccatttg gaggcgcaag 360  
aaacagcccc cggcgcgcg cgcgtgccg ccggactgcc gggaccagcg gattcgaacg 420  
ctggcgcggc ctgtc

(2) INFORMATION FOR SEQ ID NO:4272:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 145 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..145  
(D) OTHER INFORMATION: / Ceres Seq. ID 1580116  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4272:

Asp Lys Gln Ser Arg Gly Gly Arg Thr Ala Thr Ser Leu Cys Ala Ser  
1 5 10 15  
Leu Ile Ser His Gly Val Ala Ala Ala Trp Thr Ser Gly Val Val Gly  
20 25 30  
Asp Pro Glu Pro Lys Ala Pro Trp Arg Ala Gly Asp Pro Cys Arg Arg  
35 40 45  
Gly Glu Leu Ala Pro Arg Val Gly Pro Arg Arg Gly Ala His Val Pro

50 55 60  
Pro Ala Pro Pro Pro Pro Leu Pro Pro Pro Leu Arg His Ile Gln Leu  
65 70 75 80  
Arg Arg Ser Ser Arg Gly Asp His Thr Ala Arg Ala Ala Ala Arg  
85 90 95  
Gln Gln Gly Arg Pro Leu Pro Ala Glu Gln Val Gly Ala Ala Ala Ala  
100 105 110  
Gly Thr Ser Ile Trp Arg Arg Lys Lys Gln Pro Pro Ala Arg Ala Ala  
115 120 125  
Val Pro Pro Asp Cys Arg Asp Gln Arg Ser Arg Thr Leu Ala Arg Pro  
130 135 140  
Val  
145

(2) INFORMATION FOR SEQ ID NO:4273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4273:

Thr Ser Arg Val Ala Ala Ala Glu Pro Pro Pro Pro Phe Ala Pro His  
1 5 10 15  
Ser Ser Val Met Ala Ser Leu Pro Pro Gly Pro Pro Ala Trp Ser Val  
20 25 30  
Thr Leu Ser Leu Arg His Arg Gly Leu Glu Ile Arg Ala Ala Ala  
35 40 45  
Glu Asn Leu Leu Pro Gly Trp Gly Arg Gly Gly Glu Arg Met Ser Leu  
50 55 60  
Leu Leu Arg Leu Arg Arg Cys Leu Leu Leu Ser Val Thr Ser Asn Cys  
65 70 75 80  
Gly Gly Arg Pro Ala Thr Thr Gln Pro Gly Pro Pro Pro Arg Gly  
85 90 95  
Ser Arg Val Val Arg Phe Leu Arg Ser Arg Trp Ala Arg Leu Pro Arg  
100 105 110  
Ala Pro Pro Phe Gly Gly Ala Arg Asn Ser Pro Arg Arg Ala Pro Pro  
115 120 125  
Cys Arg Arg Thr Ala Gly Thr Ser Gly Val Glu Arg Trp Arg Gly Leu  
130 135 140

(2) INFORMATION FOR SEQ ID NO:4274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4274:

Met Ala Ser Leu Pro Pro Gly Pro Pro Ala Trp Ser Val Thr Leu Ser  
1 5 10 15  
Leu Arg His Arg Gly Gly Leu Glu Ile Arg Ala Ala Ala Glu Asn Leu  
20 25 30

Leu Pro Gly Trp Gly Arg Gly Gly Glu Arg Met Ser Leu Leu Leu Arg  
35 40 45  
Leu Arg Arg Cys Leu Leu Leu Ser Val Thr Ser Asn Cys Gly Gly Arg  
50 55 60  
Pro Ala Ala Thr Thr Gln Pro Gly Pro Pro Pro Arg Gly Ser Arg Val  
65 70 75 80  
Val Arg Phe Leu Arg Ser Arg Trp Ala Arg Leu Pro Arg Ala Pro Pro  
85 90 95  
Phe Gly Gly Ala Arg Asn Ser Pro Arg Arg Ala Pro Pro Cys Arg Arg  
100 105 110  
Thr Ala Gly Thr Ser Gly Val Glu Arg Trp Arg Gly Leu  
115 120 125

(2) INFORMATION FOR SEQ ID NO:4275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..379
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4275:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aaggagcgcc tgatagtcta cgattacatg ccgaacctga gcatacactc tcagctccat  | 60  |
| gggcagcacg cggcggagtg caacctcagc tgggagagga ggatgaggat cgctgtggac  | 120 |
| tccgcggaag ggatcgcccta cctgcaccac agcgcgacgc cgcacatcat ccacagagac | 180 |
| gtgaaggcga gcaacgtgct cctggacgcc gacttccagg cgcggtcgc cgacttcggc   | 240 |
| ttcgccaagc tgggtcccgga cggcgcgacg caggtcacca caagtgaaa ggcacgctgg  | 300 |
| ggtacctggc gccggagtac gcgatgctcg ggaaggcctc cgagagctgc gacgtcttca  | 360 |
| gcttcggggg cagctgct                                                |     |

(2) INFORMATION FOR SEQ ID NO:4276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4276:

Lys Glu Arg Leu Ile Val Tyr Asp Tyr Met Pro Asn Leu Ser Ile His  
1 5 10 15  
Ser Gln Leu His Gly Gln His Ala Ala Glu Cys Asn Leu Ser Trp Glu  
20 25 30  
Arg Arg Met Arg Ile Ala Val Asp Ser Ala Glu Gly Ile Ala Tyr Leu  
35 40 45  
His His Ser Ala Thr Pro His Ile Ile His Arg Asp Val Lys Ala Ser  
50 55 60  
Asn Val Leu Leu Asp Ala Asp Phe Gln Ala Arg Val Ala Asp Phe Gly  
65 70 75 80  
Phe Ala Lys Leu Val Pro Asp Gly Ala Thr His Val Thr Thr Arg  
85 90 95

(2) INFORMATION FOR SEQ ID NO:4277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

00000000-00000000



|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aatgcagagg | tcgcgttgac | ggcacaggaa | gcagcagcag | agcaggccag | gaacaagaac | 60  |
| agcaatagac | tcgcgcgcgg | gcgcagcagc | cggcggcagc | gcgcacggct | tattcgggtc | 120 |
| gggcggcatc | cgcgggttcg | gctacggcgt | cggcgtgtcc | atcggcaccc | tcctggtggc | 180 |

caccaccatc ggcgtcgcca tctacttctg cacgcgcacc tccatgcccg tgtccgcccg 240  
cgcgccagcg ccgcccgggc agggcgggcga cgccggggcg ggcacgcacg aggccacgct 300  
cgaggcggtc ccggcggtgg cctacgcgga ggcgaggaag gcggcgggcga accaggcggtg 360  
ctgctgcccc gtctgcctcg agtgctacgg cgacggcgac gtggt

(2) INFORMATION FOR SEQ ID NO:4280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4280:

Asn Ala Glu Val Ala Leu Thr Ala Gln Glu Ala Ala Ala Glu Gln Ala  
1 5 10 15  
Arg Asn Lys Asn Ser Asn Glu Leu Ala Ala Gly Arg Arg Arg Arg Arg  
20 25 30  
Gln Arg Ala Arg Leu Ile Arg Val Gly Arg His Pro Arg Val Arg Leu  
35 40 45  
Arg Arg Arg Arg Val His Arg His Pro Pro Gly Gly His His His Arg  
50 55 60  
Ala Arg His Leu Leu Leu His Ala His Leu His Ala Arg Val Arg Arg  
65 70 75 80  
Arg Ala Ser Ala Ala Ala Ala Gly Arg Arg Arg Arg Ala Gly His Arg  
85 90 95  
Arg Gly His Ala Arg Gly Val Pro Gly Gly Gly Leu Arg Gly Gly Glu  
100 105 110  
Glu Gly Gly Gly Glu Pro Gly Val Leu Leu Pro Arg Leu Pro Arg Val  
115 120 125  
Leu Arg Arg Arg Arg Arg Gly  
130 135

(2) INFORMATION FOR SEQ ID NO:4281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4281:

Met Asn Ser Pro Gly Asp Asp Gly Gly Gly Ser Ala His Gly Leu  
1 5 10 15  
Phe Gly Ser Gly Gly Ile Arg Gly Phe Gly Tyr Gly Val Gly Val Ser  
20 25 30  
Ile Gly Ile Leu Leu Val Ala Thr Thr Ile Ala Leu Ala Ile Tyr Phe  
35 40 45  
Cys Thr Arg Thr Ser Met Pro Val Ser Ala Ala Ala Pro Ala Pro Pro  
50 55 60  
Arg Gln Gly Gly Asp Ala Gly Arg Gly Ile Asp Glu Ala Thr Leu Glu  
65 70 75 80  
Ala Phe Pro Ala Val Ala Tyr Ala Glu Ala Arg Lys Ala Ala Ala Asn  
85 90 95  
Gln Ala Cys Cys Cys Pro Val Cys Leu Glu Cys Tyr Gly Asp Gly Asp  
100 105 110  
Val